

SEQUENCE LISTING

ACACCAATCCAAAAGCGTGGAACTATGTTAAAAGCTACAAACATAATATT
 AATGCTATCAAATCTCTAGCTCTCAGAAGTTTATCAATCAGTTGCAGA
 AGGAAAAATGATTGTGGGTTGACTTACGAAGACCCTAGTGTCAATTG
 AAAAAAGTGGTGCATGTTCTATTGTATATCCGACAGAAGGGACAGTT
 TTTGTCCCCTTCGGTGCATTAAAGAATGCTCCTCTATGAAAGA
 AGCAAGTTATTATTTATGCTTCTTAGATGTTCAAATGCCT
 TTGGGCAGTCACGAGTAACCGACCTATTGCTAAAGATGCCAAACGAGT
 AATGGCATGAAAGCTTTAAGGATATTGCTACTCTAAAGAAGATTATCG
 CTATGTCACTAAGCATAAGGGCCAATCCTAAACCTATAATCGTATT
 GTAGAAAATGCTGAT

SEQ ID NO. 6004

STRAIN H36B

TAAACTACTTCCACCAAAAGAATTAGTTATTCTAAAGTCCAAATAGTCAAG
 CCATTTAACAGGAACGATTCCAGCTTTGAGGAAAATACGGTATAAAA
 GTTAAGCTTATTCAAGGGGGACAGGTCAACTAAAGATAGATTAAAGTAA
 GGAGGGTAAGCAGTTGAAGGGCGGATATTTCTTGAGGAAAATTACGC
 AATTGAAAGTCATAAGGCATTGTTGAGTCTTACGTCAAAGAATATT
 CATACTGTTATTCCAGATTATATCCATCCGAGTGATAACGGGACACCTTA
 TACTATAAAATGGGAGTGTCTGATTGAAATAACGAATTAGTTAAGGGAC
 TTACCATCAAGAGTTATGAAGATTATTACAGCCTCTTAAAGGTTAA
 ATTGCCTTGAGATCCGAATACTTCCTAGTGCCTTCTCACAACCTCAC
 TAATATACTCTGGCCAAGGGGGTTACACCAATCCAAAAGCGTGGAACT
 ATGTTAAAAGCTACAACATAATTAAATGCTATAATCTAGCTCT
 TCAGAAGTTTATCAATCAGTTGCAGAAGGAAAATGATTGTTGGGTTGAC
 TTACGAAGACCCTAGTGTCAATTGCAAAAAAGTGGTGCCAATGTTCTA
 TTGTATATCCGACAGAAGGGACAGTTTGTCCCATCTCGGTTGCAATT
 ATAAAAGAATGCTCCTCTATGAAAGAAGCAAAGTTATTATTAATT
 GCTTCTTAGATGTTCAAATGCCTTGGGAGTCACAGAGTAACCGAC
 CTATTCGAAAGATGCCAAACGAGTAATGGCATGAAAGCTTAAAGGAT
 ATTGCTACTCTAAAGAAGATTATCGCTATGTCACTAAGCATAAGGGCA
 AACCTTAAACCTATAATCGTATTGCTAGAAATGCTGAT

SEQ ID NO. 6005

STRAIN 18RS21

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTTATTCTAAAGTCCAAA
 TAGTCAAGCCATTAAACAGGAACGATTCCAGCTTTGAGGAAAATACG
 GTATAAAAGTTAAGCTTATTCAAGGGGGACAGGGCAACTAAAGATAGA
 TTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTTGAGGAAA
 TTATACGCAATTGAAAGTCATAAGGCATTGTTGAGTCTTACGTATCAA
 AGAATGTTCAACTGTTATTCCAGACTATATCCATCCAAGTGATAACGGCG
 ACACCTTATACTATAATGGGAGTGTCTGATTGTAATAACGAATTAGC
 TAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGCCTTCCTTAA
 AAGTAAATTGCTTGCAGATCCGAATACTCCTAGTGCCTTCTCA
 CAACTCACTAAATACTCTGGCCAAGGGGGTTACACCAATCCAAAAGC
 GTGGAACATGTTAAAAGCTACAACATAATATTAAATGCTATCAAATCTT
 CTAGCTCTCAGAAGTTTATCAATCAGTTGCAGAAGGAAAATGATTG
 GGGCTGACTTACGAAGACCCTAGTGTCAATTGCAAAAAAGTGGTGCCAA
 TGTGTTCTATTGTTATCCGACAGAAGGGACAGTTTGTCCCATCTCGG
 TTGCAATTATAAAAAGATGCTCCTTCTATGAAAGAAGCAAAGTTATT
 AATTGTTATGCTTCTTAGATGTTCAAATGCCTTGGGAGTCACAGAG
 TAACCGACCTTACGTAAGATGCCAAACGAGTAATGGCATGAAAGCTT
 TAAAGGATATTGCTACTCTAAAGAAGATTATCGCTATGTCACTAAGC
 ATAAAGGCCAATCCTTAAACCTATAATCGTATTGCTAGAAATGCTGAT

SEQ ID NO. 6006

STRAIN M732

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT
 TATTCTAAGTCCAAATAGTCAAGCCATTAAACAGGAACGATTCCAGCTT
 TTGAGGAAAATACGGTATAAAAGTTAAGCTTATCAAGGTGGGACAGGG
 CAACTAAATAGATAGATTAAAGTAAAGGAGGGTAAGCAGTTGAAGGGCGGATAT
 TTTCTTGAGGAAAATTATACGCAATTGAAAGTCATAAGGCATTGTTG
 AGTCTTACGTATAAGAATGTTCTACTGTTATTCCAGACTATATCCAT
 CCGAGTGATAACGGGACACCTTACTATAATGGAGTGTCTTATTG

SEQUENCE LISTING

AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGAGTTAT
 TACAGCCTTCCTTAAAGTAAACCTTGCAGATCCGAATACTCC
 TCTAGTGCCTTCTCACAACACTAACTCTTGGCCAAGGGTGGTTA
 CACCAATCCAAAAGCGTGAACATGTTAAAAGCTACAACATAATATTA
 ATGCTATCAAATCTCTAGCTCTTCAGAAGTCTTCAATCAGTTGCAGAA
 GGAAAATGATTGTGGGGTTGACTTACGAAGACCCCTAGTGTCAATTGCA
 AAAAGTGGTGCCTAAGTGTCTATTGTATAACCGACAGAAGGGACAGTTT
 TTGTCCTCATCTCGGTTGCAATTATAAGAATGCTCCTTCTATGAAAGAA
 GCAAGTTATTATTATAATTGCTTCTTAGATGTTCAAATGCCTT
 TGGGCAGTCACGAGTAACCGACCTATTCTAAAGATGCCAAACAAGTA
 ATGGCATGAAAGCTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGC
 TATGTCACTAAGCATAAGAGCCAATCCTTAAACCTATAATCGCATTG
 TAGAAATGCTGAT

SEQ ID NO. 6007

STRAIN COH1

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTT
 ATTCTAAGTCCAATAGTCAGGCATTAAACAGGAACGATTCCAGCTTT
 TGAGGAAAATACGGTATAAAAGTTAACGCTTATTCAAGGTGGACAGGGC
 AACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGGGGATATT
 TTCTTGAGGAAATTACGCAATTGAAAGTCATAAGGCATTGTTGA
 GTCTTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATC
 CGAGTGTACCGCGACACCTTAACTATAATGGGAGTGTCTTGATTGTA
 AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGAGTTATT
 ACAGCCTTCTTAAAGTAAACCTTGCAGATCCGAAATACTTCCCT
 CTAGTGCCTTCTCACAACACTAACTATACTCTGGCCAAGGGTGGTTAC
 ACCAATCCAAGCGTGAACATGTTAAAGCTACAACATAATATTAA
 TGCTATCAAATCTCTAGCTCTCAGAAGTTTATCAATCAGTTGCAGAAG
 GAAAATGATTGTGGGGTTGACTTACGAAGACCCCTAGTGTCAATTGCAA
 AAAAGTGGTCCAATGTTCTATTGTATAACCGACAGAAGGGACAGTTT
 TGTCCTCATCTCGGTTGCAATTATAAGAATGCTCCTTCTATGAAAGAAG
 CAAAGTTATTATTAAATTGCTTCTTAGATGTTCAAATGCCTT
 GGGCAGTCACGAGTAACCGACCTATTCTAAAGATGCCAAACAAGTA
 TGGCATGAAAGCTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCT
 ATGTCACTAAGCATAAGAGCCAATCCTTAAACCTATAATCGCATTG
 AGAAATGCTGAT

SEQ ID NO. 6008

STRAIN M781

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGTTATT
 CTAAGTCCAATAGTCAGGCATTAAACAGGAACGATTCCAGCTTTGA
 GGAAAATACGGTATAAAAGTTAACGCTTATTCAAGGTGGACAGGGCAAC
 TAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGGGGATATTTC
 TTTGGAGGAAATTACGCAATTGAAAGTCATAAGGCATTGTTGAGTC
 TTACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATCCGA
 GTGATACGGCGACACCTTAACTATAAAATGGGAGTGTCTTGATTGTAAT
 AACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGAGTTATTACA
 GCCTTCTTAAAGTAAATTGCTTGCAGATCCGAATACTTCCCTCTA
 GTGCTTCTCACAACTCACATAATATACTCTGGCCAAGGGGGTTACACC
 AATCCAAGCGTGAACATGTTAAAGCTACAACATAATATTAAATGC
 TATCAAATCTCTAGCTTCTCAGAAGTTTATCAATCAGTTGCAGAAGGAA
 AAAATGATTGTGGGGTTGACTTACGAAGACCCCTAGTGTCAATTGCAAAA
 AGTGGTCCAATGTTCTATTGTATAACCGACAGAAGGGACAGTTTGT
 CCCATCTCGGTTGCAATTATAAGAATGCTCCTTCTATGAAAGAAGCAA
 AGTTATTATTAAATTGCTTCTTAGATGTTCAAATGCCTTGGG
 CAGTCACGAGTAACCGACCTATTCTAAAGATGCCAAACAAGTAATGG
 CATGAAAGCTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCTATG
 TCACTAAGCATAAGAGCCAATCCTTAAACCTATAATCGCATTG
 AATGCTGAT

SEQ ID NO. 6009

STRAIN CJB110

CAGCCTTTAAACTACTTCCACCAAAAGAATTAGTTATTCT
 AAGTCCAATAGTCAGGCATTAAACAGGAACGATTCCAGCTTTGAGG

SEQUENCE LISTING

AAAAATACGGTATAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTA
 ATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTT
 TGAGGAAATTATACGCAATTGAAAGTCATAAGGCATTGTTGAGCTTT
 ACGTATCAAAGAATGTTCATACTGTTATTCCAGACTATATCCATCCAAGT
 GATACGGCGACACCTTATACTATAAATGGGAGTCTTGATGTAAATAA
 CGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGC
 CTCCTTAAAGGTAAAATTGCCTTGCAGATCCGAATACTCCTCTAGT
 GCTTCTCACAACACTCACTAATATACTCTGGCCAAGGGTGGTACACCAA
 TCAAAGCGTGGAACTATGTTAAAAGCTACAACATAATATTAGCTA
 TCAAATCTCTAGCTCTCAGAAGTTATCAATCAGTTGCAGAAGGAAA
 ATGATTGTGGGCTGACTTACGAAGACCCCTAGTGTCAATTGCAAAAAAG
 TGGGCCAATGTTCTATTGTATACTCGACAGAAGGGACAGTTTGTCC
 CATCTCGGTGCAATTAAAGAATGCTCTTCTATGAAAGAAGCAAAG
 TTATTTATTAAATTATGCTTCTTAGATGTTCAAATGCCCTTGGGCA
 GTCAACGAGTAACCGACCTTACGTAAGATGCCAAACGAGTAATGGCA
 TGAAAGCTTAAAGGATATTGCTACTCTAAAGAAGATTATCGCTATGTC
 ACTAACGATAAGGGCAAATCCTTAAACCTATAATCGTATTGCTAGAAA
 TGCTGAT

SEQ ID NO. 6010

STRAIN 1169NT

ATAGTCAGGCCATTAAACAGGAACGATTCCAGCTTGTAGGAAAAATAC
 GGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAG
 ATTAAGTAAGGAGGGTAAGCATTGAAAGGCGGATATTTCTTGAGGAA
 ATTATACGCAATTGAAAGTCATAAGGCATTGTTGAGTCTACGTATCA
 AAGAATGTTCATCTGTTATTCCAGACTATATCCATCCAAGTGATAACGGC
 GACACCTTACTATAAAATGGGAGTCTTGATTGAAATAACGAAATTAG
 CTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGCCTCCTTA
 AAAGGTAATTGCCTTGCAGATCCGAATACTCCTCTAGTGTCTTCTC
 ACAACTCACCATACTCTGGCAAAGGGTGGTACCCAATCCAAAAG
 CGTGGAACTATGTTAAAAGCTACAACATAATTAAATGCTATCAAATCT
 TCTAGCTCTCAGAAGTTATCAATCAGTGTCAATTGCAAAAGTGGTGC
 GGGGTTGACTTACGAAGACCCCTAGTGTCAATTGCAAAAGTGGTGC
 ATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTCCCCTTC
 GTTGCAATTATAAAAGAATGCTCTTCTATGAAAGAACCAAAGTTATTAT
 TAAATTATGCTTCTTAGATGTTCAAATGCCCTTGGGCACTCAACGA
 GTAACCGACCTTACGTAAGATGCCAAACGAGTAATGGCATGAAAGCT
 TAAAGGATATTGCTACTCTAAAGAAGATTATCGCTATGTCACTAAGCA
 TAAGGGCAAATCCTTAAACCTATAATCGTATTGCTAGAAAATGCTGAT

SEQ ID NO. 6011

STRAIN JM91130013

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT
 TATTCTAAGTCCAAATAGTCAGGCCATTAAACAGGAACGATTCCAGCTT
 TTGAGGAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGG
 CAACTAATAGATAGATTAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATGT
 TTCTTGGAGGAATTATACGCAATTGAAAGTCATAAGGCATTGTTG
 AGCTTACGTATAAGAATGTTCATCTGTTATTCCAGACTATATCCAT
 CCGAGTGATACGGCGACACCTTACTATAAAATGGGAGTGTCTTGATTGT
 AAATAACGAAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTAT
 TACAGCCTTCTTAAAGGTTAAATTGCTTGCAGATCCGAATACTTCC
 TCTAGTGCTTCTCACAACCTACCAATATACTCTGGCAAAGGGTGGTAA
 CACCAATCCAAAAGCGTGGAACTATGTTAAAAGCTACAACATAATTAA
 ATGCTATCAAATCTCTAGCTCTCAGAAGTTATCAATCAGTTGCAGAA
 GGCAAAATGATGTGGGCTGACTTACGAAGACCCCTAGTGTCAATTGCA
 AAAAGTGGTCCAATGTTCTATTGTTATCCGACAGAAGGGACAGTTT
 TTGCTCCATCTCGGTGCAATTATAAGAATGCTCTTCTATGAAAGAA
 GCAAAGTTATTATAATTGCTTCTTAGATGTTCAAATGCCCTT
 TGGCAGTCACGAGTAACCGACCTTACGTAAGATGCCAAACGAGTA
 ATGGCATGAAAGCTTAAAGGATATTGCTACTCTAAAGAAGATTATCGC
 TATGTCACTAAGCATAAGGGCAAATCCTTAAACCTATAATCGTATTG
 TAGAAATGCTGAT

SEQ ID NO. 6012

SEQUENCE LISTING

STRAIN 2603 frame: 1
 MKEKQSKRLLIVYILLVVSIIIFISVFTYISQPSKLLPPKELVILSPNSQAILTGTIPAFEE
 KYGIVKVLIQGGTQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVIP
 DYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLQPSLKGKIAFADPNTSSAFSQ
 LTNILLAKGGYTNPKAWNYVKKLQHNINA
 QKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSLSDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 RKDAQTSNGMKALKDIATLKEDYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6013

STRAIN 090 frame: 1
 QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIVKVLIQGGTQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLQPSLKGKIAFADPNTSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGKIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSLSDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6014

STRAIN A909 frame: 1
 QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIVKVLIQGGTQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNIGHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLQPSLKGKIAFADPNTSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGKIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSLSDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6015

STRAIN H36B frame: 2
 KLLPPKELVILSPNSQAILTGTIPAFEEKYGIVKVLIQGGTQLIDRLSKEGKQLKADIF
 FGGNYTQFESHKALFESYVSKNIGHTVIPDYIHPSDTATPYTINGSVLIVNNELVKGLTIK
 SYEDLQPSLKGKIAFADPNTSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGKIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSLSDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 ILKTYNRIRRNAD

SEQ ID NO. 6016

STRAIN 18RS21 frame: 1
 QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIVKVLIQGGTQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLQPSLKGKIAFADPNTSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGKIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSLSDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6017

STRAIN M732 frame: 1
 QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIVKVLIQGGTQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLQPSLKGKIAFADPNTSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGKIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSLSDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KSQILKTYNRIRRNAD

SEQ ID NO. 6018

STRAIN COH1 frame: 1
 QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIVKVLIQGGTQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLQPSLKGKIAFADPNTSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGKIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSLSDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KSQILKTYNRIRRNAD

SEQ ID NO. 6019

STRAIN M781 frame: 1

SEQUENCE LISTING

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVQLIQGGTQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSAFAQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGMIIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSNDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKDHYRYVTKH
 KSQILKTYNRIRRNAD

SEQ ID NO. 6020

STRAIN CJB110 frame: 1
 QPFKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVQLIQGGTQLIDRLSKEGKQLKA
 DIFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSAFAQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGMIIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSNDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKDHYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6021

STRAIN 1169NT frame: 3
 SQAILTGTIPAFEEKYGIKVQLIQGGTQLIDRLSKEGKHLKADIFFGGNYTQFESHKAL
 FESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLOPSLKGKI
 AFADPNTSSAFAQLTNILLAKGGYTNPKAWNYVKKLQHNINAIAKSSSSSEVYQSVAEKG
 MIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSNDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKDHYRYVTKH
 VQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKDHYRYVTKHKGQILKTYNRIRRNAD

SEQ ID NO. 6022

STRAIN JM91130013 frame: 1
 QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVQLIQGGTQLIDRLSKEGKQLKA
 DVFFGGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSAFAQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKGMIIVGLTYEDPSVNLQKSGANVSIVYPTEGTVFVPSSVAIKNA
 PSMKEAKLFINFMLSNDVQNAFGQSTSNNRPIRKDAQTSNGMKALKDIATLKDHYRYVTKH
 KGQILKTYNRIRRNAD

SEQ ID NO. 6101

STRAIN 2603

ATGGTAAAAGTTAGTGTAAGTTCTGTAGGAACCTCAAGCATCAACAGTAGCTATTCTATG
 TTTAGTCGTATCGGCTTAAATGATGCAATAACAAAACATCATCTTTGCAGAGGCT
 GCAACTCTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGGAACGTTA
 CCGATGCTTCAAGGAATGATTCTTCTGAAACATTGAGTGGAGAAATGTACAGAATTA
 CAAACCTTATATGCTCAATTGTTGATGAGGATTAGACTCTGCTTTAGACATCA
 AAATTAGCAAGTGATAGGCATCATTAAAGATTGCTGAAGCATTAGAGCATCTAAC
 GATGATCCAGAACCTTCAAATCTGCATAAGTTCTACAAAAGTAATATTAAAAAATTA
 AAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATTAAACGCCAT
 TCAGCAACAGTATTGCGGACATTCTAATGCGACACTGCTTAACCTGTTAACAGCACTAGCG
 GCTGTTCAACAGGATTCTGGATATAATAGTAAAACGGAGCTTTGGAAAACCAACA
 TCCGGACAGATGGAATGGACAAAGACAGTTAAGAAGAATTGGAAAGAGCGGAGACGCC
 AAAGCTGAAGAACTGAAAGTAAAAGGCTGAAGAAAGTAAGAAAGCTTCAAAATTGAA
 AATACTACTAAAAAGTAATGTTCAAGTTGATAAAAAGAAATTAAATAAAAGCGGCTAAT
 GAAGCGTATAAATTAGGAGAAATTAAAAAGATACTATGAATCAATTATCAGTGGTTA
 AGTAATGCATCGGCTGCCTTACTTAAAGAGGTAGCTAAATCAAATTGACTGACACAGCT
 CGGCTATTGATG

SEQ ID NO. 6102

STRAIN 090

TTAAATGATGCAATAACAAAACATCTTTGCAGAGGCT
 GCAACTCTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGG
 AACGTTAACTCCGATGCTCAAGGAATGATTCTTCTGAAACATTGA
 GTGAGAAATGTACAGAATTACAAACCTTATATGCTCAATTGTTGGTGT
 GAGGATTAGACTCTGCTGGTTAGAATCAAATTAGCAAGTGATAGGGC
 ATCATTAAAGATTGCTGAAGCACTTTAGAGCATTAAACGATGATCCAG
 AACCTTCCAAATCTGCCATAAGTTCTACAAAAGTAATATTAAAAAATTA
 AAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATT
 TAACGCCATTCAAGTATTGCGGACATTCTAAATGCAACAGTC
 CTGTTAACCAAGCACTAGCGGCTGTTCAACAGGATTCTGGATATAAT

SEQUENCE LISTING

AGTAAAACCGGAGCTTGGAAAACCAACATCCGGACAGATGGAATGGAC
 AAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCCAAGCTGAAG
 AACTGAAAAGTAAAAAGGCTGAAGAAGTAAGAAGCTTCAAAATTGAA
 AATACTACTAAAAAAAGTAATGTTCTAGTTGATAAAAAGAAATTAAATAA
 AGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAGATAACCTATG
 AATCAATTATCAGTGGTTAAGTAATGCATCGGCTGCCTACTAAAGAG
 GTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6103

STRAIN 18RS21

TTAAATGATGCAATAACAAAACATCTTGCAGAGGC
 TGCAACTCTCAAGGGACTGTTATTCAAATGCAAAAGCTATGCTACTG
 GAACGTTAACTCCGATGCTTCAAGGAATGATTCTTCTGAAACATTG
 AGTGAGAAATGTACAGAATTACAAACCTTATATGTCATTTGTGGTGA
 TGAGGATTAGACTCTGCTGTTAGAATCAAATTAGCAAGTGTAGGG
 CATCATTAAAGATTGCTGAAGCATTAGCATCTTAACCGATGATCCA
 GAACCTTCCAATCTGCCATAAGTTCTACAAAAGTAATATAAAAATT
 AAAAAAAGTATAAAATCTAATCAAAGAAATTAGACAACCTTAATGAAT
 TTAACGCCCATTCAGCAACAGTATTGCGGACATTTCTAATGCACAGTCA
 ACTGTTAACCAAGCACTAGCGGCTGTTCAACAGGATTTCTGGATATAA
 TAGTAAAACCGGAGCTTGGAAAACCAACATCCGGACAGATGGAATGGA
 CAAAGACAGTTAAGAAGAATTGGAAAGAGCGAGAAGACGCCAAGCTGAA
 GAAGTAAAAGTAAAAGGCTGAAGAAGTAAGAAGCTTCAAAAATTGAA
 AAATACTACTAAAAAAAGTAATGTTCTAGTTGATAAAAAGAAATTAAATAA
 AAGCGGCTAATGAAGCGTATAAATTAGGAGAAATTAAAAAGATAACCTAT
 GAATCAATTATCAGTGGTTAAGTAATGCATCGGCTGCCTACTAAAGA
 GGTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6104

STRAIN 2603 frame: 1

MVKVSVSSVGTQASTVAISMFSRVSALNDAITKLSSFAEAATLQGTAYSNKSYATGTLT
 PMLQGMILFSETLSEKCTELQTLVYVSIICGDEDLDSVVLLESKLASDRASLKIIEALLEHLN
 DDPEPSKSAISSTKSNIKLKKRIKSNQKLDNLNEFNAHSATVFADISNAQSTVNQALA
 AVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWEREADAKAEELSKKAESKKASKIE
 NTTKSNVSVDKKKLIKAANEAYKLGEIKKDTYESIISGLSNASAALLKEVAKSKLTD
 RLLM

SEQ ID NO. 6105

STRAIN 090 frame: 1

LNDAITKLSSFAEAATLQGTAYSNKSYATGTLT PMLQGMILFSETLSEKCTELQTLVYV
 ICGDEDLDSVVLLESKLASDRASLKIIEALLEHLDPEPSKSAISSTKSNIKLKKRIKS
 NQKLDNLNEFNAHSATVFADISNAQSTVNQALA AVSTGFSGYNSKTGAFGKPTSGQMEW
 TKTVKKNWEREADAKAEELSKKAESKKASKIENTTTKSNVSVDKKKLIKAANEAYKLG
 EIKKDTYESIISGLSNASAALLKEVAKSKLTD TARLLM

SEQ ID NO. 6106

STRAIN 18RS21 frame: 1

LNDAITKLSSFAEAATLQGTAYSNKSYATGTLT PMLQGMILFSETLSEKCTELQTLVYV
 ICGDEDLDSVVLLESKLASDRASLKIIEALLEHLDPEPSKSAISSTKSNIKLKKRIKS
 NQKLDNLNEFNAHSATVFADISNAQSTVNQALA AVSTGFSGYNSKTGAFGKPTSGQMEW
 TKTVKKNWEREADAKAEELSKKAESKKASKIENTTTKSNVSVDKKKLIKAANEAYKLG
 EIKKDTYESIISGLSNASAALLKEVAKSKLTD TARLLM

SEQ ID NO. 6201

STRAIN 2603

ATGATTTAAAAATTGCGTGCAGCATATAGTTACAATGGGGAGGTGTTACCAATTA
 GCTTGCTGGATTATCCTCGAATTAAGGCCTTGAATTGGAAAGGATAGGAGCTTCATA
 GCTACGAGAACAAATATAAAAGAAAAGTACGAGATACAATGTGACGATAAACATCTCCTC
 GCAAAATTGTTCATTTTAAATACAATAGTTACTTTCCCTATATTCCAAATAT
 AGAGAACGGCAGCTACTTTAATGAGGATGGTATTAGTTAACCTCTGATTTTAAGC
 CATACATGTACGATTGAAACTGCAAAACTAATTAAAGAAGGTAAAATCTTATCAGCA
 GTTAAAGCCTTAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGA
 GACCTAAAGATTACTTGAATGTGATGTTGAACGGTCAATACCAATTCTGGTTAT
 CGTTAGTAATGGAAAGATTGTTAGGCAAAGCACCACATCTGAACAGGAGTTAACAGTAGGT

SEQUENCE LISTING

TTTAAGCCAGGGGTCAGTTTCACTTATCAAGATATCATCAATCATCCTGATTCT
 ATTTTGATGTTATCATCCTGCTAAAATTAAAAATCAGCTTCTTAGCAGAACATTAA
 GTTGCATGTGTTATCCAAAACATTATCAAGAAGATTATCAAAGCCTGTGCCAATGAC
 TTGAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAA
 AAAGTTTATGATTTCTTGTCAATTGGAAAATAAA

SEQ ID NO. 6202

STRAIN 090

TGGATTATCCTCTAATTAAAGCGTTGAATTGGAAAGGATAGGAGCTTTC
 ATAGCTTACGAGAACAAATATAAAAGAAAAATTGAGATACATGTGACGA
 TAAACATCTCCTCACAAAATTGTTCAATTAAAATACAATAGTTTA
 CTTTCCCTATATTCCAAATATAGAGAACGGCAGCTACTTTAATGAG
 GATGGTATTAGTTAACTCTGATTTTAAGCCATACATGTGACATTGA
 AACTGCAAACAAATATTAAAGAAGGTAATCTTATCAGCAGTTAAAG
 CCTTAATAAAGCCTGCTGAAGTACTGGTAATGATAAGAGGAATGCTGCT
 GGAGACCCCTAAAGATTACTTGAATCTGATGTTGAACCTGGTCAAATAC
 CAATTCTGGTATCGTTAGTAATGAAAGATTGTTAGGCAAAGCACCAC
 CTGAACAGGAGTTAACAGTAGCTTTAAGCCAGGGTCAGCTTCATT
 AATTaTCAAGATATCATCAATCATCCTGATTCTATTGATGGTTATCA
 TCCTGCTAAATTAAAGTCAACTTCTTAGCAGAACATTAGTTGCAT
 GTGTTATCCAAAACATTATCAAGAAGATTATCAAAGCCTGTGCTAAT
 GACTTGAAACACAGGTTTATTATTTAGATTACTGTAACGAAACACTTTA
 TGAGTGGAAATCAAAAGTTTATGATTTCTTGTCAATTGGAAAATAAA

SEQ ID NO. 6203

STRAIN A909

TTGCTGGATTATCCTCGAATTAAAGCGTTGAATTGGAAAGGATA
 GGAGCTTCATAGCTTACGAGAACAAATATAAAAGAAAAATTGAGATACA
 ATGTGACGATAAACATCTCCTCACAAAATTGTTCAATTAAAATACA
 ATAGTTTACTTTCCCTATATTCCAAATATAGAGAACGGCAGCTACT
 TTTAATGAGGATGGTATTAGTTAACTCTGATTTTAAGCCATACATG
 TACGATTGAAACTGCAAACAACTAATTAAAGAAGGTAATCTTATCAG
 CAGTTAAAGCCTTAAAGCCTGCTGAAGTACTGGTAATGATAAGAGG
 AATGCTGCTGGAGACCCCTAAAGATTACTTGAATCTGATGTTGAACCTG
 GTCAAATACCAATTCTGGTATCGTTAGTAATGAAAGATTGTTAGGCA
 AAGCACCACATGAAACAGGAGTTAACAGTAGCTTTAAGCCAGGGTCAGC
 TTTCAATTAAATTATCAAGATATCATCAATCATCCTGATTCTATTG
 TGGTTATCATCCTGCTAAATTAAAGTCAACTTCTTAGCAGAACATT
 TAGTTGCATGTGTTATCCAAAACATTATCAAGAAGATTATCAAAGCCTT
 GTGCCTAATGACTTGAAACACAGGTTTATTATTTAGATTACTGTAACGA
 AACACTTTATGAGTGGAAATCAAAAGTTTATGATTTCTTGTCAATTGG
 AAAATAAA

SEQ ID NO. 6204

STRAIN H36B

TTAAGGCCTTGAATTGGAAAGGATAGGAGCTTCATAGCTTACGAGAAA
 CAATATAAAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCAC
 AAAAATTGTTCAATTAAAATACAATAGTTTACTTTCCCTATATT
 CCAAATATAGAGAACGGCAGCTACTTTAATGAGGATGGTATTAGTTA
 ACTCTGATTTTTAAGCCTACATGTACGATTGAAACTGCAAACAACTAAT
 TTTAAAGAAGGTAATCTTATCAGCAGTTAAAGCCTTAATAAGCCTG
 CTGAAGTACTGGTAATGATAAGAGGAATGCTGGAGACCCCTAAAGAT
 TACTTTGACTATGTGATGTTGAACCTGGTCAAATACCAATTCTGGTTATCG
 TTTAGTAATGAAAGATTGTTAGGCAAAGCACCACATGAAACAGGAGTTAA
 CAGTAGCTTTAAGCCAGGGTCAGCTTCATTAAATTATCAAGATATC
 ATCAATCATCCTGATTCTATTGATGGTTATCATCCTGCTAAATTAA
 AAATCAACTTCTTTAGCAGAACATTAGTTGCATGTGTTATCCAAAAC
 ATTATCAAGAAGATTATCAAAGCCTGTGCTAATGACTTGAAACACAGA
 GTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAAA
 AGTTTATGATTTCTTGTCAATTGGAAAATAAA

SEQ ID NO. 6205

STRAIN 18RS21

TTGCTGGATTATCCTCGAATTAAAGCGTT

SEQUENCE LISTING

TGAATTGGAAAGGATAGGAGCTTCATAGCTTACGAGAAACAATATAAAA
 GAAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGAAAAATTGTT
 CATTTTAAAATACAATAGTTTACTTTCCCTATATTCCAAATATAAG
 AGAACGGCAGCTACTTTAATGAGGATGGTATTAGTTAACCTCTGATT
 TTTAAGCCATACATGTACGATTGAAACTGCAAAACTAATTAAAGAA
 GGTAAAATCTTACAGCAGTTAACGCTTAAAGCCTTAAAGCCTGCTGAAGTACT
 GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCCTAAAGATTACTTGACT
 ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTAGTAATG
 GAAAGATTGTTAGGCAAAGCACCCTGAAACAGGAGTTAACAGTAGGTTT
 TAAGCCAGGGTCAGTTTCACTTACTTATCAAGATATCATCAATCATC
 CTGATTCTATTGGTATGTTGTTATCATCCTGCTAAATTAAAGCTT
 TCTTAGCAGAACATTAGTTGATGTGTTATCCAAAACATTATCAAGA
 AGATTATCAAAGCCTTGCTGCCAATGACTTGAAACACAGGGTTATTATT
 TAGATTACTGTAACGAAACACTTTATGAGTGGAACTAAAAAGTTTATGAT
 TTTCTTGATTTGGAAAATAAA

SEQ ID NO. 6206

STRAIN M732

TTGCTGGATTATCCTCGAATTAAGGCCTT
 TGAATTGGAAAGGATAGGAGCTTCATAGCTTACGAGAAACAATATAAAA
 GAAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGAAAAATTGTT
 CATTTTAAAATACAATAGTTTACTTTCCCTATATTCCAAATATAAG
 AGAACGGCAGCTACTTTAATGAGGATGGTATTAGTTAACCTCTGATT
 TTTAAGCCATACATGTACGATTGAAACTGCAAAACTAATTAAAGAA
 GGTAAAATCTTACAGCAGTTAACGCTTAAAGCCTTAAAGCCTGCTGAAGTACT
 GGTAAAAGATAAGAGGAATGCTGCTGGAGACCCCTAAAGATTACTTGACT
 ATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTAGTAATG
 GAAAGATTGTTAGGCAAAGCACCCTGAAACAGGAGTTAACAGTAGGTTT
 TAAGCCAGGGTCAGTTTCACTTACTTATCAAGATATCATCAATCATC
 CTGATTCTATTGGTATGTTGTTATCATCCTGCTAAATTAAAGCTT
 TCTTAGCAGAACATTAGTTGATGTGTTATCCAAAACATTATCAAGA
 AGATTATCAAAGCCTTGCTGCCAATGACTTGAAACACAGGGTTATTATT
 TAGATTACTGTAACGAAACACTTTATGAGTGGAACTAAAAAGTTTATGAT
 TTTCTTGATTTGGAAAATAAA

SEQ ID NO. 6207

STRAIN COH1

TTGCTGGAT
 TATCCTCGAATTAAGGCCTTGAATTGGAAAGGATAGGAGCTTCATAGC
 TTACGAGAAACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAAC
 ATCTCCTCGAAAAATTGTTCATTTTAAATACAATAGTTTACTTTT
 CCCTATATTCCAAATATAGAGAACGGCAGCTACTTTAATGAGGATGG
 TATAGTTAACCTCTGATTTTAAAGCCATACATGTACGATTGAAACTG
 CAAAATATTAAAGAGTAAATCTTACAGCAGTTAAAGCCTT
 AATAAGCCTGCTGAAGTACTGGTAAAGATAAGAGGAATGCTGCTGGAGA
 CCCTAAAGATTACTTGACTATGTGATGTTGAACTGGTCAAATACCAATT
 CTGGTTATCGTTAGTAATGGAAAGATTGTTAGGCAAAGCACCCTGAA
 CAGGAGTTAACAGTAGGTTAAGCCAGGGTCAGTTTCACTTTACTTA
 TCAAGATATCATCAATCATCCTGATTCTATTGGTTATCATCCTG
 CTAAAATTAAAAATCAGCTTCTTAAAGCAGAACATTAGTTGATGTGTT
 ATCCAAAACATTATCAAGAAGATTATCAAAGCCTTGCTGCCAATGACTT
 GAAACACAGGGTTATTATTAGATTACTGTAACGAAACACTTTATGAGT
 GGAATCAAAAGTTATGATTCTTGGCATTGGAAAATAAA

SEQ ID NO. 6208

STRAIN M781

TTGCTGGA
 TTATCCTCGAATTAAGGCCTTGAATTGGAAAGGATAGGAGCTTCATAG
 CTTACGAGAAACAATATAAAAGAAAAACTGAGATACAATGTGACGATAAA
 CATCTCCTCGAAAAATTGTTCATTTTAAATACAATAGTTTACTTT
 CCCTATATTCCAAATATAGAGAACGGCAGCTACTTTAATGAGGATGG
 GTATTAGTTAACCTCTGATTTTAAAGCCATACATGTACGATTGAAACT
 GCAAAACTAATTAAAGAAGGTTAAAGCAGTTAAAGCCTT
 TAATAAGCCTGCTGAAGTACTGGTAAAGATAAGAGGAATGCTGCTGGAG

SEQUENCE LISTING

ACCTCTAAAGATTACTTGTACTATGTGATGTTGAACTGGTCAAATACCAAT
 TCTGGTTATCGTTAGTAATGGAAAGATTGTTAGGCAAAGCACCACATCTGA
 ACAGGAGGTTAACAGTAGGTTAAGCCAGGGGTCAGTTTCACTTTACTT
 ATCAAGATATCATCAATCATCCTGATTCTATTGATGGTTATCATCCT
 GCTAAAATTAAACATCAGCTTCTTAGCAGAACATTAGTTGCATGTGT
 TATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCAATGACT
 TGAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTATGAG
 TGGAAATCAAAAGTTATGATTTCTTGTCAATTGGAAAATAAA

SEQ ID NO. 6209

STRAIN CJB110

TTGCTGGATTATCCTCGAATTAAGGC
 GTTTGAATTGGAAAGGATAGGAGCTTCATAGCTTACGAGAAAACAATATA
 AAAGAAAATTGAGATAACATGTGACGATAAACATCTCCTCACAAAATT
 GTTCATTTTAAACATACAATAGTTTACTTTCCCTATATCCCAAATA
 TAGAGAACGGCAGCTACTTTAATGAGGATGGTATTAGTTAACCTCG
 ATTTTTAAGCCATACATGTACGATTGAAACTGCAAAACTAATTTTAA
 GAAGGTTAAACCTTACAGCAGTTAAGCCTTAAAGCCTGCTGAAGT
 ACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCTAAAGATTACTTG
 ACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCGTTAGTA
 ATGGAAAGATGTTAGGCAAAGCACCACATGAACAGGAGTTAACAGTAGC
 TTTAAGCCAGGGTCAGCTTCAATTAACTTCAAGATAATCATCAATC
 ATCCTGATTCTATTGATGGTTATCATCCTGCTAAAATTAAAATCAA
 CTTCTTCTAGAGAACATTAGTTGCATGTGTTATCCCAAACATTATCA
 AGAAGATTATCAAAGCCTTGTGCTAATGACTGAAACACAGAGTTATT
 ATTTAGATTACTGTAACGAAACACTTATGAGTGAATCAAAAGTTAT
 GATTTCTTGTCAATTGGAAAATAAA

SEQ ID NO. 6210

STRAIN 1169NT

AATTAAGGCCTTGAATTGGAAAGGATAGGAGCTTCATAGCTTACGAGA
 AACAAATATAAAAGAAAAACTGAGATAACATGTGACGATAAACATCTCCTC
 GCAAAATTGTCATTTTAAACATACAATAGTTTACTTTCCCTATAT
 TCCCAAATATAGAGAACGGCAGCTACTTTAATGAGGATGGTATTAGTT
 TAACTTCTGATTTTAAAGCCATACATGTACGATTGAAACTGCAAAACTA
 ATTTTAAAGAAGGTAACATCTTACAGCAGTTAAGCCTTAAAGCC
 TGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCTAAAG
 ATTACTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTAT
 CGTTTAGTAATGGAAAGATGTTAGGCAAAGCACCACATGAACAGGAGTT
 AACAGTAGGTTAAAGCAGGGTCAGCTTCAATTGATGGTTATCATCCTGCTAAAATT
 TCAATCATCCTGATTCTATTGATGGTTATCATCCTGCTAAAATT
 AAAAATCAGCTTCTTCTAGAGAACATTAGTTGCATGTGTTATCCCAA
 ACATTATCAAGAAGATTATCAAACATTGTGCCAATGACTGAAACACA
 GAGTTTATTATTTAGATTACTGTAACGAAACACTTATGAGTGAATCAA
 AAAGTTATGATTTCTTGTCAATTGGAAAATAAA

SEQ ID NO. 6211

STRAIN JM9130013

ATAGGAGCTTCATAGCTTACGAGAAAACAATATAAAAGAAAAATTGAGAT
 ACAATGTGACGATAAACATCTCCTCACAAAATTGTCATTTTTAAAC
 ACAATAGTTTACTTTCCCTATATCCCAAATATAGAGAACGGCAGCT
 ACTTTAATGAGGATGGTATTAGTTAACCTCTGATTTTAAAGCCATAC
 ATGTACGATTGAAACTGCAAAACTAATTTTAAAGAAGGTAACATTCTT
 CAGCAGTTAACCTTAAAGCCTGCTGAAGTACTGGTAAATGATAAG
 AGGAATGCTGCTGGAGACCTAAAGATTACTTGTACTATGTGATGTTGA
 CTGGTCAAATACCAATTCTGGTTATGTTAGTAATGGAAAGATTGTTAG
 GCAAAGCACCACATCTGAAACAGGAGTTAACAGTAGCTTAAAGCCAGGGGTC
 AGCTTCAATTATCAAGATAATCATCAATCATCCTGATTCTATT
 TGATGGTTATCATCCTGCTAAAATTCAACTTTCTTAGCAGAAC
 ATTAGTTGCATGTGTTATCCCAAACATTATCAAGAAGATTATCAAAGC
 CTGTGCCATATGACTGAAACACAGAGTTATTAGATTACTGTA
 CGAAACACTTATGAGTGAATCAAAAGTTATGATTTCTTGTCAATT
 TGGAAAATAAA

SEQUENCE LISTING

SEQ ID NO. 6212

STRAIN 2603 frame: 1

MILKICRAAYSILQWGGVYQLALLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNNSFTFPYIPKREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKA

FKPGVSFHFYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK

SEQ ID NO. 6213

STRAIN A909 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNNSFTFPYIPKREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKA

FKPGVSFHFYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK

SEQ ID NO. 6214

STRAIN H36B frame: 3

KAFELERIGAFIAYEKQYKRKIEIQCDDKHLLAKIVHFLKYNNSFTFPYIPKREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKA

FKPGVSFHFYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK

SEQ ID NO. 6215

STRAIN 18RS21 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNNSFTFPYIPKREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKA

FKPGVSFHFYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK

SEQ ID NO. 6216

STRAIN M732 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNNSFTFPYIPKREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKA

FKPGVSFHFYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK

SEQ ID NO. 6217

STRAIN COH1 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNNSFTFPYIPKREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKA

FKPGVSFHFYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK

SEQ ID NO. 6218

STRAIN M781 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNNSFTFPYIPKREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKA

FKPGVSFHFYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK

SEQ ID NO. 6219

STRAIN CJB110 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNNSFTFPYIPKREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKA

FKPGVSFHFYQDIINHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQK

SEQUENCE LISTING

SEQ ID NO. 6220

STRAIN 1169NT frame: 2
 IKA FELERIGAFIAYEKQYKRKTEIQCDDKHLLAKIVHFLKYNSTFPYIPKYREAAATF
 NEDG ISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEV LVNDKRNAAGDPKDYFD
 YVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFTYQDIINHPDSIFDGYHP
 AKIKNQQLS LAEHLVACVIPKHYQEDYQNLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLC
 HLENK

SEQ ID NO. 6221

STRAIN JM9130013 frame: 1
 IGA FIA YEKQYKRKIEIQCDDKHLTKIVHFLKYNSTFPYIPKYREAAATF NEDG ISLT
 SDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEV LVNDKRNAAGDPKDYFDYVMLNWSN
 TNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHNYQDIINHPDSIFDGYHPAKIKNQLS
 LAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVYDFLC HLENK

SEQ ID NO. 6222

STRAIN 090 frame: 3
 DYPLIKA FELERIGAFIAYEKQYKRKIEIQCDDKHLLTKIVHFLKYNSTFPYIPKYREA
 AATF NEDG ISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEV LVNDKRNAAGDPK
 DYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHNYQDIINHPDSIFD
 GYHPAKIKNQQLS LAEHLVACVIPKHYQEDYQSLVPNDLKHRVYYLDYCNETLYEWNQKVY
 DFLCHLENK

SEQ ID NO. 6301

STRAIN 2603

ATGAAAAGTCGAAAAAAAGATAAATTGGTATTGAGGTTAACACAAACACTATTGGTTTT
 GGTGTTGGGTGGGTTTGGTTTATAATTATAAAATGATAATGTCGAACCGACAGTC ACT
 AGTGCATCGGATCAAACGACGACTTTATTCAAACGATTCTCCAACAGCTATTGAAATT
 TCTAACGACTATGATTGTATGCGTCAGTCTTATTAGCACAAGCTATTGGAATCATCC
 AGTGGACAATCAGATTGTCTAAGGCTCTAATTATAACCTCTTGGCATCAAAGGAGAA
 TATAAAGGTAATCTGTCTAAATGCCTACTTTAGAAGATGATGGAAAGGCAATATGACT
 CAAATCCAAGCTCTTTCGCGCTATCCAAATTATTCTGCTTCACTATATGATTATGCT
 GAGTTAGTATCTAGTCAAAGATGATCTGTTGGAAATCAAACCTCTTCTTATAAG
 GATGCTACTGAGCTCTAACAGGTCTTATGCGACAGATACTGCTTATGCTAGTAAATTAA
 AACCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6302

STRAIN 090

GGGGTTTGGTTTATAATTATAA
 AAAATGATAATGTCGAACCGACAGTC ACTAGTGCATCGGATCAAACGACGA
 CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTCTAAAGACCTAT
 GATTGTATGCGTCAGTCTTATTAGCACAAGCTATTGGAATCATCCAG
 TGGACAATCAGATTGTCTAAGGCTCTAATTATAACCTCTTGGCATCA
 AAGGAGAATATAAAGGTAATCTGTCTAAATGCTACTTTAGAAGATGAT
 GGGAAAGGCAATATGACTCAAATCCAAGCTCTTTCGCGCTATCCAAA
 TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
 ATGCATCTGTTGGAAATCAAACCTCTTCTTATAAGGATGCTACTGCA
 GCTCTAACAGGTCTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
 CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6303

STRAIN A909

GGGGTTTGGTTTATAATTATAA
 AAAATGATAATGTCGAACCGACAGTC ACTAGTGCATCGGATCAAACGACGA
 CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTCTAAAGACCTAT
 GATTGTATGCGTCAGTCTTATTAGCACAAGCTATTGGAATCATCCAG
 TGGACAATCAGATTGTCTAAGGCTCTAATTATAACCTCTTGGCATCA
 AAGGAGAATATAAAGGTAATCTGTCTAAATGCTACTTTAGAAGATGAT
 GGGAAAGGCAATATGACTCAAATCCAAGCTCTTTCGCGCTATCCAAA
 TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
 ATGCATCTGCTTGGAAATCAAACCTCTTCTTATAAGGATGCTACTGCA
 GCTCTAACAGGTCTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
 CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQUENCE LISTING

SEQ ID NO. 6304

STRAIN H36B

```
GGGGTTGGTTTATAATTATAAAAATGATA
ATGTCGAACCGACAGTCACTAGTCATCGGATCAAACGACGACTTTATT
CAAACGATTTCTCCAACAGCTATTGAAATTCTAAGACCTATGATTGTA
TGCCTCAGTCTTATTAGCACAAGCTATTGGAATCATCCAGTGGACAAT
CAGATTGCTAAGGCTCTAATTATAACCTCTTGGCATCAAAGGAGAA
TATAAAGGTAATCTGCTTAACTGCTACTTTAGAAGATGATGGGAAAGG
CAAATATGACTCAAATCCAAGCTCCTTCGCGCTATCAAATTATTCTG
CTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTGTGCA
GCTTGGAAATCAAATACCTCTTATAAGGATGCTACTGCAAGCTAAC
AGTCTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTA
TTGAAACCTACAGTCTAGATGCTTATGATAAA
```

SEQ ID NO. 6305

STRAIN 18RS21

```
GGGGTTGGTTTATAATTATAAAAATGATAATG
TCGAACCGACAGTCACTAGTCATCGGATCAAACGACGACTTTATTCAA
ACGATTTCTCCAACAGCTATTGAAATTCTAAGACCTATGATTGATG
GTCAGTCTTATTAGCACAAGCTATTGGAATCATCCAGTGGACAATCAG
ATTGCTAAGGCTCTAATTATAACCTCTTGGCATCAAAGGAGAATAT
AAAGGTAATCTGCTTAACTGCTACTTTAGAAGATGATGGGAAAGGCAA
TATGACTCAAATCCAAGCTCCTTCGCGCTATCAAATTATTCTGCTT
CACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCACTGTT
TGGAAATCAAATACCTCTTATAAGGATGCTACTGCAAGCTAACAGG
TCTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTG
AAACCTACAGTCTAGATGCTTATGATAAA
```

SEQ ID NO. 6306

STRAIN M732

```
GGGGTTGGTTTATAATTATAAA
AAATGATAATGTCGAACCGACAGTCACTAGTCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTCTAAGACCTAT
GATTGCTATGCGTCAGTCTTATTAGCACAAGCTATTGGAATCATCCAG
TGGACAATCAGATTGCTAAGGCTCTAATTATAACCTCTTGGCATCA
AAGGAGAATATAAAGGTAATCTGCTTAACTGCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTCGCGCTATCAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
ATGCATCTGTTGGAAATCAAATACCTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA
```

SEQ ID NO. 6307

STRAIN COH1

```
GGGGTTGGTTTATAATTATAAA
AAATGATAATGTCGAACCGACAGTCACTAGTCATCGGATCAAACGACGA
CTTTTATTCAAACGATTTCTCCAACAGCTATTGAAATTCTAAGACCTAT
GATTGCTATGCGTCAGTCTTATTAGCACAAGCTATTGGAATCATCCAG
TGGACAATCAGATTGCTAAGGCTCTAATTATAACCTCTTGGCATCA
AAGGAGAATATAAAGGTAATCTGCTTAACTGCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTCGCGCTATCAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
ATGCATCTGTTGGAAATCAAATACCTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTATGCGACAGATACTGCTTATGCTAGTAAATTAAA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA
```

SEQ ID NO. 6308

STRAIN M781

```
GGGGTTGGTTTATAATTATAAAAATGA
TAATGTCGAACCGACAGTCACTAGTCATCGGATCAAACGACGACTTTA
TTCAAACGATTTCTCCAACAGCTATTGAAATTCTAAGACCTATGATTG
TATGCGTCAGTCTTATTAGCACAAGCTATTGGAATCATCCAGTGGACA
ATCAGATTGCTAAGGCTCTAATTATAACCTCTTGGCATCAAAGGAG
ATAATAAAGGTAATCTGCTTAACTGCTACTTTAGAAGATGATGGGAAA
```

SEQUENCE LISTING

GGCAATATGACTCAAATCCAAGCTCCTTTCGCGCTATCCAAATTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAGGAACTGATCTAAGGATGCTACTGCAGCTACAGGTCCTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6309

STRAIN CJB110

GGGGTTGGTTTATAATTATAAAAATGATAATGT
CGAACCGACAGTCACTAGTCATCGGATCAAACGACGACTTTATTCAAA
CGATTTCCTCAACAGCTATTGAAATTCTAAGACCTATGATTGTATGCG
TCAGTCCTTATTAGCACAAGCTATTGGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCTAATTATAACCTCTTGGCATCAAAGGAGAATATA
AAGGTAATCTGCTAAATGCCTACTTTAGAAGATGATGGAAAGGCAAT
ATGACTCAAATCCAAGCTCTTTCGCGCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAGGATGCTACTGCAGCTAACAGGT
CTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6310

STRAIN 1169NT

GGGGTTGGTTTATAATTATAAAAATGATAATGT
CGAACAGACAGTCACTAGTCATCGGATCAAACGACGACTTTATTCAAA
CGATTTCCTCAACAGCTATTGAAATTCTAAGACCTATGATTGTATGCG
TCAGTCCTTATTAGCACAAGCTATTGGAATCATCCAGTGGACAATCAGA
TTTGTCTAAGGCTCTAATTATAACCTCTTGGCATCAAAGGAGAATATA
AAGGTAATCTGCTAAATGCCTACTTTAGAAGATGATGGAAAGGCAAT
ATGACTCAAATCCAAGCTCTTTCGCGCTATCCAAATTATTCTGCTTC
ACTATATGATTATGCTGAGTTAGTATCTAGTCAGGATGCTACTGCAGCTAACAGGT
CTTATGCGACAGATACTGCTTATGCTAGTAAATTAAACCAAATTATTGA
AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6311

STRAIN JM9130013

TTGGTTTATAATTATAAAAATGATAATGTCGAACCGACAGTCACTAGT
GCATCGGATCAAACGACGACTTTATTCAAACGATTCCCCAACAGCTAT
TGAAATTCTAAGACCTATGATTGTATGCGTCAGTCTTATTAGCACAAG
CTATTTGGAATCATCCAGTGGACAATCAGATTGTCTAAGGCTCTAAT
TATAACCTCTTGGCATCAAAGGAGAATATAAAGTAAATCTGTTCAAAT
GCCTACTTTAGAAGATGATGGAAAGGTAATATGACCCAAATCCAAGCTC
CTTTCGCGCTATCAAATTATTCTGCTTCACTATATGATTATGCTGAG
TTAGTATCTAGTCAGGATGCTACTGCAGCTAACAGGTCTTATGCGACAGATACTG
CTTATGCTAGTAAATTAAACCAAATTATTGAAAACACTACAGTCTAGATGCT
TATGATAAA

SEQ ID NO. 6312

STRAIN 2603 frame: 1

MKSRRKKDKLVLRLTTTLLVGLGGWFNYKNDNVEPTVTSASDQTTTFIGTISPTAIEI
SKTYDLYASVLLAQAILESSSGQSDLSKAPNLYFGIKGEYKGKSVQMPTEEDDGKGNMT
QIQAPFRAYPNYSASLYDYAELVSSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKL
NQIETYSLDAYDK

SEQ ID NO. 6313

STRAIN 090 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIGTISPTAIEIISKTYDLYASVLLAQAILESSSGQ
SDLSKAPNLYFGIKGEYKGKSVQMPTEEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNNQIETYSLDAYDK

SEQ ID NO. 6314

STRAIN A909 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIGTISPTAIEIISKTYDLYASVLLAQAILESSSGQ

SEQUENCE LISTING

SDL SKAPN YNLFGIKGEYKGKSVQM PTLE DDGKGNMTQI QAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6315

STRAIN H36B frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIGTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDL SKAPN YNLFGIKGEYKGKSVQM PTLE DDGKGNMTQI QAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6316

STRAIN 18RS21 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIGTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDL SKAPN YNLFGIKGEYKGKSVQM PTLE DDGKGNMTQI QAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6317

STRAIN M732 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIGTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDL SKAPN YNLFGIKGEYKGKSVQM PTLE DDGKGNMTQI QAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6318

STRAIN M781 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIGTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDL SKAPN YNLFGIKGEYKGKSVQM PTLE DDGKGNMTQI QAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6319

STRAIN CJB110 frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIGTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDL SKAPN YNLFGIKGEYKGKSVQM PTLE DDGKGNMTQI QAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6320

STRAIN 1169NT frame: 1

GVWFYNYKNDNVEPTVTSASDQTTTFIGTISPTAIEISKTYDLYASVLLAQAILESSSGQ
SDL SKAPN YNLFGIKGEYKGKSVQM PTLE DDGKGNMTQI QAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6321

STRAIN JM9130013 frame: 3

WFYNYKNDNVEPTVTSASDQTTTFIGTISPTAIEISKTYDLYASVLLAQAILESSSGQSD
LSKAPN YNLFGIKGEYKGKSVQM PTLE DDGKGNMTQI QAPFRAYPNYSASLYDYAELVSS
QKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIENYSLDAYDK

SEQ ID NO. 6401

STRAIN 2603

ATGAACAAGTCTAAGAAAATTATCAATTATTACTACAAGCGCAAGCTCTA
TTCTCAGATGAAACAAATGCTCTGCCAACTTATCAAATGCTTCAGCTATGCTAAATGCT
ATGCTTCCAAATTCTGTATTACAGGCTTTATTATTTGATGGAGAAGAGTTAATTCTT
GGCCCTTCCAGGGTGGTGTATCATGTGTGCATATTACTTGTAGAAAAGGTGTTGTGGT
GAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGTTACAAAGCATGCTAACAT
ATCTCTGTGATTCAAAGCTATGAGTGAATCGTAGTACCTATGTTAAAATGCCAA
CTTCTAGGAGTTCTAGATTAGATTCTTCTTGTAGCAGATTATGATGAGATTGATCAA
GAATACTTAGAAAATTGTAGGTATTCTAGTAGAACATACGATTGGAAATTGGATATG
TTTGGAGTTGAAAAG

SEQ ID NO. 6402

STRAIN 090

CTCTATTCTCAGATGAAACAAATGCTCTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCCAAATTCTGTATTTAC
AGGCTTTTATTATTTGATGGAAAGGAGTTAATTCTTGGCCCTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTGTAGAAAAGGTGTTGTGGTGA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGTTACAAAGCATGC

SEQUENCE LISTING

TAACATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTCTTCTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAATTGTAGG
TATTCTAGTAGAACATACGATTGGAATTGGATA

SEQ ID NO. 6403

STRAIN A909

CTCTATTCTCAGATGAAACAAATGCTCTTGC
CTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCAAATTCTGTAT
TTACAGGCTTTATTATTGATGGAGAAGAGTTAATTCTTGGCCCTTC
CAGGGTGGTGTATCATGTGTCATATTACTTAGGAAAAGGTGTTGTGG
TGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGC
ATGCTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTA
CCTATGTTAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTCTTC
TTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAATTG
TAGGTATTCTAGTAGAACATACGATTGGAATTGGATATGTTGGAGTT
GAAAAG

SEQ ID NO. 6404

STRAIN H36B

CTCTATTCTCAGATGAAACAAATGCTCTG
CAACTTATCAAATGCTTCAGCTATGCTAAaTGCTATGCTTCAAATTCTG
TATTTCAGGGCTTTATTATTGATGGAGAAGAGTTAATTCTTGGCCCT
TTCCAGGGTGGTGTATCATGTGTCATATTACTTAGGAAAAGGTGTTTG
TGGTGAATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAA
AGCATGCTAACTATATCTCCTGTGATCAAAGCTATGAGTGAAATCGTA
GTACCTATGTTAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTTC
TTCTTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAT
TTGTAGGTATTCTAGTAGAACATACGATTGGAATTGGATATGTTGGAA
GTTGAAAAG

SEQ ID NO. 6405

STRAIN 18RS21

CTCTATTCTCAGATGAAACAAATGCTCTTGC
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCAAATTCTGTATT
CAGGCTTTATTATTGATGGAGAAGAGTTAATTCTTGGCCCTTCAG
GGTGGTGTATCATGTGTCATATTACTTAGGAAAAGGTGTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCT
ATGTTAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAATTGTAG
GTATTCTAGTAGAACATACGATTGGAATTGGATATGTTGGAGTTGAA
AAG

SEQ ID NO. 6406

STRAIN M732

CTCTATTCTCAGATGAAACAAATGCTCTTGC
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCAAATTCTGTATT
CAGGCTTTATTATTGATGGAGAAGAGTTAATTCTTGGCCCTTCAG
GGTGGTGTATCATGTGTCATATTACTTAGGAAAAGGTGTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAATTGTAG
GTATTCTAGTAGAACATACGATTGGAATTGGATATGTTGGAGTTGAA
AAG

SEQ ID NO. 6407

STRAIN COH1

CTCTATTCTCAGATGAAACAAATGCTCTTGC
TTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCAAATTCTGTATT
TACAGGCTTTATTATTGATGGAGAAGAGTTAATTCTTGGCCCTTC
AGGGTGGTGTATCATGTGTCATATTACTTAGGAAAAGGTGTTGTGGT
GAATCTGCACAAACTGCTAAGACGCTGATTGATGATGTTACAAAGCA

SEQUENCE LISTING

TGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTCAAATCGTAGTAC
 CCATGTTAAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCT
 TTAGTAGCAGATTATGATGAGATTGATCAAGAAACTTAGAAAAATTGTT
 AGGTATTCTAGTAGAACATACGATTGGAAATTGGATATGTTGGAGTTG
 AAAAG

SEQ ID NO. 6408

STRAIN M781

CTCTATTCTCAGATGAAACAAATGCTCTGCCAACTT
 ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCAAATTCTGTATTTA
 CAGGTTTATTATTTGATGGAGAGGAGTTAATTCTGGCCCTTTCA
 GGTGGTGTATCATGTGTGCATATTACTTAGGAAAAGGTGTTGTGGTGA
 ATCTGCACAAACTGCTAAGACGCTGATTGTGATGTTACAAAGCATG
 CTAACTATATCTCCTGTGATTCAAAGCTATGAGTCAAATCGTAGTACCC
 ATGTTAAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCTT
 AGTAGCAGATTATGATGAGATTGATCAAGAAACTTAGAAAAATTGTT
 GTATTCTAGTAGAACATACGATTGGAAATTGGATATGTTGGAGTTGAA
 AAG

SEQ ID NO. 6409

STRAIN CJB110

CTCTATTCTCAGATGAAACAAATGCTCTGCCAACTT
 TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCAAATTCTGTATTTAC
 AGGTTTATTATTTGATGGAGAAGAGTTAATTCTGGCCCTTTCCAGG
 GTGGTGTATCATGTGTGCATATTACTTAGGAAAAGGTGTTGTGGTGA
 TCTGCACAAACTGCTAAGACGCTGATTGTGATGTTACAAAGCATGC
 TAACTATATCTCCTGTGATTCAAAGCTATGAGTCAAATCGTAGTACCTA
 TGTTAAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCTT
 GTAGCAGATTATGATGAGATTGATCAAGAAACTTAGAAAAATTGTT
 TATTCTAGTAGAACATACGATTGGAAATTGGATATGTTGGAGTTGAAA
 AG

SEQ ID NO. 6410

STRAIN 1169NT

CTCTATTCTCAGATGAAACAAATGCTCTGCCAACTT
 TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCAAATTCTGTATTTAC
 AGGTTTATTATTTGATGGAGAAGAGTTAATTCTGGCCCTTTCCAGG
 GTGGTGTATCATGTGTGCATATTACTTAGGAAAAGGTGTTGTGGTGA
 TCTGCACAAACTGCTAAGACGCTGATTGTGATGTTACAAAGCATGC
 TAACTATATCTCCTGTGATTCAAAGCTATGAGTCAAATCGTAGTACCC
 TGTTAAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCTT
 GTAGCAGATTATGATGAGATTGATCAAGAAACTTAGAAAAATTGTT
 TATTCTAGTAGAACATACGATTGGAAATTGGATATGTTGGAGTTGAAA
 AG

SEQ ID NO. 6411

STRAIN JM9130013

CTCTATTCTCAGATGAAACAAATGCTCTGCCAACTT
 TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCAAATTCTGTATTTAC
 AGGTTTATTATTTGATGGAGAAGAGTTAATTCTGGCCCTTTCCAGG
 GTGGTGTATCATGTGTGCATATTACTTAGGAAAAGGTGTTGTGGTGA
 TCTGCACAAACTGCTAAGACGCTGATTGTGATGTTACAAAGCATGC
 TAACTATATCTCCTGTGATTCAAAGCTATGAGTCAAATCGTAGTACCTA
 TGTTAAAAAATGGCAAACCTCTAGGAGTTCTAGATTTAGATTCTTCTT
 GTAGCAGATTATGATGAGATTGATCAAGAAACTTAGAAAAATTGTT
 TATTCTAGTAGAACATACGATTGGAAATTGGATATGTTGGAGTTGAAA
 AG

SEQ ID NO. 6412

STRAIN 2603 frame: 1

MNKSKKIENYQLLLQALFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGEELIL
 GPFQGGVSCVHITLGKGVCGESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGK
 LLGVLDLDSSLVADYDEIDQEYLEKFVGILVEHTIWNLDMFGEVK

SEQ ID NO. 6413

SEQUENCE LISTING

STRAIN 090 frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGKELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLD

SEQ ID NO. 6414
 STRAIN A909 frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEEELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQ ID NO. 6415
 STRAIN H36B frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEEELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQ ID NO. 6416
 STRAIN 18RS21 frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEEELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQ ID NO. 6417
 STRAIN M732 frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEEELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQ ID NO. 6418
 STRAIN COH1 frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEEELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQ ID NO. 6419
 STRAIN M781 frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEEELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQ ID NO. 6420
 STRAIN M781 frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEEELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQ ID NO. 6421
 STRAIN CJB110 frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGKELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQ ID NO. 6422
 STRAIN 1169NT frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEEELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQ ID NO. 6423
 STRAIN JM9130013 frame: 3
 LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDGEEELILGPQGGVSCVHITLGKGVC
 GESAQTAKTLIVDDVTKHANYISCDSKAMSEIVVPMFKNGKLLGVLDLDSLADYDEID
 QEYLEKFVGLVEHTIWNLDMFGVEK

SEQUENCE LISTING

SEQ ID NO. 6501

STRAIN 2603

ATGAAAAAGAGTACCCAAATAACTACTAATAGTTGCA
 TTATTCTACTGTGTTAGCGGAGGATTTATATGAAAGAACAAACAAAGAAAAGAAGAA
 CTAACACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAATTCTATGAG
 AATATAGAAGAAATAAAATCACACATCCTGTTCAACTGAAATTCTGGAGATTGGCAT
 TGTACTGTAAAGATTTCATTTAATGATAAAAATCTATTGTTATAATATTACACATAAT
 TTGGAATCGAAAAAAATTATAGCGGAAATTAAATGAAAAAAATATGAATTGGAT
 TCAAGAATTGGTAAACAAAAAAACTATAAAATTATTTTCAGATGGTCAGGAGAAG
 ATACAA

SEQ ID NO. 6502

STRAIN 090

GGAGGATTTATATGAAAGAACAA
 ACAAAAGAGAAACTAAACGGAATCGAGAATATGAAGTTAGTCTAG
 TCAAGCATTGAAAATTCTATGAGAATATAGAAGAAATAAAATCACA
 CATCCTGTTCAACTGAAATTCTGGAGATTGGCATTGTACTGTAAAGAT
 TTCATTAAATGATAAAAATCTATTGTTATAATATTACACATAATTG
 AATCGAAAAAAATTATAGCGGAAATTAAATGAAAAAAATATGAATT
 TTTGATTCAAGAATTGGTAAACAAAAAAACTATAAAATTATTTTC
 AGATGGtCAGGAGAACATAAA

SEQ ID NO. 6503

STRAIN A909

GGAGGATTTATATGAAAGAACAA
 AGAAAAAGAGAACTAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAA
 AGCATTGAAAATTCTATGAGAATATAGAAGAAATAAAATCACACATC
 CTGTTCAACTGAAATTCTGGAGATTGGCATTGTACTGTAAAGATTCA
 TTTAATGATAAAAATCTATTGTTATAATATTACACATAATTGGAATC
 GAAAAAAATTATAGCGGAAATTAAATGAAAAAAATATGAATTGG
 ATTCAAGAATTGGTAAACAAAAAAACTATAAAATTATTTTCAGAT
 GGtCAGGAGAACATAAA

SEQ ID NO. 6504

STRAIN H36B

GGAGGATTTATATGAAAGAACAA
 ACAAAAGAGAAACTAAACGGAATCGAGAATATGAAGTTAGTCTAG
 TCAAGCATTGAAAATTCTATGAGAATATAGAAGAAATAAAATCACA
 CATCCTGTTCAACTGAAATTCTGGAGATTGGCATTGTACTGTAAAGAT
 TTCATTAAATGATAAAAATCTATTGTTATAATATTACACATAATTG
 AATCGAAAAAAATTATAGCGGAAATTAAATGAAAAAAATATGAATT
 TTTGATTCAAGAATTGGTAAACAAAAAAACTATAAAATTATTTTC
 AGATGGtCAGGAGAACATAAA

SEQ ID NO. 6505

STRAIN 18RS21

GGAGGATTTATATGAAAGAACAA
 AAAGAAAAGAGAACTAAACGGAATCGAGAATATGAAGTTAGTCTAGTC
 AAAGCATTGAAAATTCTATGAGAATATAGAAGAAATAAAATCACACA
 TCCGTGTTCAACTGAAATTCTGGAGATTGGCATTGTACTGTAAAGATT
 CATTAAATGATAAAAATCTATTGTTATAATATTACACATAATTGGA
 TCGAAAAAAATTATAGCGGAAATTAAATGAAAAAAATATGAATT
 TGATTCAAGAATTGGTAAACAAAAAAACTATAAAATTATTTTCAG
 ATGGtCAGGAGAACATAAA

SEQ ID NO. 6506

STRAIN M781

GGAGGATTTATATGAAAGAACAAAGAAAA
 GAAGAACTAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATT
 GAAAATTCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTT
 CAACTGAAATTCTGGAGATTGGCATTGTACTGTAAAGATTCAATTAA
 GATAAAAATCTATTGTTATAATATTACACATAATTGGAATCGAAAAA
 AAATTATAGCGGAAATTAAATGAAAAAAATATGAATTGGATTCAA

SEQUENCE LISTING

GAATTGGTAAAACAAAAAAACTATAAAATTATTTTCAGATGGTCAG
GAGAAGATACAA

SEQ ID NO. 6507

STRAIN CJB110

GGAGGATTTATATGAAAGAACAAACAAAGAAAAGAAGAA
CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAGCATTGAAAAA
TTCCTATGAGAATATAGAAGAATAAAATCACACATCCTGTTCAACTG
AAATTCTGGAGATTGGCATTGTACTGAAAGATTCTATTAAATGATAAA
AAATCTATTGTTATAATATTACACATAATTGGAATCGAAAAAAATTA
TAGCGGAAATTTAATGAAAAAAATATGAATTGATTGATTCAAGAATTG
GTAACACAAAAAAACTATAAAATTATTTTCAGATGGTCAGGAGAAG
ATACAA

SEQ ID NO. 6508

STRAIN 1169NT

GGAGGATTTATATGAAAGAACAAACAAAG
AAAAGAAGAACTAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAG
CATTGAAAATTCTATGAGAATATAGAAGAATAAAATCACACATCCT
GTTCACTGAAATTCTGGAGATTGGCATTGTACTGAAAGATTCTATT
TAATGATAAAAATCTATTGTTATAATATTACACATAATTGGAATCGA
AAAAAAATTATAGTGGAAATTAAATGAAAAAAATATGAATTGTTGAT
TCAAGAATTGTAACAAAAAAACTATAAAATTATTTTCAGATGG
TCAGGAGAAGATACAA

SEQ ID NO. 6509

STRAIN JM9130013

GGAGGATTTATATGAAAGAACAAAC
AAAGAAAAGAAGAACTAAACGGAATCGAGAATATGAAGTTAGTCTAGTC
AAAGCATTGAAAATTCTATGAGAATATAGAAGAATAAAATCACACA
TCCTGTTCACTGAAATTCTGGAGATTGGCATTGTACTGAAAGATT
CATTAAATGATAAAAATCTATTGTTATAATATTACACATAATTGGA
TCGAAAAAAATTATAGCGGAAATTAAATGAAAAAAATATGAATTGTT
TGATTCAAGAATTGGTAAACAAAAAAACTATAAAATTATTTTCAG
AtGGtCAGGAGAAGATACAA

SEQ ID NO. 6510

STRAIN 2603 frame: 1

MKKSTQIILLIVLFLVSGGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNSGKFNEKNMNFFDSRIGTK
KTIKIIIFSDQEKIQ

SEQ ID NO. 6511

STRAIN 090

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNSGKFNEKNMNFFDSRIGTK
KTIKIIIFSDGQ

SEQ ID NO. 6512

STRAIN A909

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNSGKFNEKNMNFFDSRIGTK
KTIKIIIFSDGQ

SEQ ID NO. 6513

STRAIN H36B

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNSGKFNEKNMNFFDSRIGTK
KTIQ

SEQ ID NO. 6514

STRAIN 18RS21

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNSGKFNEKNMNFFDSRIGTK
KTIKIIIFSDGQE

SEQUENCE LISTING

KIQ

SEQ ID NO. 6515

STRAIN CJB110
 GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVK
 ISFNDKKSIVYNITHNLESKKNYSGNFNEKNMNFDSRIGTKKTIKIIIFSDGQEKIQ

SEQ ID NO. 6516

STRAIN JM9130013
 GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDW
 HCTVKISFNDKKSIVYNITHNLESKKNYSGFNEKNMNFDSRIGTKKTIKIIIFSDGQE
 KIQ

SEQ ID NO. 6517

STRAIN 1169NT frame: 1
 GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
 NDKKSIVYNITHNLESKKNYSGFNEKNMNFDSRIGTKKTIKIIIFSDGQEKIQ

SEQ ID NO. 6518

STRAIN M781 frame: 1
 GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
 NDKKSIVYNITHNLESKKNYSGFNEKNMNFDSRIGTKKTIKIIIFSDGQEKIQ

SEQ ID NO. 6601

STRAIN 2603

TTGACAAGGCATATAAAATTCTATACTAAATTACAAAATGAAGGAGAGGAACTATG
 GAAATACTGATTGCAGGTGGTAGTGGTTTTAGGAAAGCAGATAATAAAAGCAGCGTT
 ACAAAAGGGCATAAAAGTGGCTTACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAG
 GATCCTAGATTAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCTTAAAG
 GACAGAACTTTGATATATTAAATTGACTGTATTGGAGCGATTAGCCAACTCAACTAGAT
 GAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCAGTCTGTACAAAAATCAAATACCA
 AAGTTAGTTATATTTCAGCCAACAGCGGTATTAGCTTACATTAAAGTAAAGGAAG
 GCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTGTAAGGACAGGTTGATG
 TATGGTAAGAGCGACCTCTCGATTTCAGCCAAGCTGATAAAAGTTATTAGTCAT
 TTGCTTCTAGGTATTGTTGACAAAAGGTCTTCAACTAAGGTTGATAGTGGCA
 GAAGCAATCGTTACTACGCTTAGGAAAAACCAACCCAAAAATCCTTCTATTGAAGAA
 TTAATAATAAA

SEQ ID NO. 6602

STRAIN 090

ACAAGGCATATAAAATTCTATACTAAATTACAAAAT
 GAAGGAGAGGAACTATGAAATACTGATTGCAGGTGGTAGTGGTTTT
 AGGAAAGCAGATAATAAAAGCAGCGTTACAAAAGGGCATAAAGTGGCTT
 ACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTA
 ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCTTAAAG
 CAGAACCTTGATATATTAAATTGACTGTATTGGAGCGATTAGCCAACTC
 AACTAGATGAGCTTAAAGCAACCCAAAAGCAGTAGCAGTCTGT
 CACAAAAATCAAATACAAAGTTAGTTATATTCAAGCCAACAGCGGCTA
 TTCAAGGCTGTTACATTAAAGGAAAGGAGCAGACAGATAATCAAAGCAA
 CGGGTCTGGATTATCTTTGTAAGGACCAAGGTGATGTTGAGAG
 CGACCTCTCGATTTCAGCCAAGCTGATAAAAGTTATTAGTCATT
 GCTTCTAGGTATTGTTGACAAAAGGTCTTCAACTAAGGTTGTA
 TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAACCAACCCAAAA
 ATCCTTCTATTGAAGAATTAAATAAA

SEQ ID NO. 6603

STRAIN A909

ACAAGGCATATAAAATTCTATACTAAATTACAAAATG
 AAAGGAGAGGAACTATGAAATACTGATTGCAGGTGGTAGTGGTTTT
 GGAAGCAGATAATAAAAGCAGCGTTACAAAAGGGCATAAAGTGGCTT
 CCTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTA
 CCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCTTAAAGAGAC
 AGAACCTTTGATATATTAAATTGACTGTATTGGAGCGATTAGCCAACTCA
 ACTAGATGAGCTTAAAGCAACCCAAAAGCAGTAGCAGTCTGTC

SEQUENCE LISTING

ACAAAAAATCAAATACCAAAAGTTAGTTATTTAGCCAACAGCGGCTAT
 TCAGCTTACATTAAAGTAAAGGAGAGCAGAGATAATCAAAGCAAG
 CGGTCTGGATTATCTTTGTAAGACCAGGTTGATGTATGGTGAAGAGC
 GACCTCTCTCGATTTCCAAGCCAAGTGTATAAAGTTATTTAGTCATTG
 CCTTCTTAGGTATTGTTGACAAAAGGTCTTCCAACTAAGGTTGTGAT
 AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAACCAACCCAAAAAA
 TCCCTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6604

STRAIN H36B

TATAAAAATTCTATACAAATTACAAAATGAAGGGAGAGGAACATATGG
 AAATACTGATTGCAGGTGGTAGTGGTTTTAGGAAAGCAGATAATAAA
 GCAGCGCTTACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGG
 TAAAGGTGATATATTAAAGGATCCTAGATTAACCTACATTAGGGGAGATA
 TTACAGAAGCTGATAAGATTCAAGACAGAACTTTGATATATTAA
 ATTGACTGTATTGGGAGATTAAGCCCAATCAACCTAGATGAGCTTAACGT
 TAAAGCAACCCAAAAGCAGTAGCAGTGTCAACAAAATCAAATACCAA
 AGTTAGTTATATTCAAGGCAACAGCGGCTATTAGCTTACATTAAAGT
 AAAAGGAAGGGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTT
 TGTAAGACCAGGTTGATGTATGGTGAAGAGCGACCTCTCGATTTC
 AAGCCAAGTGTATAAAGTTAGTCAGGCTTCTAGGTATTGTT
 GTACAAAAGGTCTTCCAACTAAGGTGTGATAGTGGCAGAAGCAATCGT
 TACTACGCTTAGGAAAAACCAACCCAAAAATCCTTCTATTGAAGAAT
 TAAATAATAAA

SEQ ID NO. 6605

STRAIN 18RS21

ACAAGGCATATAAAAATTCTATACAAATTACAAAAT
 GAAGGGAGGGAACTATGAAACTATGATTGCAGGTGGTAGTGGTTTT
 AGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
 ACTTATCAAGACATGAAGGTAAGGTGATATATTAAAGGATCCTAGATTA
 ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTAGAAGA
 CAGAACTTTGATATATTAAAGTACTGTATTGGAGCGATTAAGCCAAATC
 AACTAGATGAGCTTAAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGT
 CACAAAATCAAATACCAAAAGTTAGTTATATTCAAGCCAACAGCGGCTA
 TTCAGCTTACATTAAAGGAAAGGAGCAGAGCAGATAATCAAAGCAA
 CGGGTCTGGATTATCTTTGTAAGACCAGGTTGATGTATGGTGAAGAG
 CGACCTCTCTCGATTTCAGGCAAGTGTATAAAGTTATTAGTCATT
 GCCTTCTTAGGTATTGTTGACAAAAGGTCTTCCAACTAAGGTTGTGA
 TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAACCAACCCAAAAA
 ATCCTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6606

STRAIN M732

CAAATGAAGGAGAgGGAACATATGgAAATACTGATTGCAGGTGGTAGTGG
 TTTCTAGGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGG
 TGGCTTACTTATCAAGGCATGAAGGTAAGGTGATATATTAAAGGATCCT
 AGATTAACCTACATTAAAGGGAGATATTACAGAAGCTGATAAGATTCA
 AGAACATAGAAATTGATATATTAAAGTACTGTATTGGAGCGATTAAGC
 CCAATCAACTAGATGAGCTTAAAGCAACCCAAAAGCAGTAGCA
 CTCTGTACACAAAATCAAATACCAAAAGTTAGTTACATTCAAGCCAATAG
 CGGTATTAGCTTACATTAAAGGAAAGGAGCAGAGCAGATAATCA
 AAGCAAGCGGTCTGGATTATCTTTGTAAGACCAGGTTGATGTATGGT
 GAAGAGCGACCTCTCGATTTCAGGCAAGTGTATAAAGTTATTAG
 TCATTTGCCTTCTTAGGTATTGTTGACAAAAGTCTTCCAACTAAGG
 TTGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACT
 CAAAAATCCTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6607

STRAIN COH1

ACAAGGCATATAAAAATTCTATACAAATTAC
 AAAATGAAGGGAGGGAACTATGAAATACTGATTGCAGGTGGTAGTGGT
 TTTCTAGGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGG
 GGCTTACTTATCAAGGCATGAAGGTAAGGTGATATATTAAAGGATCCTA

SEQUENCE LISTING

GATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCACTTA
 GAACATAGAAATTGATATATTAAATTGACTGTATTGGAGCGATTAAGCC
 CAATCAACTAGATGAGCTAACGTTAACAGCAACCCAAAAGCAGTAGCAC
 TCTGTCAACAAAATCAAATACCAAAAGTTAGTTACATTTCAAGCCAATAGC
 GGCTATTCAAGCTTACATTAAGGAAAGGAAGGCAGAGCAGATAATCAA
 AGCAAGCGGTCTGGATTATCTTTGTAAGGACCGAGTTGATGTATGGTG
 AAGAGCGACCTCTCTCGATTTCAGGAAAGCTTAAAGGTTAGTATAAAATTATTTAGT
 CATTGCGCTTCTTAGGTATTGTTGTAACAAAAGCTTTCAACTAAGGT
 TGTGATAGTGGCAGAAGCAATCGTTACTCGCTTAGGAAAAACCAACTC
 AAAAATCCTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6608

STRAIN M781

ACAAGGCATATAAAAATTCTATACAAATTTC
 AAATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTT
 TTCTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGTG
 GCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTAAAGGATCCTAG
 ATTAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCACTTAG
 AACATAGAAATTGATATTAAATTGACTGTATTGGAGCGATTAAGGCC
 AATCAACTAGATGAGCTAACGTTAACAGCAACCCAAAAGCAGTAGCACT
 CTGTCACAAAATCAAATACCAAAAGTTAGTTACATTTCAAGCCAATAGCG
 GCTATTCAAGCTTACATTAAGGAAAGGAAGGCAGAGCAGATAATCAA
 GCAAGCGGTCTGGATTATCTTTGTAAGGACCGAGGTTGATGTATGGTG
 AGAGCGACCTCTCTCGATTTCAGGAAAGCTTAAAGGTTAGTATAAAATTATTTAGTC
 ATTGCGCTTCTTAGGTATTGTTGTAACAAAAGCTTTCAACTAAGGT
 GTGATAGTGGCAGAAGCAATCGTTACTCGCTTAGGAAAAACCAACTCA
 AAAAATCCTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6609

STRAIN 1169NT

ACAAGGCATATAAAAATTCTATACAAATTTC
 ATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTT
 TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC
 TTACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGAT
 TAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCACTTAGAA
 GACAGAACTTTGATATATTAAATTGACTGTATTGGAGCGATTAAGCCAA
 TCAACTAGATGAGCTAACGTTAACAGCAACCCAAAAGCAGTAGCACTCT
 GTCACAAAATCAAATACCAAAAGTTAGTTACATTTCAAGCCAACAGCGGC
 TATTCAAGCTTACATTAGAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGC
 AAGCGGTCTGGATTATCTTTGTAAGGACCGAGGTTGATGTATGGTGAAAG
 AGCGACCTCTCTCGATTTCAGGAAAGCTTAAAGGTTAGTATAAAATTATTTAGTCAT
 TTGCGCTTCTTAGGTATTGTTGTAACAAAAGGTCTTCAACTAAGGTTG
 GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGACAAAACCAACTCAA
 AAAATCCTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6610

STRAIN CJB110

ACAAGGCATATAAAAATTCTATACAAATTTC
 ATGAAGGAGAGGGAACTATGGAAATACTGATTGCAGGTGGTAGTGGTT
 TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGTGGC
 TTACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGAT
 TAACCTACATTAAGGGAGATATTACAGAAGCTGATAAGATTCACTTAGAA
 GACAGAACTTTGATATATTAAATTGACTGTATTGGAGCGATTAAGCCAA
 TCAACTAGATGAGCTAACGTTAACAGCAACCCAAAAGCAGTAGCACTCT
 GTCACAAAATCAAATACCAAAAGTTAGTTATATTTCAGCCAACAGCGGC
 TATTCAAGCTTACATTAAAGTAAAAGGAAGGCAGAGCAGATAATCAAAGC
 AAGCGGTCTGGATTATCTTTGTAAGGACCGAGGTTGATGTATGGTGAAAG
 AGCGACCTCTCTCGATTTCAGGAAAGCTTAAAGGTTAGTATAAAAGTTATTTAGTCAT
 TTGCGCTTCTTAGGTATTGTTGTAACAAAAGGTCTTCAACTAAGGTTG
 GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGACAAAACCAACCCAAA
 AAAATCCTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6611

STRAIN JM9130013

SEQUENCE LISTING

ACAAGGCATATAAAATTCATACTAAATTTACAAAATG
 AAGGAGAGGAACTATGAAACTGATTGCGAGGTGGTAGTGGTTTTA
 GAAAGCAGATAATAAAGCAGCGTTACAAAAGGGCATAAAGTGGCTTA
 CTTATCAAGACATGAAGGTAAAGGTGATATTTAAGGATCTAGATTAA
 CcTACATTAGGGAGATATTACAGAACGCTGATAAGATTCTAGATTAA
 AGAACTTTGATATATTAAATTGACTGTATTGGAGCGATTAAGCCCAATCA
 ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGTC
 ACAAAAATCAAATACCAAAGTTAGTTATTTAGCCAACAGCGGCTAT
 TCAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
 CGGTCTGGATTATCTTTGTAAGACCAGGTTGATGTATGGTGAAGAGC
 GACCTCTCTGATTTCCAAGCCAAGTGTATAAAGTTATTAGTCATTG
 CCtTTCTTAgtATTGTTGACAAAGGTCTTCAACTAAGGTTGTGAT
 AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAACCAACCCAAAAAA
 TCCTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6612

STRAIN 2603 frame: 1

TRHIKISILNLQNEGEGETMEILIAAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLYIRGDITEADKIHLEDRFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPK
 LVYISANSGYSAYIKSKRKAQIIKASGLDYLFPVPGMYGEERPLSIFQAKC1KLFSHL
 PFLGIVVQKVFPKVVIVAEAVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6613

STRAIN 090 frame: 1

TRHIKISILNLQNEGEGETMEILIAAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLYIRGDITEADKIHLEDRFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPK
 LVYISANSGYSAYIKSKRKAQIIKASGLDYLFPVPGMYGEERPLSIFQAKC1KLFSHL
 PFLGIVVQKVFPKVVIVAEAVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6614

STRAIN A909 frame: 1

TRHIKISILNLQNEGEGETMEILIAAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLYIRGDITEADKIHLEDRFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPK
 LVYISANSGYSAYIKSKRKAQIIKASGLDYLFPVPGMYGEERPLSIFQAKC1KLFSHL
 PFLGIVVQKVFPKVVIVAEAVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6615

STRAIN H36B frame: 2

IKISILNLQNEGEGETMEILIAAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPR
 TYIRGDITEADKIHLEDRFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPKLVY
 ISANSGYSAYIKSKRKAQIIKASGLDYLFPVPGMYGEERPLSIFQAKC1KLFSHLPFL
 GIVVQKVFPKVVIVAEAVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6616

STRAIN 18RS21 frame: 1

TRHIKISILNLQNEGEGETMEILIAAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLYIRGDITEADKIHLEDRFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPK
 LVYISANSGYSAYIKSKRKAQIIKASGLDYLFPVPGMYGEERPLSIFQAKC1KLFSHL
 PFLGIVVQKVFPKVVIVAEAVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6617

STRAIN M732 frame: 1

QNEGEGETMEILIAAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKDPRLYIKGDIT
 EADKIHLEHRNFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPKLVYISANSGYS
 AYIKSKRKAQIIKASGLDYLFPVPGMYGEERPLSIFQAKC1KLFSHLPFLGIVVQKV
 PTKVVIVAEAVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6618

STRAIN COH1 frame: 1

TRHIKISILNLQNEGEGETMEILIAAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIFKD
 PRLYIKGDITEADKIHLEHRNFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPK
 LVYISANSGYSAYIKSKRKAQIIKASGLDYLFPVPGMYGEERPLSIFQAKC1KLFSHL
 PFLGIVVQKVFPKVVIVAEAVTSLRKKPTQKILSIEELNNK

SEQUENCE LISTING

SEQ ID NO. 6619

STRAIN M781 frame: 1

TRHIKISILNLQNEGEGETMEILIAGGSGFLGQIIKAALTGHKVAYLSRHEGKGDIFKD
 PRLTYIKGDITEADKIHLEHRNFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPK
 LVYISANSGYSAYIKSKRKAQEIIKASGLDYLFRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPKVVIVAEAIVTSLRKPKTQKILSIEELNNK

SEQ ID NO. 6620

STRAIN 1169NT frame: 1

TRHIKISILNLQNEGEGETMEILIAGGSGFLGQIIKAALTGHKLAYLSRHEGKGDIFKD
 PRLTYIKGDITEADKIHLEDRTFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPK
 LVYISANSGYSAYIRSKRKAQEIIKASGLDYLFRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPKVVIVAEAIVTTLRKPKTQKILSIEELNNK

SEQ ID NO. 6621

STRAIN CJB110 frame: 1

TRHIKISILNLQNEGEGETMEILIAGGSGFLGQIIKAALTGHKVAYLSRHEGKGDIFKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPK
 LVYISANSGYSAYIKSKRKAQEIIKASGLDYLFRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPKVVIVAEAIVTTLRKPKTQKILSIEELNNK

SEQ ID NO. 6622

STRAIN JM9130013 frame: 1

TRHIKISILNLQNEGEGETMEILIAGGSGFLGQIIKAALTGHKVAYLSRHEGKGDIFKD
 PRLTYIRGDITEADKIHLEDRTFDILIDCIGAIKPQLDELNVKATQKAVALCHKNQIPK
 LVYISANSGYSAYIKSKRKAQEIIKASGLDYLFRPGLMYGEERPLSIFQAKCIKLFSHL
 PFLGIVVQKVFPKVVIVAEAIVTTLRKPKTQKILSIEELNNK

SEQ ID NO. 6701

STRAIN 090

CAATAACAAACATTGAAAATAAAAAGTTAGCTTGGTTAGCACGA
 TCTGGAGAACCGCCTGCACGTTGTTAGCTAAGTTAGGAGCAATAGTGAC
 AGTTAATGATGGCAACCAATTGATGAAAATCCAACAGCACAGTCAGTCTTGT
 TGGAAAGAGGTATTAAAGTGGTTGTTAGCTCATCCTTAAAGTGGTTAGCTAAGTGGAA
 GATGAGGATTGTTACATGATGAAAATCCAGGAATACCTTATAACAA
 TCCTATGGTCAAAAAAGCATTAGAAAACAAATCCGTGTTGACTGAAG
 TGGATTAGCATACTTAGTTCAGAACCTCAGCTAATAGGTATTACAGGC
 TCTAACGGAAAAGACAACGACAACGATGATTGAGCAAGTCTTAAATGC
 TGGAGGTCAAGAGAGGTTAGCTGGAATATCGGCTTCTGCTAGTG
 AAGTTGTTCAAGGCTGCGGATGATAAGATATTCTAGTTATGGAATTATCA
 AGTTTCACTGCTAATGGGAGTTAAGGAATTCTGCTCATATTGCACTGAA
 TACTAATTAAATGCAACTCATTTAGATTATCATGGGTCTTTGAAGATT
 ATGTTGCTGCAAAATGGAAATATCCAATCCTTAAATGCTTCTGATT
 TTGGTACTTAATTAAATCAAGGTATTCTAAAGAGTTAGCTAAAGACTAC
 TAAAGCAACAATGTTCTTCTACTACGGAAAAGTTGATGGTGCT
 ACGTACAAGACAAGCAACTTTCTATAAAGGGGAGAATATTATGTTAGTA
 GATGACATTGGTGTCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
 TATTGCGGTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
 CTTTAAGCAATTGGAGGTAAACACCGCTTGCACATCACTCGGTAAG
 GTTCATGGTATTAGTTCTATAACGACAGCAAGTCACAACTATATTGGC
 AACTCAAAAAGCATTATCTGGCTTGTATAACTAAAGTTATCCTAATTG
 CAGGGAGGTCTGATCGGTAATGAGTTGATGATAACAGGATATC
 ACTGGACTTAAACATATGTTAGGGAAATCGGCATCTCGAGTAA
 ACGTGCTGCAACAAAGCAGGAGTAACCTTATAGCGATGCTTGTAGTTA
 GAGATGCGGTACATAAAGTTATGAGGTGGCACAAACAGGGGATGTTATC
 TTGCTAAGTCCTGCAAAATGCATCATGGGACATGTATAAGAATTGCAAGT
 CCGTGGTGTGATTCAATTGATACTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6702

STRAIN A909

CAATAACAAACATTGAAAATAAAAAGTTAGCTTGGTTAGCACGA
 TCTGGAGAACGCTGCTGCACGTTGTTAGCTAAGTTAGGAGCAATAGTGAC
 AGTTAATGATGGCAACCAATTGATGAAAATCCAACAGCACAGTCAGTCTTGT
 TGGAAAGAGGTATTAAAGTGGTTGTTAGCTCATCCTTAAAGTGGTTA

SEQUENCE LISTING

GATGAGGAGTTTGTACATGATTAACCCAGGAATACCTTATAACAA
 TCCTATGGTCAAAAAGCATTAGAAAAACAAATCCCTGTTTGACTGAAG
 TGGAAATTAGCATACTTAGTTCAGAATCTCAGCTAATAGGTATTACAGGC
 TCTAACGGAAAAGCACAACGACAACGATGATTGAGAAGTCCTAAATGC
 TGGAGGTAGAGGTTGTTAGCTGGAATATCGGCTTCTGCTAGTG
 AAGTTGTTAGCTGGAATGATAAAAGATACTCTAGTTATGGAATTATCA
 AGTTTTCAGCTAATGGAGGTTAAGGAATTTCGCTCATATTGCACTAAT
 TACTAATTAAATGCCACTCATTAGATTATCATGGGCTTCTGATTGAGATT
 ATGGTGCTGAAAATGGAATATCCAAATCAAATGCTTCACTGATT
 TTGGTACTTAATTAACTAAGGTATTCTAAAGAGTTAGCTAAACTAC
 TAAAGCaACAATCGTCCCTCTACTACGGAAAAAGTTGATGGTCTT
 ACGTACAAGACAAGCAACTTTCTATAAAGGGAGAATATTATGTCAGTA
 GATGACATTGGTGTCCCAGGAAGGCCATAACGTAnAGAATGCTCTAGCAAC
 TATTGCGGTTGCTAAACTGGTGTGATCAGTAATCAAGTTATTAGAAA
 CTTAACGAAATTGGAGGTTGAAACACCGCTTGCACACTCGGTAAG
 GTTCACTGGTATTAGTTCTATAACGACAGCAAGTCAACTAATATATTGGC
 AACTACAAAAGCATTATCTGGCTTGTAAATACTAAAGTTATCCTAATTG
 CAGGGAGGTCTGATCGCGTAATGAGTTGATGATTGATACCAAGATA
 ACTGGACTTAAACATATGGTTGTTAGGGAAATCGGCATCTGAGTAA
 ACGTGCTGCACAAAAGCAGGAGTAACCTATAGCGATGCTTAGATGTTA
 GAGATGCGGTACATAAAGCTTATGAGGTGGCACAAACAGGGCATGTTAC
 TTGCTAAGTCTGCAAAATGCATCATGGACATGTATAAGAATTGCAAGT
 CGGTGATGATTGATACTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6703

STRAIN H36B

GGACGAGTAATGAAAACAATAACAACATTGAAAAT
 AAAAAGTTTAGTCCTGGTTAGCACGATCTGGAGAAGCTGCTGCACCG
 TTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCAT
 TTGATGAAAATCCAACAGCACAGTCTTGTGGAAGAGGGTATTAAAGTG
 GTTGTGTTAGTCATCCTTAGAATTGTTAGATGAGGATTGGTACAT
 GATTAACATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAGCAT
 TAGAAAACAAATCCCTGTTGACTGAAGTGGAAATTAGCATACTTAGTT
 TCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGAAAACGACAAC
 GACAACGATGATTGCAAGTCTTAATGCTGGAGGTCAGAGAGGTTGT
 TAGCTGGGAATATCGGCTTCTGCTAGTGAAAGTTGTTAGGCTGCAAT
 GATAAACATACTCTAGTTATGAAATTATCAAGTTTCAGCTAATGGAGT
 TAAGGAATTTCGTCCTCATATTGCACTAATTACTAATTAAATGCCAACTC
 ATTAGATTATCATGGCTTTGAAGATTATGTTGCTGAAAATGGAAT
 ATCCAAAATCAAATGCTTCATCTGATTGGTACTTAATTAAATCA
 AGGTATTCTAAAGAGTTAGCTAAACTACTAAAGCAACAATCGTCCCT
 TCTCTACTACGGAAAAGTTGATGGTGTACGACAAGACAACACTT
 TTCTATAAAAGGGGAATAATTATGTCAGTAGATGACATTGGTGTCCCAGG
 AAGCCATAACGTTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACTGG
 CTGGTATCAGTAATCAAGTTATTAGAGAAACTTAAAGCAATTGGAGGT
 GTAAACACCGCTTGCACACTCGGTAAGGTTGATGGTATTAGTTCTA
 TAACGACAGCAAG

SEQ ID NO. 6704

STRAIN 18RS21

GGACGAGTAATGAAAACAATAACAACATTG
 AAAAATAAAAAGTTTAGTCCTGGTTAGCACGATCTGGAGAAGCTGCT
 GCACGTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA
 ACCATTTGATGAAAATCCAACAGCACAGTCTTGTGGAAGAGGGTATTA
 AAGTGGTTGTTGAGTGTAGTCATCCTTAAAGTTGTTAGATGAGGATTGGT
 TACATGATTAACCCAGGAATACCTTATAACAATCCTATGGTCAAAA
 AGCATTAGAAAACAAATCCCTGTTGACTGAAGTGGAAATTAGCATACT
 TAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGAAAACG
 ACAACGACAACGATGATTGCAAGAAGTCTTAAATGCTGGAGGTCAGAGAGG
 TTGTTAGCTGGGAATATCGGCTTCTGCTAGTGAAAGTTGTTAGGCTG
 CGAATGATAAAAGACTCTAGTTAGGAAATTCAAGTTTCAGCTAATG
 GGAGTTAAGGAATTTCGTCCTCATATTGCACTAATTACTAATTAAATGCC
 AACTCATTAGATTATCATGGGCTTTGAAGGATTGTTGCTGCAAAAT
 GGAATATCCAAAATCAAATGTCCTCATCTGATTGGTACTTAATT

SEQUENCE LISTING

AATCAAGGTATTCCTAAAGAGTTAGCTAAACTACTAAAGCAACAATCGT
 TCCTTCTACTACGGAAAAAGTTGATGGTGCCTACGTACAAGACAAGC
 AACTTTCTATAAAGGGAGAATATTATGTCAGTAGATGACATTGGTGTGTC
 CCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGGGTTGCTAA
 ACTGGCTGGTATCGTAATCAAGTTATTAGAGAACTTTAACAAATTG
 GAGGTGTTAACACCGCTGCAATCACTCGGTAAGGTTCATGGTATTAGT
 TTCTATAACGACAGCAAGTCAACTAATATATTGCAACTCAAAAGCATT
 ATCTGGCTTGATAACTAAAGTTATCCTAATTGCAAGGAGGTCTGATC
 CGGTAATGAGTTGATGAATTGATACCAAGATATCACTGGACTAAACAT
 ATGGGTGTTTAGGGAAATCGGCATCTCGAGTAAACGTGCTGCACAAAA
 AGCAGGAGTAACCTATAGCGATGCTTAGATGTTAGAGATGCGGTACATA
 AAGCTTATGAGGTGGCACACAGGGCATGTTATCTGCTAAGTCCTGCA
 AATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGTGAATT
 CATTGATACTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6705

STRAIN M732

GGACGAGTAATGAAAACAATAACAAACATTGAAA
 ATAAAAAAAGTTTAGTCCTGGTTAGCACGATCTGGAGAACCGCTGCA
 CGTTGTTAGCTAAGTTAGGAGCAATAGTGCAGCTTAATGATGGCAAACC
 ATTGATGAAAATCCAACAGCACAGCTTGTGGAGAGGGTATTAAAG
 TGGTTGTTGAGTGCATCCTTCTAGAATTGTTAGATGAGGATTGTTAC
 ATGATTAAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAGC
 ATTAGAAAACAATCCCTGTTGACTGAAGTGGAAATTAGCATACTTAG
 TTTCAGAATCTCAGCTAATAGGTATTACAGGCTTAACGGAAAACGACA
 ACCACAACGATGATTGCAAGTCTTAATGCTGGAGGTAGAGGAGGTT
 GTTAGCTGGGAATATCGGCTTCTGCTAGTGAAGTTGTTCAAGGCTGCG
 aTGATAAAAGATATTCTAGTTATGAAATTATCAAGTTTCAGCTAATGGGA
 GTTAAGGAATTTCGTCCTCATATTGCAAGTAAATTACTAATTAAATGCCAAC
 TCAATTAGATTATCATGGCTTTGAAAGATTATGATGCTGCAAATGGA
 ATATCCAAAATCAAATGCTTCATCTGATTGTTGGTACTTAATTAAAT
 CAAGGTATTCTAAAGAGTTAGCTAAAACACTAAAGCAACAAATCGTTCC
 TTTCTCTACTACGGAAAAGTTGATGGTGCCTACGTACAAGACAAGCAAC
 TTTCTATAAAGGGAGAATATTATGCAAGTAAATTGCAACTCAAAAGCATTATC
 GGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTGCTAAACT
 AGCTGGTATCAGTAATCAAGTTATTAGAGAACTTAAAGCAATTGGAG
 GTGTTAACACCGCTTGCATCACTCGGTAAGGTCATGGTATTAGTTCT
 TATAACGACAGCAAGTCAACTAATATTGGCAACTCAAAAGCATTATC
 TGGCTTGTATAACTAAAGTTACCTAATTGCAAGGAGGTCTGATCGCG
 GTAATGAGTTGATGAATTGATACCAAGATATCACTGGACTAAACATATG
 GTGTTTGTGGAGATCGGCATCTCGAGTAAACGTGCTGCACAAAAAGC
 AGGAGTAACCTATAGCGATGCTTAGATGTTAGAGATGCGGTACATAAG
 CTTATGAGGTGGCACACAGGGCATGTTATCTGCTAAGTCCTGCAATT
 GCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGTGAATTCAT
 TGATACTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6706

STRAIN COH1

GGACGAGTAATGAAAACAATAACAAACATTG
 AAATAAAAAGTTTAGTCCTGGTTAGCACGATCTGGAGAACCGCTG
 CACGTTGTTAGCTAAGTTAGGAGCAATAGTGCAGCTTAATGATGGCAA
 CCATTGATGAAAATCCAACAGCACAGCTTGTGGAGAGGGTATTAA
 AGTGGTTGTTGAGTGCATCCTTCTAGAATTGTTAGATGAGGATTGTT
 ACATGATTAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAA
 GCATTAGAAAACAATCCCTGTTGACTGAAGTGGAAATTAGCATACTT
 AGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTTAACGGAAAACGA
 CAACGACAAACGATGATTGCAAGTCTTAATGCTGGAGGTAGAGGAGG
 TTGTTAGCTGGAAATATCGGCTTCTGCTAGTGAAGTTGTTCAAGGCTG
 GGAATGATAAAAGATATTCTAGTTATGAAATTATCAAGTTTCAGCTATGG
 GAGTTAAGGAATTTCGTCCTCATATTGCAAGTAAATTACTAATTAAATGCCA
 ACTCATTAGATTATCATGGCTTTGAAAGATTATGTTGCTGCAAATG
 GAATATCCAAAATCAAATGCTTCTGATCTGATTGTTGGTACTTAATT
 ATCAAGGTATTCTAAAGAGTTAGCTAAAACACTAAAGCAACATCGT
 CCTTCTACTACGGAAAAGTTGATGGTGCCTACGTACAAGACAAGCA

SEQUENCE LISTING

ACTTTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGGTGTCC
 CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAA
 CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTGG
 AGGTGTTAAACACCGCTTGCACACTCGGTAAAGGTTATGGTATTAGT
 TCTATAACGACAGCAACTAACTATATTGCGCAACTCAAAAGCATTA
 TCTGGCTTGTATAACTAAAGTTATCCTAATTGCGAGGAGGCTTGATCG
 CGGTAAATGAGTTGATGATGATACCAAGAGATATCACTGGACTTAAACATA
 TGTTGTTAGGGAAATCGGCATCTCGAGTAAACAGTGCTGCACAAAAA
 GCAGGAGTAACCTATAGCGATGCTTAGATGTTAGAGATGCGGTACATAA
 AGCTTATGAGGTGGCACACAGGGCGATGTTATCGCTAAGTCTGCAA
 ATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGTGATGAATT
 ATTGATACTTCGAAA

SEQ ID NO. 6707

STRAIN M781

GGACGAGTAATGAAAACAATAACAAACATT
 TGGAAAATAAAAAGTTTACTCCTGGTTAGCACGATCTGGAGAAGCCG
 CTGCACGTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGCC
 AAACCATTTGATGAAAATCCAACAGCACAGTCTTGTGGAGAGGGTAT
 TAAAGTGGTTGTGGTAGTCATCCTTAGAATTGTTAGATGAGGATTTT
 GTTACATGATTAACCCAGGAATACCTTATAACAATCCTATGGTCAA
 AAAGCATTAGAAAACAATCCCTGTTTGACTGAAGTGGATTAGCATA
 CTAGTTCAAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAA
 CGACAACGACAACGATGTTGAGAAGTCTTAAATGCTGGAGGTCAGAGA
 GGGTTGTTAGCTGGAAATTCGGCTTCTGCTAGTGAAGTTGTTCAAGG
 TGGGGATGATAAGATATTCTAGTTATGAAATTATCAAGTTTCAGCTAA
 TGGGAGTTAGGAATTTCGTCCTCATATTGCAAGTAATTACTAATTAAATG
 CCAACTCATTAGATTATCATGGGTCTTGTAAAGGATTATGTTGCTGCAA
 ATGGAATATCCAAAATCAAATGTCATCTGATTTTGGTACTTAATT
 TTAATCAAGGTATTTCTAAAGAGTTAGCTAAACTACTAAAGCAaCAATC
 GTCTCTTCTACTACGGAAAAGTTGATGGTGTCTACGTACAAGACAA
 GCAACTTTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGGTG
 TCCCAGGAAGCCATAACGCTAGAGAATGCTCTAGCAACTATTGCGGTTGCT
 AAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTAAAGCAATT
 TGGAGGTGTTAAACACCGCTTGCACACTCGGTAAAGGTTATGGTATT
 GTTTCTATAACGACAGCAACTAAATATGGCAACTCAAAAGCA
 TTATCTGGCTTGTATAACTAAAGTTATCCTAATTGCAAGGAGGCTTGA
 TCGCGGTAAATGAGTTGATGAATTGATACCAGATATCACTGGACTTAAAC
 ATATGGTTTTAGGGAAATCGGCATCTCGAGTAAACAGTGCTGCACAA
 AAAGCAGGAGTAACTTATAGCGATGCTTAGATGTTAGAGATGCGGTACA
 TAAAGCTTATGAGGTGGCACACAGGGCGATGTTATCGCTAAGTCTG
 CAAATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGTGAA
 TTCAATTGATACTTCGAAGTCTTAGAGGAGAG

SEQ ID NO. 6708

STRAIN CJB110

GGACGAGTAATGAAAACAATAACAAACATTGA
 AAATAAAAAAGTTTACTCCTGGTTAGCACGATCTGGAGAAGCCGCTG
 CACGTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGCCAA
 CCATTGATGAAAATCCAACACAGCACAGTCTTGTGGAGAGGGTATTAA
 AGTGGTTGTGGTAGTCATCCTTAGAATTGTTAGATGAGGATTTGTT
 ACATGATTAACCCAGGAATACCTTATAACAATCCTATGGTAAAAAA
 GCATTAGAAAACAATCCCTGTTGACTGAAGTGGATTAGCATACTT
 AGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGA
 CAACGACAACGATGATTGAGAAGTCTTAAATGCTGGAGGTCAGAGAGGT
 TTGTTAGCTGGAAATATCGGCTTCTGCTAGTGAAGTTGTTCAAGGCTGC
 GGATGATAAAGATATTCTAGTTATGAAATTATCAAGTTTCAGCTAATGG
 GAGTTAAGGAATTTCGTCTCATATTGCAAGTAATTACTAATTAAATGCCA
 ACTCATTAGATTATCATGGGTCTTTGAGAATATGTTGCTGCCAAATG
 GAATATCCAAAATCAAATGTCCTCATGATTGTTGGTACTTAATT
 ATCAAGGTATTCTAAAGAGTTAGCTAAACTACTAAAGCAACAATCGT
 CCTTCTACTACGGAAAAGTTGATGGTGTCTACGTACAAGACAAGCA
 ACTTTCTATAAAGGGGAGAATATTATGTTAGTAGAGATGACATTGGTGTCC
 CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA

SEQUENCE LISTING

CTAGCTGGTATCAGTAATCAAGTTAGAGAAACTTAAAGCAATTTGG
 AGGTGTTAACACCGCTGCAATCACTCGGTAAAGGTCATGGTATTAGTT
 TCTATAATGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTA
 TCTGGCTTGTATAACTAAAGTTATCCTAATTGCAGGAGGTCTGATCG
 CGGTAAATGAGTTGATGAATTGATACAGATATCACTGGACTTAAACATA
 TGGTTGTTAGGGATCGGCATCTCGAGTAAACGTCGACAAAAAA
 GCAGGAGTAACCTATAGCGATGCTTAGATGTTAGAGATGCGGTACATAA
 AGCTTATGAGGTGGCACACAGGGCATGTTATCTGCTAAGTCCTGCAA
 ATGCATCATGGGACATGTATAAGAATTGAAAGTCGAACTCCGTGATGAATT
 ATTGATACTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6709

STRAIN 1169NT

CAATAACACATTGAAAATAAAAAAGTTAGTCCTGGTTAGCACGA
 TCTGGAGAACGGCTGCACGTTGTTAGCTAAGTTAGGAGCAATAGTGAC
 AGTAATGATGGAAACCAATTGATGAAAATCCAACAGCACAGTCCTTGT
 TGGAAAGGGTATTAAAGGTTGTTAGTCATCCTTAAAGGTTA
 GATGAGGATTGTTGTTACATGATGATGAAAATCCAGGAATACCTTATAACAA
 TCCTATGGTCAAAAAGCATTAGAAAAACAAATCCCTGTTTGAAGTGAAG
 TGGAAATTAGCATACCTAGTTCAGAATCTCAGCTAATAGGTATTACAGGC
 TCTAACGGGAAACGACAACGACAACGATGATTGAGAAGTCCTGAAATGC
 TGGAGGTAGAGAGGTTGTTAGCTGGAAATATCGGCTTCCTGCTAGTG
 AAGTTGTTCAAGGCTGCGGATGATAAAAGATACTCTAGTTATGAAATTATCA
 AGTTTCAGCATATGGGAGTTAAGGAATTCTGCTCATATTGAGTAAT
 TACTAATTAAAGCCAACCTATTAGATTATCATGGGCTTTGAAGAATT
 ATGTTGCTGCAAAATGGAATATCCAAATCAAATGCTTCACTGATT
 TTGGTACTTAATTAACTAAGGTTATTCTAAAGGTTAGCTAAACACTAC
 TAAAGCAACAACTCGTCCTTCTACTACGGAAAAGTTGATGGTCTT
 ACGTACAAGACAAGCAACTTTCTATAAAGGGGAGAATATTATGTCAGTA
 GACCGACATTGGTCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
 TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
 CTTAAGCAATTGAGGTTAAACACCGCTGCAATCACTCGGTAAAG
 GTTCATGGTATTAGTTCTATAACGACAGTAAGTCAACTAATATATTGGC
 AACTCAAAAAGCATTATCTGGCTTGTATAACTAAAGTTATCCTAATTG
 CAGGAGGTCTTGTGATCGCGGAATGAGTTGATGAATTGATACCAGATATC
 ACTGGACTTAAGCATATGGTTGTTAGGGGAATCGGCATCTCGAGTAAA
 ACGTGCTGCACAAAAGCAGGAGTAACCTATAGCAATGCTTAgATGTTA
 GAGATGCGATGACATAAGCTTATGAGGTGGCACACAGGGCATGTTATC
 TTGTTAGTCTGCGAATGCACTGATGGACATGTATAAGAATTGAAAGT
 CGTGGTGTGATGAATTCAATTGATACTTCG

SEQ ID NO. 6710

STRAIN JM9130013

GGACGAGTAATGAAAACAATAACAACA
 TTTGAAAATAAAAAGTTAGTCCTGGTTAGCACGATCTGGAGAAGC
 TGCTGCACGTTGTTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATG
 GCAAAACATTGATGAAAATCCAACAGCACAGTCCTTGTGAAAGAGGGT
 ATTAAAGTGGTTGTGGTAGTCATCCTTAAAGTGTAGATGAGGATT
 TTGTTACATGATTAAAATCCAGGAATACCTTATAACAATCCTATGGTCA
 AAAAGCATTAGAAAAACAAATCCCTGTTTGACTGAAGTGGAAATTAGCA
 TACTTAGTTCTCAGCTAATAGGTATTACAGGCTCTAACGGGAA
 AACGACAACGACAACGATGATTGAGAAGTCTTAAATGCTGGAGGTAGA
 GAGGTTGTTAGCTGGGAATATCGGCTTCTGCTAGTGAAGTTGTTAG
 GCTGCGAATGATAAGATACTCTAGTTATGGAATTATCAAGTTTCAGCT
 AATGGGAGTTAAGGAATTCTGCTCATATTGCAAGTAATTACTAATTAA
 TGCCAACCTATTAGATTATCATGGGCTTTGAAGATTATGTTGCTGCA
 AAATGGAATATCCAAAATCAAATGTCCTCATCTGATTGGTACTTAA
 TTTAATCAAGGTTATTCTAAAGAGTTAGCTAAACTACTAAAGCAACAA
 TCGTTCCCTTCTACTACGGAAAAGTTGATGGTCTACGTACAAGAC
 AAGCAACTTTCTATAAAGGGAGAATATTATGTCAGTAGATGACATTGG
 TGCCCCAGGAAGCCATAACGTTAGAGAATGCTAGCAACTATTGCGGTTG
 CTTAAACTGGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTAAAGCAAT
 TTTGGAGGTGTTAACACCGCTTGCAATCACTCGGTAAAGGTTATGGTAT
 TAGTTCTATAACGACAGCAAGTCAACTAATATTGCAACTCAAAAAG

SEQUENCE LISTING

CATTATCTGGCTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTT
 GATCGCAGTAATGAGTTGATGAATTGATACCAGATATCACTGGACTTAA
 ACATATGGTTAGGGAAATCGGCATCTCGAGTAAAACGGTGCAC
 AAAAAGCAGGAGTAACCTATAGCGATGCTTAGATGTTAGAGATGCGGTAA
 CATAAAGCTTATGAGGTGGACAACAGGGCAGTGTATCTGCTAAGTCC
 TGCAAATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGTGATG
 AATTCAATTGATACTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6710

STRAIN 2603

ggacgagtaatgaaaacaataacaacatttggaaaataaaaaagtttagt
 ccttggtagcagatctggagaagctgctgcacgttttagctaagt
 taggacaatgtgacagttaatgtggcaaacattttagaaaaatcca
 acagcacagtctttgttggaaagagggtttagaaaaatccatgatc
 tcctttagatttttagatgaggatgtttagatgatgatgatgatc
 gaatacacctataacaatctatggtcaaaaagcattagaaaaacaaatc
 cctgttttactgaatgtgaaatttagcataacttagttcagaatctcagct
 aataggattacaggcttaacggaaaacgcacacgcacatgatgattt
 cagaatgtttaatgtggaggttcagagaggtttagtggatata
 ggctttccctgtctgttgcaggatgttgcaggctgcgaatgatc
 agttatggattatcaaggatcttgcataatggatggatggatattcg
 ctcatattgcataacttgcataatggatggatattcat
 gggcttttgcaggatgttgcataatggatggatattcat
 gtttcatctgttgcaggatgttgcaggatgttgcaggatgttgc
 agttatggatggatggatggatggatggatggatggatggatggat
 aatattatgtcagtagatgacattgggtgtcccgaggatggatggat
 agaatgtcttagcaacttgcgggtgtctaaactggctgttgc
 caagttattagagaaacttgcataatggatggatggatggatggat
 gcaatcactcggtaaaggatgttgcataatggatggatggatggat
 caactaatatattggcaactcaaaagcattatctggcttgcataat
 aaatggatggatggatggatggatggatggatggatggatggatggat
 attgataccatgttgcaggatgttgcaggatgttgcaggatgttgc
 gatgttttagatgttgcaggatgttgcaggatgttgcaggatgttgc
 acaggggatgttgcaggatgttgcaggatgttgcaggatgttgc
 ataagaatttgcaggatgttgcaggatgttgcaggatgttgcaggat
 cttagaggagag

SEQ ID NO. 6711

STRAIN 090 frame: 3

ITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLEEGIKVVCGS
 HPLELLDEDFCYMIKNGPIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGITGSNGK
 TTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQADDKDILVMELOSSFQLMGVKEFRPHI
 AVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSDFLVLNFNQGISKELAKTTKATIVPF
 STTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
 LSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQALSGFDNTKVILIAAGGLDRGNEFD
 ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP
 ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6712

STRAIN A909 frame: 3

ITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLEEGIKVVCGS
 HPLELLDEDFCYMIKNGPIPYNNPMVKKALEKQIPVLTEVELAYLVSESQLIGITGSNGK
 TTTTMTIAEVLNAGGQRGLLAGNIGFPASEVVQADDKDILVMELOSSFQLMGVKEFRPHI
 AVITNLMPTHLDYHGSFEDYVAAKWNIQNQMSSDFLVLNFNQGISKELAKTTKATIVPF
 STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNFXNALATIAVAKLAGISNQVIRET
 LSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQALSGFDNTKVILIAAGGLDRGNEFD
 ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP
 ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6713

STRAIN H36B frame: 1

GRVMKTITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLEEGI

SEQUENCE LISTING

KVVCGSHPLELLDEDFCYMIKNPNGIPYNNPMVKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVAQANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSDFLVLNFNQGISKELAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETSLNFGGVKHRLQSLGKVGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD

SEQ ID NO. 6714
 STRAIN 18RS21 frame: 1
 GRVMKTITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLL
 KVVCGSHPLELLDEDFCYMIKNPNGIPYNNPMVKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVAQANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSDFLVLNFNQGISKELAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETSLNFGGVKHRLQSLGKVGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
 RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTVYSDALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6715
 STRAIN M732 frame: 1
 GRVMKTITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLL
 KVVCGSHPLELLDEDFCYMIKNPNGIPYNNPMVKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVAQANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSDFLVLNFNQGISKELAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETSLNFGGVKHRLQSLGKVGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
 RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTVYSDALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6716
 STRAIN COH1 frame: 1
 GRVMKTITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLL
 KVVCGSHPLELLDEDFCYMIKNPNGIPYNNPMVKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVAQANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSDFLVLNFNQGISKELAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETSLNFGGVKHRLQSLGKVGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
 RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTVYSDALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6717
 STRAIN M781 frame: 1
 GRVMKTITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLL
 KVVCGSHPLELLDEDFCYMIKNPNGIPYNNPMVKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVAQANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNIQNMSSDFLVLNFNQGISKELAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETSLNFGGVKHRLQSLGKVGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
 RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTVYSDALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6718
 STRAIN CJB110 frame: 1
 GRVMKTITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLL
 KVVCGSHPLELLDEDFCYMIKNPNGIPYNNPMVKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVAQANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPTHLDYHGSFEEYVAAKWNIQNMSSDFLVLNFNQGISKELAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETSLNFGGVKHRLQSLGKVGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
 RGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTVYSDALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6719
 STRAIN 1169NT frame: 3
 ITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLL
 EGIKVVC

SEQUENCE LISTING

HPLELLDEDFCYMIKNPGIPYNNPMVKALEKQIPVLTEVELAYLVSESQLIGITGSNGK
 TTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAADDKDTLVMELSSFQLMGVKEFRPHI
 AVITNLMPHTLDYHGSFEDYVAAKWNIQNQMSSDFLVLNFNQGISELAKTTKATIVP
 STTEKVDGAYVQDKQLFYKGENIMSVDIGVPGSHNVENALATIAVAKLAGISNQVIRET
 LSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD
 ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSNALDVRDAVHKAYEVAQQGDVILXSP
 ANASWDMYKNEFVRGDEFIDT

SEQ ID NO. 6720

STRAIN JM9130013 frame: 1
 GRVMKTITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKFDENPTAQSLLEEGI
 KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPHTLDYHGSFEDYVAAKWNIQNQMSSDFLVLNFNQGISELAKTTK
 ATIVPSTTEKVDGAYVQDKQLFYKGENIMSVDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
 RSNEFDELIPIITGLKHMVVLGESASRVKRAAQKAGVTYSNALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNEFVRGDEFIDTFSLRGE

SEQ ID NO. 6721

STRAIN 2603 frame: 1
 GRVMKTITTFENKKVLVGLARSGEAAARLLAKLGAIVTVNDGKFDENPTAQSLLEEGI
 KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKALEKQIPVLTEVELAYLVSESQLIGI
 TGSNGKTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPHTLDYHGSFEDYVAAKWNIQNQMSSDFLVLNFNQGISELAKTTK
 ATIVPSTTEKVDGAYVQDKQLFYKGENIMSVDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLD
 RGNEFDELIPIITGLKHMVVLGESASRVKRAAQKAGVTYSNALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNEFVRGDEFIDTFSLRGE

SEQ ID NO. 6801

STRAIN 2603
 ATGGCTAAAGAGAGGGTAGATGTTCTGCCTATAAACAGGGACTTTTGATACAGGAGAG
 CAAGCGAAACCGTGGTGTATGGCAGGAATGGTGAATACGTATCAATGGAGAACGTAT
 GATAAACCGAGGTGAAAAGGTTGCAGACGATACTGAATTAAAACCTAAAAGGTGAAAACAA
 AAATATGTTAGTAGAGGTTGATTGAAATTAGAAAAAGCTTACAAGTTTGAAATTCTCA
 GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTACTGATGTTATG
 CTACAATCAGGAGCGCCTTAGTTACGCAGTAGATGTAGGAACAAATCAATTAGTTGG
 AAGTTACGTCAGGATCATCGTGGTCTATGGAACAATATAATTAGGTATGCCAA
 AAAGAAGATTCAAGGAGGGACTGCCTGAATTGCGATCGATAGATGTCATTTATCTCT
 CTTAATTGATTTCACAGCTCTAAAGAAATTAGTTAGTGGATGGTGGACAAGTAGTGGCA
 TTAATTAAACACAAATTGAGGAGCTGAGCAAATTGGTAAAGATTGTTAGTCAAA
 GACAAGTTGGTTCATGAAAGGTTGACAACAGTCAGGAAATTCTCACGAAAGATTGGA
 TATACGGTTAACATCTTGATTTGCCATTCAAGGTGGACATGAAATATTGAGTT
 TTAATGCATTGCAAAGTGTCAAGATCCACAAATCTTGCTTGACCAAATACAAGAT
 GTTATAGAAAAAGCACATAAGGAATTAGAAAAATGAAGAAGAG

SEQ ID NO. 6802

STRAIN 090
 GCTAAAGAGAGGGTAGATGTTCTGCCT
 ATAAACAGGGACTTTTGATACACGAGAGCAAGCGAAACGTTGTTATG
 GCAGGAATGGTGAATTAACGTTATCAATGGAGAACGTTATGATAAACAGG
 TGAAAAGGTTGCAGACGATACTGAATTAAAACCTAAAAGGTGAAAACAA
 AATATGTTAGTAGAGGTTGATTGAAATTAGAAAAGCTTACAAGTT
 GAAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
 TGGTTTACTGATGTTATGCTACAATCAGGAGCGCTTAGTTACGCAG
 TAGATGTAGGAACAAATCAATTAGTTGGAAGTTACGTCAGGATCATCGT
 GTTCGTTCTATGGAACAATATAATTAGGTATGCCAAAAAGAAGATT
 CAAGGAGGGACTGCCTGAATTGCGATCGATAGATGTCATTTATCTCTC
 TTAATTGATTTCACAGCTCTAAAGAAATTAGTTAGTGGATGGTGGACAA
 GTAGTGGCATTAAATTAAACACAAATTGAGCAGGTCGTGAGCAAATTG
 TAAAAATGGTATTGTCAAAGACAAGTTGGTCATGAAAAGGTTTGACAA
 CAGTGCACCAATTCAAGAAAGATTATGGATACGGTAAACATCTTGAT
 TTTCGCCCATTCAAGGTGGACATGAAATATTGAGTTTAATGCATT

SEQUENCE LISTING

GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATG
TTATAGAAAAGCACATAAGGAATTAGAAGAAAATGAAGAAGAG

SEQ ID NO. 6803

STRAIN A909

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGAATGGTGTATCAACGTTATCAATGGAGAACGTTATGATAAAACCAGGT
GAAAAGGGTGCAGACGATACTGAATTAAAACGTTAAAGGTGAAAAGGTAAA
ATATGTTAGTAGAGGGATTGAAATTAGAAAAAGCTTACAAGTGGTGT
AAATTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCTCTACGGGT
GGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTACGCAGT
AGATGAGGAACAATCAATTAGTTGGAGTTACGTCAAGGATCATCGTG
TTCGTTCTATGGAAACAATATAATTAGGTATGCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTGTCATCGATAGATGCTCATTATCTCT
TAATTTGATTTTACAGCTCTAAAGAAATTAGTTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACACAATTGAAAGCAGGTGAGCAAATTGGT
AAAAATGGTATTGTCAGAAAGCAGGTGGTGTGACAAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTGATT
TTTCGCCATTCAAGGTGGACATGGAAATTAGTGGTTAAATGCATTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
TATAGAAAAGCACATAAGGAATTAGAAGAAAATGAAGAAGAG

SEQ ID NO. 6804

STRAIN H36B

GCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGG
GACTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGGCAGGAATG
GTGATTAACGTTATCAATGGAGAACGTTATGATAAAACCAGGTGAAAAGGT
TGCAGACGATACTGAATTAAAACGTTAAAGGTGAAAAGCTAAATATGTTA
GTAGAGGGATTGAAATTAGAAAAAGCTTACAAGTGGTGTGAAATTTC
GTGAGATAAGCTAACTATAGATATTGGCGCTCTACGGGTGGTTTAC
TGATGTTATGCTACAATCAGGAGCGCGTTAGTTACGCAGTAGATGTTAG
GAACAAATCAATTAGTTGGAGTTACGTCAAGGATCATCGTGTGTTCT
ATGGAAACAATAATTAGGTATGCCAAAAAGAAGATTCAAGGAGGG
ACTGCCTGAATTGTCATCGATAGATGCTCATTATCTCTTAATTG
TTTACAGCTCTAAAGAAATTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAAACACAATTGAAAGCAGGTGAGCAAATTGGTAAAGGTTTG
TATTGTCAGAAAGCAGGTGGTGTGACAAACAGTGTGACCA
ATTTCACGAAAGATTATGGATATACGGTTAAACATCTGATTTCGCC
ATTCAAGGTGGACATGGAAATTAGTGGTTAAATGCATTGCAAAAGTG
TCAAGATCCACAAAATCTTGTGCTTGACCAAATAAGATGTTATAGAAA
AAGCACATAAGGAATTAGAAGAAAATGAAGAAGAG

SEQ ID NO. 6805

STRAIN 18RS21

GCTAAACAGAGGGTAGATGTTCTTGCCTA
TAAACAGGGACTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
CAGGAATGGTGTATCAACGTTATCAATGGAGAACGTTATGATAAAACCAGGT
GAAAAGGGTGCAGACGATACTGAATTAAAACGTTAAAGGTGAAAAGGTAAA
ATATGTTAGTAGAGGGATTGAAATTAGAAAAAGCTTACAAGTGGTGT
AAATTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCTCTACGGGT
GGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTACGCAGT
AGATGAGGAACAATCAATTAGTTGGAGTTACGTCAAGGATCATCGTG
TTCGTTCTATGGAAACAATATAATTAGGTATGCCAAAAAGAAGATTTC
AAGGAGGGACTGCCTGAATTGTCATCGATAGATGCTCATTATCTCT
TAATTTGATTTTACAGCTCTAAAGAAATTAGTGGATGGTGGACAAG
TAGTGGCATTAATTAAACACAATTGAAAGCAGGTGAGCAAATTGGT
AAAATGGTATTGTCAGAAAGCAGGTGGTGTGACAAAC
AGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTGATT
TTTCGCCATTCAAGGTGGACATGGAAATTAGTGGTTAAATGCATTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATAAGATGT
TATAGAAAAGCACATAAGGAATTAGAAGAAAATGAAGAAGAG

SEQ ID NO. 6806

SEQUENCE LISTING

STRAIN M732

GCTAAAGAGAGGGTAGATGTTCTTGCTA
 TAAACAGGGACTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGACTGGTGAACGTTATCAATGGAGAACGTTATGATAAAACCAGGC
 GAAAAGGTTGCAGACGATACTGAATTAAAACCTAAAGGTGAAAAACTAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTACAAGTTTG
 AAATTCAGTGCAGATAAGCTAACATAGATATTGGCGCCTACGGGT
 GGTGTTACTGATGTTATGCTACAATCAGGAGCGTTAGTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTGGAAGTTACGTACGGATCATCGTG
 TTGTTCTATGGAACAAATATAATTAGGTATGCCAAAAAGAAGATTTC
 AAGGAGGGACTGCCTGAATTGACATCGATAGATGTCCTCATTATCTCTC
 TAATTGATTTACAGCTCTAAAAGAAATTAGTGGATGGACAAG
 TAGTGGCATTAAATTAAACCAATTGAAAGCAGGTGAGCAAATTGGT
 AAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTGACAAC
 AGTACCAATTTCAGGAAAGATTATGGATATAACGGTTAACATCTGATT
 TTGCGCCGTTCAAGGTGGACATGGAATTAGTGGTTTAAATGCATTG
 CAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAATACAAGATGT
 TTATAGAAAAGCACATAAGGAATTAGAAAATGAAGAAGAG

SEQ ID NO. 6807

STRAIN COH1

GCTAAAGAGAGGGTAGATGTTCTTGCT
 ATAAACAGGGACTTTGATACACGAGAGCAAGCGAAACGTGGTGTATG
 GCAGGACTGGTGAACGTTATCAATGGAGAACGTTATGATAAAACCAGG
 CGAAAAGGTTGCAGACGATACTGAATTAAAACCTAAAGGTGAAAAACTAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTACAAGTTTG
 GAAATTCAGTGCAGATAAGCTAACATAGATATTGGCGCCTACGGG
 TGTTTACTGATGTTATGCTACAATCAGGAGCGTTAGTACGTACGG
 TAGATGTAGGAACAAATCAATTAGTTGGAAGTTACGTACGGATCATCGT
 GTTCGTTCTATGGAACAAATATAATTAGTGTGGTACGGTAAAGGTTTG
 CAAGGAGGGACTGCCTGAATTGACATCGATAGATGTCCTCATTATCTC
 TTAATTGATTTACCAAGCTCTAAAAGAAATTAGTGGATGGTGGACAA
 GTAGTGGCATTAAATTAAACCAATTGAAAGCAGGTGAGCAAATTGG
 TAAAATGGTATTGTCAGGAAAGATTATGGATATAACGGTTAACATCTGAT
 TTGCGCCGTTCAAGGTGGACATGGAATTAGTGGTTTAAATGCATT
 GCAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAATACAAGATG
 TTATAGAAAAGCACATAAGGAATTAGAAAATGAAGAAGAG

SEQ ID NO. 6808

STRAIN M781

GCTAAAGAGAGGGTAGATGTTCTTGCT
 ATAAACAGGGACTTTGATACACGAGAGCAAGCGAAACGTGGTGTATG
 GCAGGACTGGTGAACGTTATCAATGGAGAACGTTATGATAAAACCAGG
 CGAAAAGGTTGCAGACGATACTGAATTAAAACCTAAAGGTGAAAAACTAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTACAAGTTTG
 GAAATTCAGTGCAGATAAGCTAACATAGATATTGGCGCCTACGGG
 TGTTTACTGATGTTATGCTACAATCAGGAGCGTTAGTACGTACGG
 TAGATGTAGGAACAAATCAATTAGTTGGAAGTTACGTACGGATCATCGT
 GTTCGTTCTATGGAACAAATATAATTAGTGTGGTACGGTAAAGGTTTG
 CAAGGAGGGACTGCCTGAATTGACATCGATAGATGTCCTCATTATCTC
 TTAATTGATTTACCAAGCTCTAAAAGAAATTAGTGGATGGTGGACAA
 GTAGTGGCATTAAATTAAACCAATTGAAAGCAGGTGAGCAAATTGG
 TAAAATGGTATTGTCAGGAAAGATTATGGATATAACGGTTAACATCTGAT
 TTGCGCCGTTCAAGGTGGACATGGAATTAGTGGTTTAAATGCATT
 GCAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAATACAAGATG
 TTATAGAAAAGCACATAAGGAATTAGAAAATGAAGAAGAG

SEQ ID NO. 6809

STRAIN CJB110

GCTAAAGAGAGGGTAGATGTTCTTGCT
 TAAACAGGGACTTTGATACACGAGAGCAAGCGAAACGTGGTGTATG
 CAGGAATGGTGAACGTTATCAATGGAGAACGTTATGATAAAACCAGGT

SEQUENCE LISTING

GAAAAGGTTGCAGACGATACTGAATTAAAACAAAAGGTGAAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTG
 AAATTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTACGCAGT
 AGATGTTAGGAACAAATCAATTAGTTGGAAAGTTACGTCAAGGATCATCGT
 TTCGTTCTATGGAACAATATAATTAGGTATGCCAAAAGAAGATTTC
 AAGGAGGGACTGCCTGAATTGCACTGATCGATAGATGTCTCATTATCTCT
 TAATTTGATTTCAGCTCTAAAAGAAATTAGGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAAACCAATTGAAAGCAGGTGAGCAAATTGGT
 AAAATGGTATTGCTAAAGACAAGTTGGTTCATGAAAGGTTTGACAAC
 AGTACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTCGCCCCATTCAAGGTGGACATGGAAATTATGGAGTTTAATGCATTG
 CAAAAGTGTCAAGATCCACAAAATCTGTGCTGACCAATACAAGATGT
 TATAGAAAAGCACATAAGGAATTAAAGAAAATGAAGAAGAG

SEQ ID NO. 6810

STRAIN 1169NT

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
 TAAACAGGGACTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGACTGGTGTATCAACGTTATGATAAAACCAAGGC
 GAAAAGGTTGCAGACGATACTGAATTAAAACAAAAGGTGAAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTG
 AAATTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTACGCAGT
 AGATGTTAGGAACAAATCAATTAGTTGGAAAGTTACGTCAAGGATCATCGT
 TTCGTTCTATGGAACAATATAATTAGGTATGCCAAAAGAAGATTTC
 AAGGAGGGACTGCCTGAATTGCACTGATAGATGTCTCATTATCTCT
 TAATTTGATTTCAGCTCTAAAAGAAATTAGGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAAACCAATTGAAAGCAGGTGAGCAAATTGGT
 AAAATGGTATTGCTAAAGACAAGTTGGTTCATGAAAGGTTTGACAAC
 AGTACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTCGCCCCATTCAAGGTGGACATGGAAATTATGGAGTTTAATGCATTG
 CAAAAGTGTCAAGATCCACAAAATCTGTGCTGACCAATACAAGATGT
 TATAGAAAAGCACATAAGGAATTAAAGAAAATGAAGAAGAG

SEQ ID NO. 6811

STRAIN JM9130013

GCTAAAGAGAGGGTAGATGTTCTTGCCTA
 TAAACAGGGACTTTGATACACGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGAATGGTGTATCAACGTTATGATAAAACCAAGGT
 GAAAAGGTTGCAGACGATACTGAATTAAAACAAAAGGTGAAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTG
 AAATTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTAGTTACGCAGT
 AGATGTTAGGAACAAATCAATTAGTTGGAAAGTTACGTCAAGGATCATCGT
 TTCGTTCTATGGAACAATATAATTAGGTATGCCAAAAGAAGATTTC
 AAGGAGGGACTGCCTGAATTGCACTGATAGATGTCTCATTATCTCT
 TAATTTGATTTCAGCTCTAAAAGAAATTAGGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAAACCAATTGAAAGCAGGTGAGCAAATTGGT
 AAAATGGTATTGCTAAAGACAAGTTGGTTCATGAAAGGTTTGACAAC
 AGTACCAATTTCACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTCGCCCCATTCAAGGTGGACATGGAAATTATGGAGTTTAATGCATTG
 CAAAAGTGTCAAGATCCACAAAATCTGTGCTGACCAATACAAGATGT
 TATAGAAAAGCACATAAGGAATTAAAGAAAATGAAGAAGAG

SEQ ID NO. 6812

STRAIN 2603 frame: 1

MAKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEVKADDTELKLKGEKLK
 YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLKYAVDVGTNQLVWK
 LRQDHVRVSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNILPALKEILVDGGQVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGTVKHLDfspIQQGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKEFKNEEE

SEQ ID NO. 6813

SEQUENCE LISTING

STRAIN 090 frame: 1
 AKERDVVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLKYAVDVTNQLVWK
 LRQDHRRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNILPALKEILVDGGQVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKNEEE

SEQ ID NO. 6814

STRAIN A909 frame: 1
 AKERDVVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLKYAVDVTNQLVWK
 LRQDHRRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNILPALKEILVDGGQVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKNEEE

SEQ ID NO. 6815

STRAIN 18RS21 frame: 1
 AKERDVVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLKYAVDVTNQLVWK
 LRQDHRRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNILPALKEILVDGGQVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKNEEE

SEQ ID NO. 6816

STRAIN M732 frame: 1
 AKERDVVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLKYAVDVTNQLVWK
 LRQDHRRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNILPALKEILVDGGQVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKNEEE

SEQ ID NO. 6817

STRAIN COH1 frame: 1
 AKERDVVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLKYAVDVTNQLVWK
 LRQDHRRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNILPALKEILVDGGQVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKNEEE

SEQ ID NO. 6818

STRAIN M781 frame: 1
 AKERDVVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLKYAVDVTNQLVWK
 LRQDHRRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNILPALKEILVDGGQVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKNEEE

SEQ ID NO. 6819

STRAIN CJB110 frame: 1
 AKERDVVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLKYAVDVTNQLVWK
 LRQDHRRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNILPALKEILVDGGQVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKNEEE

SEQ ID NO. 6820

STRAIN 1169NT frame: 1
 AKERDVVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLKYAVDVTNQLVWK
 LRQDHRRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNILPALKEILVDGGQVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKNEEE

SEQ ID NO. 6821

SEQUENCE LISTING

STRAIN JM9130013 frame: 1
 AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVTGNQLVWK
 LRQDHVRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKKNEEE

SEQ ID NO. 6822

STRAIN H36B frame: 1
 AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLK
 YVSRRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVTGNQLVWK
 LRQDHVRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
 IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDGYTVKHLDFSPIQGGHGNIEFL
 MHLQKCQDPQNLVLDQIQDVIEKAHKFKKNEEE

SEQ ID NO. 6901

STRAIN 2603

ATGAATAAAAGGTACTATTGACATCGACAATGGCAGTCGCTATTATCAGTCGCAAGT
 GTTCAAGCACAAGAACAGATACGACGTGGACAGCACGTACTGTTCAGAGGTAAAGGCT
 GATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATAACTAAC
 GTTATTCAGAAGCAATGCAATTGATATGAATGCTTAGCAAAAATAAATAACATTGCA
 GATATCAATCTTATTTACTCTGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCAT
 ACTGCCACTTCAATGAAAATAGAAAACCAGCAACAAATGCTGCTGGTCAAACAAACAGCT
 ACTGTGGATTGAAAACCAATCAAGTTCTGAGCAGACAACTCAGACGTCAAGTCAACAA
 ATTTCGGAAGGTATGACACCGAGCAACAAACGATTGTTGAGACAAAGACTTCTCAATACA
 TCTCTGCGCCAGCTTGAATCAAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTC
 GCAGCAGCTAATGAACAGGTATCAGCAGCTCCTGTAAGTCAGTCAAGTTC
 GCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAAGTCAACAAACAGTATCA
 CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCAGTAAGA
 GTAGCAGCCCCTAGAGTGCAAGTGTAAAGTAGTCACCTCTAAAGTAGAAACTGGTG
 TCACCGAGCAGTATGACTCAGCTCAGTTCCTGACTACAGACTTCACAGCTACAGAC
 AGTAAGTTACAAGCAGTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCA
 ACACCGGTAGACAACAGCTTCAACAAACAAATGCACTGACATCCTGAAAATGCA
 GGGCTCAAACCTCATGTTGAGCTTAAAGAAAAGTAGCGTCAACTTATGGAGTTAAT
 GAATTCACTACATACCGTGGGGAGATCCAGGTGATCATGGTAAAGGTTAGCAGTTGAC
 TTTATTGTAGGTACTAATCAAGCACTGGTAAATAAGTTGCAACAGTACTCTACAAAAT
 ATGGCAGCAAATAACATTCTATATGTATCTGGCAACAAAAGTTTACTCAAATACAAAC
 AGTATTATGGACCTGCTAAACTTGAATGCAATGCCAGATCGTGGTGGCCTACTGCC
 AACCACTATGACCACGTTACGTATCATTAAACAAATAATATAAAAAGGAAGCTATTG
 GCTTCTTTTATATGCCCTGAATAGACTTCAAGGTTCTTATATAATTTTTATTA

SEQ ID NO. 6902

STRAIN 090

TGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTT
 CAATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACACCCAGCT
 ACTGTGGATTGAAAACCAATCAAGTTCTGTTGAGACCAAAAGTTTC
 TCTCAATACAATTCGGAAGGTATGACACCAGAAGCAGCAACAAACGATTG
 TTTCGCCAATGAAGACATAATTCTGCGCCAGCTTGAATCAAAAGAA
 GTATTAGCACAAGCAAGCTGTTAGTCAGCAGCAGCTAATGAACAGGT
 ATCAACAGCTCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAG
 AGGAAGTTAAACCAACTCAGACGTCAAGTCAGTCAACAAACAGTATCA
 CCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACC
 GGTAAGAACTGTAGCAGCCCCTAGAGTGGCAAGGTGTTAAAGTAGTC
 CTTGACTACGACTTCACACAGCTACAGACAGTAAGTTACAAGCAGTGA
 AGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAG
 CACAACCAAGCTCAACAAACAAATGCACTGACATCCTGAAAATGCA
 GGGCTCAAACCTCATGTTGAGCTTAAAGAAAAGTAGCGTCAACTTA
 TGGAGTTAATGAATTCACTACATACCGTGCAGGTGATCCAGGTGATCATG
 GTAAAGGTTAGCAGTCGACTTATTGAGTAAAGCAAGCAACTTGGT
 AATGAAGTTGCCAGACTCTACACAAAATATGGCAGCAAATAACATTTC
 ATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTATG
 GACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCCTACTGCC
 AACCAATTGACCAGTGTACGTATCATTAAACAAATAATATAAAAAGG

SEQUENCE LISTING

AAGCTATTTGGCTTCTTTTATATGCCTTGAATAGACTTCAAGGTTCT
TATATAATTTTATTAA

SEQ ID NO. 6903

STRAIN A909

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAA
ATATGGTATACACTAACCGTTATTCAGAAGCAATGTCAATTGATATGA
ATGTCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTCCT
GAGACAACACTGAGCTAAGTACGATCAGAAGAGTCATACTGCTACTTC
AATGAAAATAGAACACCAAGCAACAAATGCTGCTGGTCAAACAAcAGCTA
CTGTCGATTGAAAACCAATCAAGTTCTGTTGCAGACCAAAAGTTCT
CTCAATACAATTCGGAAGGTATGACACCAGAAGCAGCAACACGATTGT
TTCGCCAATGAAGACATATTCTTcTGGCCAGCTTGAAATCAAAGAAG
TATTAGCACAAGGGCaAGCTGTTAGTCAAGCAGCAGCTAATGAAACAGGTA
TCACAGCTcCTGTGAAGTCGATTACTTCAGAAGTTCCAgCAGCTAAAGA
GGAAGTTAAACCAATCAGACGTCAGTCAGTCAACAAACAGTATCAC
CAgCTTCTGTGCCGCTGAAACACCAAGCTCCAgTAGCTAAaGTAGCACCG
GTAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCC
TAAAGTAGAAACTGGTGCAATCACCAGAGCATGTATCAGCTCAGCAGTT
CTGTGACTACGACTTCACAGCTACAGACAGTAAGTTACAAGCGACTGAA
GTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGC
ACAACCAAGCTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAA
GGCTCCAACCTCATGTTGCAGCTTATAAGAAAAGTAGCGTCAACTTAT
GGAGTTAATGAATTcAGTACATACCCTGCGGGAGATCCAGGTGATCATGG
TAAAGGTTAGCAGTTGACTTTATTGTAgtGAAAAACCAAGCATTGGTA
ATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCaAATAACATTCA
TATGTTATCTGGCAACAAAGTTTACTCAAAtCAAATAGTATTATGG
ACcTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTAcTGCCA
ACCaCTATGACCACGTTCACGTATCATTAAACAAAtaATATAAAAAGGA
AGCTaTTGGCTTCTTTTATATGCCTTGCATAGACTTCAAGGTTCTT
ATATAATTTTATTAA

SEQ ID NO. 6904

STRAIN H36B

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATA
TGGTGTACACACTAACCGTTATTCAGAAGCAATGTCAATTGATATGAATG
TCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTCCTGAG
ACAACCaCTGAGCTAACGTCAGTACGATCAGAAGAGTCATACTGCTACTTC
GAAAATAGAACACCAAGCAACAAATGCTGCTGGTCAAACACAGCTACTG
TCGATTTGAAAACCAATCAAGTTCTGTTGCAGACCAAAAGTTCTCTC
AATACAATTCGGAAGGTATGACACCAAGCAGCAACACGATTGTTTC
GCCAACTGAAGACATATTCTTCTGCGCAGCTTGAAATCAAAGAAGTAT
TAGCACAAGGGCAAGCTGTTAGTCAAGCAGCAGCTAAAGCAGGTATCA
CCAGCTCTGTGAAGTCGATTACTTCAGAAGTCTCAGCAGCTAAAGAGGA
AGTTAAACCAACTCAGACGTCAGTCAGTCAACAAACAGTATCACCAG
CTTcTGGTGCCTGAAACACCAAGCTCCAGTAGCTAAAGTAGCACCAGGTA
AGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCTAA
AGTAGAAAATGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTG
TGACTACGACTTCAACAGCTACAGACAGTAAGTACAAGCGACTGAAGTT
AAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACA
ACCAAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAAGGC
TCCAACTCTCATGTTGCAGCTTATAAGAAAAGTAGCGTCAACTTATGGAA
GTTAATGAATTCACTACCGTGCAGGGAGATCCAGGTGATCATGGTAA
AGGTTTAGCAGTTGACTTTATTGTAAGTAAAACCAAGCACTTGGTAATG
AAGTTGCACAGTACTCTACACAAAAtaTGGCAGCAAATAACATTTCATAT
GTTATCTGGCaACAAAAGTTTACTCAAATACAAATAGTATTATGGACC
TGCTAATACTTGAATGCAATGCCAgATCGTGGTGGCGTTACTGCCAAC
ACTATGACCACGTTCACGTATCATTAAACAAATAATATAAAAAGGAAGC
TATTTGGCTTCTTTTATATGCCTTGCATAGACTTCAAGGTTCTTATA
TAAATTTTATTAA

SEQ ID NO. 6905

STRAIN 18RS21

CTGATTTGGTAAAGCAAGACAAT

SEQUENCE LISTING

AAATCATCATATACTGTGAAATATGGTGATACAcTAAGcGTTATTCAGA
 AGCAATGTCAATTGATATGAATGTCTAGCAAAAATAAATAACATTGCAG
 ATATCAATCTTATTTCAGAGACAACTGAGACAACTGAGACAACTGAG
 AAGAGTCATACTGCCaCTTCAGGAAATAGAAACACCAGCAaCAAATGC
 TGCTGGTCAaACAaCAGCTACTGTGGATTGAAACCAATCAaGTTTCTG
 TTGCAGACAAAAGTTCTCTCAATACAATTCGGAAGGTATGACACCA
 GAAGCAGCAACAAAGTGTTCGCCAATGAAGACaTATTCTCAGCGCC
 AGCTTGAAaTCAAAAGAAGTATTAGCACAAGAGCAAGCTTGTCAAG
 CAGCAGCTAATGAACAGGTATCACCAGCTCTGTGAAGTCGATTACTCA
 GAAGTTCCAGCAGCTAAAGAGGAAGTAAACCAACTCAGACGTCAGTCAG
 TCAGTCAACAAACAGTATCACCAGCTCTGTGCCGTGAAACACCAAGCTC
 CAGTAGCTAAAGTAGCACCAGTAAGAAGTGTAGCAGCCCTAGAGTGGCA
 AGTGTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGCATCACCAGAGCA
 TGTATCAGCTCCAGCAGTCTCTGTGACTACGACTCACCAGCTACAGACA
 GTAAGTTACAAGCGACTGAAGTTAAGAGCGTCCGGTAGCACAAAAGCT
 CCAACAGCAACACCGGTAGCACAACCCAGCTTCAACAAACAAATGCAGTAGC
 TGCACATCCTGAAAATGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAG
 AAAAGTAGCGTCAACTTATGGAGTTAATGAATTCACTACATACCGTGC
 GGAGATCCAGGTGATCATGGTAAAGGTTAGCAGTTGACTTTATTGTAGG
 TACTAATCAAGCACTTGGTAAATAAAGTTGACAGTACTcTACACAAAATA
 TGGCAGCAAATAACATTTCATATGTTATCTGGCAACAAAAGTTTACTCA
 AATACAAACAGTATTTATGGACCTGCTAATACTTGGAAATGCCAATGCCAGA
 TCGTGGTGGCCTTACTGCCAACCCTATGACCACGTTCACGTATCATT
 ACAAAATAATAAAAAAGGAAGCTATTGGCTTCTTTTATATGCCCTTG
 AATAGACTTTCAAGGTTCTTATATAATTTTTATT

SEQ ID NO. 6906

STRAIN COH1

CTGATT

GGTAAAGCAAGACAATAATCATCATATACTGTGAAATATGGTGATACAC
 TAAGCGTTATTCAGAAGCAATGTCAATTGATATGAATGTCTAGCAAAA
 ATTAATAACATGCGAGATATCAATCTTATCTGAGACAAACACTGAC
 AGTAACCTTACGATCAGAAGAGTCATACTGCCACTCAATGAAAATAGAAA
 CACCAAGCAACAAATGCTGCTGGTCAAACAAACAGcTACTGTGATTGAAA
 ACCAATCAAGTTTTGTCAGACCAAAAGTTTCTCTCAATACAATTTC
 GGAAGGTATGACACCAGaaGCAGCAACAACGATTGTTGCCAATGAAGA
 CaTATTCTTCTGCGCCAGTTGAAATCAAAGAAGTATTAGCACAAGAG
 CAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAGCTCTGT
 GAAGTCGATTACTTCAGAAGTCCAGCAGCTAAAGAGGAAGTTAAACCAA
 CTCAGACGTCACTGAGTAAACACAGTATCACCAGCTCTGTGCC
 GCTGAAACACCAAGCTCCAGTAGCTAAAGTAGCACCAGTAAGAAACTGTAGC
 AGCCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCTGACTACGACT
 GTGCATCACCAGAGCATGTATCAGCTCCAGCAGTCTGTGACTACGACT
 TCACCAAGCTACAGACAGTAAAGTTACAAGCGACTGAAGTTAAGAGCGTTCC
 GGTAGCACAAAAGCTCAACAGCAACACCGGTAGCACAACCCAGCTTCAA
 CAACAAATGCAGTAGCTGCACATCTGAAAATGCAGGGCTCCAACCTCAT
 GTTGCAGCTTATAAAGAAAAGTAGCGTCAACTTATGGAGTTAATGAATT
 CAGTACATACCGTGCAGGGAGATCCAGGTGATCATGGTAAAGGTTAGCAG
 TTGACTTTATTGTAGGTAAGAAGCACTTGGTAATGAAGTTGCACAG
 TaCTCTACACAAAATATGGCAGCAAATAACATTTCATATGTATCTGGCA
 ACAAAAGTTTATTCAAATACAAATAGTATTATGGACCTGCTAATACTT
 GGAATGCAATGCCAGATCGTGGTGGCCTACTGCCAACCACTATGACCAC
 GTTCACGTATCATTAAACAAATAATATAAAAAGGAAGCTATTGGCTTC
 TTTTTATATGCCCTGAATAGACTTTCAAGGTTCTTATATAATTTTTATT
 A

SEQ ID NO. 6907

STRAIN M732

CTGATTGGTAAAGCAAGACAATAATCATCATATACTGTGAAATATGGT
 GATACAnTAAGCGTTATTCAGAAGCAATGTCAATTGATATGAATGTCTT
 AGCAAAATTAATAACATGCGAGATATCAATCTTATCTGAGACAA
 CACTGACAGTAACCTACGATCAGAAGAGTCATCTGCCACTCAATGAAA
 ATAGAAACACCAAGCAACAAATGCTGCTGGTCAAACAAACAGCTACTGTcGA
 TTTGAAAACCAATCAAGTTGGTGCAGACCAAAAGTTCTCTCAATA

SEQUENCE LISTING

CAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTGCCA
 ATGAAGACATATTCTCTGCCAGCTTGAATCAAAAGAAGTATTAGC
 ACAAGAGCAAGCTGTAGTCAGTAGCAGCTAATGAACAGGTATCACCAG
 CTCTGTGAAGTCGATTACTTCAGAAGTCCAGCAGCTAAAGAGGAAGTT
 AAACCAACTCAGACGTAGTCAGTTAACACAGTATCACCAGCTTC
 TGTTGCCGCTGAAACACCAAGCTCCAGTAGCTAAAGTAGCACCAGTAAGAA
 CTGTAGCAGCCCCTAGAGTGGCAAGTGTAAAGTAGTCAGTCACTCCTAAAGTA
 GAAACTGGTGCATCACCAAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC
 TACGACTTCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGA
 GCGTTCCGGTAGCACAAAAGCTCAAACAGCAaCACCGGTAGCACAACCA
 GCTTCAACAACAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA
 ACCTCATGTTGAGCTTAAAGAAAAAGTAGCTGCAACTTATGGAGTTA
 ATGAATTCACTACATACCGTGCAGGGAGATCCAGGTGATCATGGTAAAGGT
 TTAGCAGTTGACTTTAttttagttaaaaaccAAGCAGCTGGTAATGAAGT
 TGACAGTACTcTACACAAAATATGGCAGCAAATAACATTTCATATGTTA
 TCTGGCAACAAAAGTTTATTCAAATAACAAATAGTATTTATGGACCTGCT
 AATACTTGGAAATGCAATGCCAGATCGTGGTGGCCTACTGCCAACCACTA
 TGACCACGTTACGTATCATTAAACAAATAATATAAAAAGGAAGCTATT
 TGGCTTCTTTTATATGCCCTGAATAGACTTCAAGGTTCTTATATAAT
 TTTTATTA

SEQ ID NO. 6908

STRAIN M781

CTGATTTGGTAAAGCAAGACAATAATCATCATATACTGTGAAATATGGT
 GATACACTAAGCCTTATTCAAGCAATGTCAATTGATATGAATGTCTT
 AGCAAAAATTAATAACATTGCAGATATCAATCTTATTATCTGAGACAA
 CACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTTCAATGAAA
 ATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTCGA
 TTGAAAACCAATCAAGTTTGTGAGACCAAAAGTTCTCTCAATA
 CAAITTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTGCCA
 ATGAAGACATATTCTCTGCCAGCTTGAATCAAAGAAGTATTAGC
 ACAAGAGCAAGCTGTAGTCAGTAGCAGCTAATGAACAGGTATCACCA
 CTCTGTGAAGTCGATTACTTCAGAAGTCCAGCAGCTAAAGAGGAAGTT
 AAACCAACTCAGACGTAGTCAGTTAACACAGTATCACCAAGCTTC
 TGTTGCCGCTGAAACACCAAGCTCCAGTAGCTAAAGTAGCACCAGTAAGAA
 CTGTAGCAGCCCCTAGAGTGGCAAGTGTAAAGTAGTCAGTCACTCCTAAAGTA
 GAAACTGGTGCATCACCAAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC
 TACGACTTCACCAGCTACAGACAGTaaGTTACAAGCGACTGAAGTTAAGA
 GCGTTCCGGTAGCACAAAAGCTCAAACAGCAACACCAGTAGCACAACCA
 GCTTCAACAAACATTCAGCTGCAACATCCTGAAAATGCAGGGCTCCA
 ACCTCATGTTGAGCTTAAAGAAAAAGTAGCGTCAACTTATGGAGTTA
 ATGAATTCACTACATACCGTGCAGGGAGATCCAGGTGATCATGGTAAAGGT
 TTAGCAGTTGACTTTATTGTAGGTAACCAAGCAGCTGGTAATGAAGT
 TGACAGTACTCTACACAAAATATGGCAGCAAATAACATTTCATATGTTA
 TCTGGCAACAAAAGTTTATTCAAATAACAAATAGTATTTATGGACCTGCT
 AATACTTGGAAATGCAATGCCAGATCGTGGTGGCCTACTGCCAACCACTA
 TGACCACGTTACGTATCATTAAACAAATAATATAAAAAGGAAGCTATT
 TGGCTTCTTTTATATGCCCTGAATAGACTTCAAGGTTCTTATATAAT
 TTTTATTA

SEQ ID NO. 6909

STRAIN CJB110

CTGATTTGGTAAAGCAAGACAATAATCATCATATACTGTGAAA
 TATGGTGTACACTAAGCCTTATTCAAGCAATGTCAATTGATATGAA
 TGTCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTATCTG
 AGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTTCA
 ATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACACCCAGCTAC
 TGTTGGATTTGAAAACCAATCAAGTTcTGTGCAAGCAGCAACAAAGTTCTC
 TCAATACAATTTCGGAAGGTATGACACCAGAAGCAGCAACAAACGATTGTT
 TCGCCAATGAAGACATATTCTCTGCCAGCTTGAATCAAAGAAGT
 ATTAGCACAAGAGCAAGCTGTAGTCAGCAGCAGCTAATGAACAGGTAT
 CAACAGCTCTGTGAAGTCGATTACTTCAGAAGTCCAGCAGCTAAAGAG
 GAAGTTAAACCAACTCAGACGTAGTCAGTCAGTCAACACAGTATCACC
 AGCTTCTGTGCGCTGAAACACCAAGCTCCAGTAGCTAAAGTAGCACCAGG

SEQUENCE LISTING

TAAGAACTGTAGCAGCCCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCT
 AAAGTAGAAACTGGTGCATCACAGAGCATGTATCAGCTCCAGCAGTTCC
 TGTGACTACGACTTCAACAGCTACAGACAGTaaAGTTaCAAGCGACTGAAG
 TTAAGAGCGTCTCGGTAGCACAAAAAGCTCAACAGCAACACCGGTAGCA
 CAACCAGCTTCAACAAACAAATGCAGTAGCTGCACATCCTGAAATGCAGG
 GCTCCAACCTCATGTTGAGCTTATAAAGAAAAGTAGCGTCAACTTATG
 GAGTTAATGAATTCACTGACATCCGTCAGGTGATCCAGTGTGATCATGGT
 AAAGGTTTAGCAGTcGACTTTATTGTAGTAAAGAAAACCAAGCACTTGGTAA
 TGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTCAT
 ATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTTATGGA
 CCTGCTAACTACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAA
 CCATTATGACCATGTTCACGTATCATTAAACAATAATATAAAAAAGGAA
 GCTATTGGCTTCTTTTATATGCCCTGAATAGACTTCAAGGTTCTTA
 TATAATTTTATTA

SEQ ID NO. 6910

STRAIN 1169NT
 CTGATTTG

GTAAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTACACT
 AAGCGTTATTCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAA
 TTAATAACATTGCAGATATCAATCTTATTTCATCCTGAGACAACACTGACA
 GTAACCTACGATCAGAAGAGTCATACTGCCACTTCAATGAAAATAGAAC
 ACCAGCAACAAATGCTGCTGGTCAAACAAACAGCTACTGTGGATTGAAAA
 CCAATCAAGTTTCTGTCAGACAAAAAGTTCTCTCAATACAATTTCG
 GAAGGTATGACACCAGAACGAGCAACAAACGATTGTTTCGCCAATGAAGAC
 ATATTCTTCTGCGCCAGCTTgAAATCAAAAGAAGTATTAGCACAAGAGC
 AAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCACCAGCTCTGTG
 AAGTCGATTACTTCAGAAGTCCAGCAGCTAAAGAGGAAGTTAGACCAAC
 TcAGACGTCAGTCAGTCAGTCAACAAACAGTATCACCAGCTTCTGTTGCCG
 CTGAAAACACCAGCTCAGTAGCTAAAGTAGCACCGGTAAGAAGACTGTAGCA
 GCCCCAGCCCCCTAGAGTGGCAAGTGTAAAGTAGTACTCCCTAAAGTAGA
 AAactGGTGCATCACAGAGCATGTACAGCTCCAGCAGTTCCTGTGACTA
 CGACTTCAACAGCTACAGAACTAACAGCAACACCGGTaGCACAACCAGC
 GtTCCGGTgGCACAAAAAGCTCCAACAGCAACACCGGTaGCACAACCAGC
 TTcAACAAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGACTCCAAC
 CTCATGTTGCAGCTTATAAAGAAAAGTAGCGTCAACTTATGGAGTTAA
 GAATTCACTGACATCCGTCAGGAGATCCAGGTGATCATGGTAAAGGTT
 AGCAGTTGACTTTATTGTAGTAAAGAACCAAGCACTTGGTAAAGTTG
 CACAGTACTCTACACAAATATGGCAGCAAATAACATTCTATGTTATC
 TGGCAACAAAAGTTTACTCAAATACAAATAGTATTTATGGACCTGCTAA
 TACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACACTATG
 ACCACGTTCACTGATCATTAACAAATAATATAAAAAGGAAGCTATTG
 GCTCTTTTATATGCCCTGAATAGACTTCAAGGTTCTTATATAATT
 TTATTA

SEQ ID NO. 6911

STRAIN JM9130013

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACT
 GTGAAATATGGTACACTAAGCGTTATTCAGAAGCAATGTCAATTGA
 TATGAATGTCTTAGAAAAAATAACATTGCACTATCAATCTTATT
 ATCCtGAGACAACACTGACAGTAACTTACGATCAGAAGAGTCATACTGCC
 ACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAAAC
 AGCTACTGTGGATTGAAAACCAATCAAGTTCTGTCAGACAGCAACAAAG
 TTTCTCTCAATACAATTTCGGAAGGTATGACACCCAGAAGCAGCAACAAAC
 ATTGTTTCGCCAATGAAGACATATTCTCTGCCAGCTTGAATCAAA
 AGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAAC
 AGGTATCACAGCTCCTGTGAAGTCGATTACTCAGAAGTCCAGCAGCT
 AAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAAACAGT
 ATCACCAAGCTTCTGTTGCCGCTGAAAACACCAGCTCCAGTAGCTAAAGTAG
 CACCGGTAAAGAAGTGTAGCAGCAGCCCCCTAGAGTGGCAAGTGTAAAGTAGTC
 ACTCCTAAAGTAGAAACTGGTGCATCACCAAGAGCATGTATCAGCTCCAGC
 AGTTCCTGTGACTACGACTTACCCAGTACAGAGCACTGAAAGTTACAAGCGA
 CTGAAAGTTAAAGAGCGTTCGGTAGCACAAAAAGCTCCAACAGCAACACCG
 GTAGCaCAACCAGCTTCAACAAACAAATGCAGTAGCTGCACATCCTGAAA

SEQUENCE LISTING

TGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAA
 CTTATGGAGTTAATGAATTCACTACATACCGTGGGGAGATCCA_gGTGAT
 CATGGTAAAGGTTAGCAGTTGACTTATTGTTAGGACTAATCAAGCACT
 TGGTAATAAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACA
 TTTCATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAACAGTATT
 TATGGACCTGCTAATACTTGAATGCCAGATCGTGGTGGCGTTAC
 TGCCAAACCACTATGCCAGCAGTACGTTACATTAAACAAATAATAAAA
 AAGGAAGCTATTGGCTCTTTTATATGCCCTGAATAGACTTTCAAGG
 TTCTTATATAATTTTATTAA

SEQ ID NO. 6912

STRAIN 2603 frame: 1

MNKVLLTSTMAASLLSVASVQAQETDTWTARTVSEVKADLVKQDNKSSYTVKYGDTLS
 VISEAMSIDMNVLAKINNIADINLIYPETTLLTVYDQKSH
 TATDLKTNQSVADQKVSINTISEGMPTEAATTIVSPMKTYSAPALKSKEVLAQEQAVSQ
 AAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVQSTTVSPASVAAETPAPVAKVAPVRT
 VAAPRVASVVKVTPKVEHGASPEHVSAPAVPVTTSPATDSKLQATEVKSVPAQKAPTA
 TPVAPQAPSTTNAVAAHPENALQPHVAAYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVD
 FIVGTNQALGNKVAQYSTQNMANNISYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTA
 NYDHVHVSFNK. YKKGSYLASFYALNRLSRFLYNFY

SEQ ID NO. 6913

STRAIN 090 frame: 2

ETTLTVTYDQKSHATSMKIEPATNAAGQTPATVDLKTNQSVADQKVSINTISEGMP
 EAATTIVSPMKTYSAPALKSKEVLAQEQAVSQAAANEQVSTAPVKSITSEVPAAKEEVK
 PTQTSVQSTTVSPASVAAETPAPVAKVAPVRTVAAPRVASVVKVTPKVEHGASPEHVS
 PASVAAETPAPVAKVAPVRTVAAPRVASVVKVTPKVEHGASPEHVSAPAVPVTTTSTATD
 SKLQATEVKSVPAQKAPTA TPVAPQAPSTTNAVAAHPENALQPHVAAYKEKVASTYGV
 NYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTAHYDHVHVSFNK. YKKGSYLASFYAL
 NRLSRFLYNFY

SEQ ID NO. 6914

STRAIN A909 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLLTVYDQKSH
 TATSMKIEPATNAAGQTTATVDLKTNQSVADQKVSINTISEGMPTEAATTIVSPMKTYS
 SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVQSTTV
 PASVAAETPAPVAKVAPVRTVAAPRVASVVKVTPKVEHGASPEHVSAPAVPVTTTSTATD
 SKLQATEVKSVPAQKAPTA TPVAPQAPSTTNAVAAHPENALQPHVAAYKEKVASTYGV
 NYEFSTYRAGDPGDHGKGLAVDFIVGKQALGNEVAQYSTQNMANNISYVIWQQKFYSNTNS
 SIYGPANTWNAMPDRGGVTAHYDHVHVSFNK. YKKGSYLASFYALHRLSRFLYNFY

SEQ ID NO. 6915

STRAIN H36B frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLLTVYDQKSH
 TATSMKIEPATNAAGQTTATVDLKTNQSVADQKVSINTISEGMPTEAATTIVSPMKTYS
 SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVQSTTV
 PASVAAETPAPVAKVAPVRTVAAPRVASVVKVTPKVEHGASPEHVSAPAVPVTTTSTATD
 SKLQATEVKSVPAQKAPTA TPVAPQAPSTTNAVAAHPENALQPHVAAYKEKVASTYGV
 NYEFSTYRAGDPGDHGKGLAVDFIVGKQALGNEVAQYSTQNMANNISYVIWQQKFYSNTNS
 SIYGPANTWNAMPDRGGVTAHYDHVHVSFNK. YKKGSYLASFYALHRLSRFLYNFY

SEQ ID NO. 6916

STRAIN 18RS21 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLLTVYDQKSH
 TATSMKIEPATNAAGQTTATVDLKTNQSVADQKVSINTISEGMPTEAATTIVSPMKTYS
 SSAPALKSKEVLAQEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVQSTTV
 PASVAAETPAPVAKVAPVRTVAAPRVASVVKVTPKVEHGASPEHVSAPAVPVTTTSTATD
 SKLQATEVKSVPAQKAPTA TPVAPQAPSTTNAVAAHPENALQPHVAAYKEKVASTYGV
 NYEFSTYRAGDPGDHGKGLAVDFIVGKQALGNEVAQYSTQNMANNISYVIWQQKFYSNTNS
 SIYGPANTWNAMPDRGGVTAHYDHVHVSFNK. YKKGSYLASFYALHRLSRFLYNFY

SEQ ID NO. 6917

STRAIN M732 frame: 3

DLVKQDNKSSYTVKYGDTXSVISEAMSIDMNVLAKINNIADINLIYPETTLLTVYDQKSH

SEQUENCE LISTING

TATSMKIEPATNAAGQTATVDLTNQVFVADQKVSINTISEGMTPEAATTIVSPMKT
 SSAPALKSKEVLAQEQAQSVAANEQVSPAPVKSITSEVPAKEEVKPTQTSVSQLTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTSPATD
 SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
 EFSTYRAGDPGDHGKGGLAVDFIVGKQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFYALNRLSRFLYNFY

SEQ ID NO. 6918

STRAIN COH1 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIEPATNAAGQTATVDLTNQVFVADQKVSINTISEGMTPEAATTIVSPMKT
 SSAPALKSKEVLAQEQAQSVAANEQVSPAPVKSITSEVPAKEEVKPTQTSVSQLTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTSPATD
 SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
 EFSTYRAGDPGDHGKGGLAVDFIVGKQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFYALNRLSRFLYNFY

SEQ ID NO. 6919

STRAIN M781 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIEPATNAAGQTATVDLTNQVFVADQKVSINTISEGMTPEAATTIVSPMKT
 SSAPALKSKEVLAQEQAQSVAANEQVSPAPVKSITSEVPAKEEVKPTQTSVSQLTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTSPATD
 SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
 EFSTYRAGDPGDHGKGGLAVDFIVGKQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFYALNRLSRFLYNFY

SEQ ID NO. 6920

STRAIN CJB110 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIEPATNAAGQTATVDLTNQVFVADQKVSINTISEGMTPEAATTIVSPMKT
 SSAPALKSKEVLAQEQAQSVAANEQVSPAPVKSITSEVPAKEEVKPTQTSVSQLTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTSPATD
 SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
 EFSTYRAGDPGDHGKGGLAVDFIVGKQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFYALNRLSRFLYNFY

SEQ ID NO. 6921

STRAIN 1169NT frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIEPATNAAGQTATVDLTNQVFVADQKVSINTISEGMTPEAATTIVSPMKT
 SSAPALKSKEVLAQEQAQSVAANEQVSPAPVKSITSEVPAKEEVKPTQTSVSQLTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTSPATD
 SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
 VNEFSTYRAGDPGDHGKGGLAVDFIVGKQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
 TNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFYALNRLSRFLYNFY

SEQ ID NO. 6922

STRAIN JM9130013 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIEPATNAAGQTATVDLTNQVFVADQKVSINTISEGMTPEAATTIVSPMKT
 SSAPALKSKEVLAQEQAQSVAANEQVSPAPVKSITSEVPAKEEVKPTQTSVSQLTTVS
 PASVAAETPAPVAKVAPVRTVAAPRVASAKVVTPKVETGASPEHVSAPAVPVTTSPATD
 SKLQATEVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVN
 EFSTYRAGDPGDHGKGGLAVDFIVGKQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK. YKKGSYLASFYALNRLSRFLYNFY

SEQ ID. NO. 7001

STRAIN 2603

ATGGGAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGAGCCACTATTCCTC
 GTGATAGAGCCTTGCTTGAGGCATTTTATATTACCAAGCAGAGCATTGATGAGGAGT
 GGGATAGTCTATTCACTAGTTATGACCAATAGGCAAGAAAATAAGTCTGTTCAAG
 TACITCACTTGAGACAGATGTTCAGCTTTGTCAGGCTAGTCCTTATGATACTGCTC
 ATGATCTATTGACCTATAACACAAGTTCGGCCAAAGTGGCTTCAAAACTAGATAAAC

SEQUENCE LISTING

TATCGCCGCTGAAAAAAACTTGGTGATAGAAGTGGCCTTGTCAATCTGGCCACTCGTT
 TTCAATTATTGGATTCCAATGGACACTACCAAACCATATCGCCGGATTCACTCTTACAAA
 AGAGTAGGGGAGCTAATTGGTCAATGTATCGTGTGGCTAATAATTAGCGGATCGTA
 TTAGTCGAGATATTGAACAGTTCTCTTAACTTACAGGCGCTGAGCTGAAACTAGAGCTG
 ATGAAACTGTTCTAGAAAATGAAGAAACTGTTGATGAGCACAAAACAAGTGTTCATCAAG
 CAATATCTTTCGAGAAGAGGGCTCTGGTTATTGCTAGTTGGATGTAGATTGTCTC
 AACTAGATGTCAAATAGGAAACCAAGTCATCTGCCAGCTATGAAGAGTTATCCTTAC
 GACGTAACATTGAGATTCTAACATATTGACCAAATCGAAATGAACGTTCAAAGTCC
 CAAGTTTAGCAGGGTGAACAGAGATGGAATGACACCAGTCTTGATGGCG
 AGGAATTACTTACTTATCTGAAGCTGATGGCAGTCCCTATGAGCTGAACGAACGCTGA
 CTACAGTCGAAGAAAAGGAATTAGAAAAATTGGACAAGCATTAGGATAGAAAATCAAG
 AAAAATTGACTCAGCTAGGGATTGATTATCTCAGTTGACCCAGACCGAGTCGGTATTT
 TATTGGATGCAGCAGGTGTTTCGTTAAAAATGCAGACCTTGCTTTACTAGGTGTT
 ATCCCAAAGCCTCGGTAACCTAACACTAGCCCTTGGACAGAACTACTCCAAATGGGACTAA
 GTCATGAAAAGGGTGAATTCTTCTGGTAGCCAGCTTCCATTGAAGAGCTGCGACAAG
 TTGCGCTACGCCATTATACCAAGAACACTCAGCAGAGATGGGAGCAATTGAAAAG
 ATAAAGGTAATCAGCCAGATTAACTCTCAGAGATTGGAAGCAAGCTAGAGAAAGCTG
 AGGGAAAAGAAGTAGTTGATGAAGAAATCGCGAAAATCCACTGGTTAGAGAGTATTGG
 ACACTTATCCTCTGGGGTATTGGTTCCCTATAAGGGACAGGACTTGGAGGTGATGCGG
 TCAGCGATGCTGATTGAACGGTTGATTGGATTGAGTTAGTCATGACTTTGGATA
 TCATTGAACAAAATCCAGTTCTTATGTGAGGACCTGGGAAGAAGTCAGTCAGGCACCTC
 ATCAGCCAAAGGCAGAACACAAACAGAGTTAGAAGAAGCGGACCAAGAATTAAACCTAT
 TCTCATTCTGGAAGAGGGAGCCAGTTAGAGTATTGGACTATTGGAAACCAAGATGATTG
 AAAATGGTCATAACGATACTGATCTGAAGAACACAGATAATCAAATTCCGAAAGAGGAAG
 TCGCGAAGGAAATTCCAGAGATTCCAGTAACGGACTTTATTCCAGAGGAGTTGACGG
 ACTTTTATCCTAAAGACTGCTAGAGATAAGGTTGAGACAAACATTGTGGCATTGTTGG
 TAAAAAAATCTAGAAGTAGAGCACCGCAATGCTTCAACAGTAAGAACTCCTGCCA
 AGTATGTAGGCTGGGGTGGACTAGCCAAATGAATTTCGATGACTATAATCCAAAATTTT
 CTAAGGAACGAGAAGAAGTGAAGAGCCTAGTCACAGATAAAGAGTATTGGATATGAAAC
 AGTCCTCCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTCAAGATGTGGATAAGT
 TGGAAAGAGATGGCTTACAGGTGGAAAATCCTAGATCCTCCATGGGAACAGGGAAATT
 TCTTTCGCGCTATGCCAAACACTTAAGAGAAAAGAGTGAAGTTGATGGCTAGAGTTAG
 ATACTTACAGGAGCTATTGCCAAACCCCTCATCCAAATAGTCATATTGAAATTAAAGG
 GATTGAGAGGGCTTAAACGAAATAGTTGATTTGGTGAATTGAAATGTGCCCT
 TTGCCAATATCGAATGGGATAATAGGTACGATAGGCCTACATGATTGACTACT
 TTGTCAAAAGTCATTGATTGCTCATGATGGTGGACAAGTAGCATTATCTTCCA
 CAGGAACATAGGATAAGCGAACAGAAAACATCTTACAAGATAATTGAGACAAACTGAAAT
 TTCTGGTGGGGTTCGACTGCCACTCTGCTTAAGGCCATTGCAAGGAACGAGTGTCA
 CAACGGATATGTTATTCTCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTAG
 CCTTTTCAGGTTCCATTGCTATGACAAGGATAGTCGCAATTGGCTCAATCCTTATTGG
 ATGGAGAATACAATAGCCAGGTGCTAGGAACCTACAGGAGTCAGGAATTGAAACGGGAA
 CACTTCTGTTAAGGGGACTAGTGATGACTTGATTGCAAGTGGTGAACACAGCTCTAAATC
 ACCTTCTGTTAAGGGGACTAGTGATGACTTGATTGCAAGTGGTGAACACAGCTCTAAATC
 CAAACAAAGTCATGATGACCTTCATTGAGTCATCTTAAACCCAGATGTGTTGA
 CCAAACAAGTCATGATGACCTTCATTGAGTCATCTTAAACCCAGATGTGTTGA
 GTTTGGTTATCAGGGCTCTACAGTTACTATCGAGATAACAAAGGCATTCGAGTCGGAA
 CCAAGACGGAGAAAATCAGTTACTATGTCATGAGAGGGCAACTTCAAAGCATGGACA
 CCAAACATTCTCAAAAGCAGATTGATGCTTTAATGCCCTAGAAGTGAATGACTAAACACTG
 CTCTGGATGTCATGTGACCGATGATGCAAGCCAAACGTTGTCAGTTAAGGGTATTATA
 AAAAGACAGTTTCTATGAAGCTCATTGCTTATAAGAAAGTGGCACGTATCAAAGGAA
 TGTTGCGATATTGCAATGCCATTCCAAGAAGTTATTGCCATTCAACGCTATTGACTATG
 ATAAGGAGACCTTAAACCAACTGTTAGGCAAACCTACGTCACCTATGATAGCTTGTCA
 AACACTATGGTATTGAAATAGTGCTGTGAACCCGAATTCTTGTGATAGTGATGATAAGT
 ATTGCTCTGCTAGTTGGAAGATGAAAGTCGCTTCAAGTGGAAAGTCTGTTATCT
 ATACTAAATCCCTTGCTTGAAGGCTCTAGTGCTGCTGACGGACGAGGGTGTGATTTCG
 CTTATATGATGTCATCTACAGGTTGAATCGCAGATGACCTTGATTGAGGAGTTAGGCG
 ACCTCATTATGCCATTGCTGAGAAGTATTGAATGGAGAATTGACCTATGTTCTCGCC
 AAGACTTCTTCAGGGAGTCGTCAGTAAAGTGAAGTGGTAGATCTATTGTCACAAAC
 AAGACAATCAGGACTTTAACCTGGTACACATTATGCCGGACTCTAGAAGCTATCAAACCAAG
 CCCGTATTACTTGGCAGACATTGATTATGAAATCGGTTCACTGCTGGATTCTGGCTG
 TTATGAAAATTGCCAAAGAACCTTATGGGAAAGCCATTGAAACTGTCAGACCAAG
 AAGTAGCGACAGTCTAGAAGTCAGTCCCATTGACGGGGTTATCCTACCAATCTAAGT
 TTGCGCTACACCTATTCCAACGCAACGGATAGGAGTTAGGTGCTCTGCTTCACTG
 ATAGTGGTCGAAAATCTTGAATTCCTGAAATTCCAACCAACCATCACAAAC

SEQUENCE LISTING

AAGTTGTCGAAGGGGATAAGAAAAAGAATGTGACGGATGTAGAGAAAACAACGGTCTGC
 GTGCCAAGGAAACACACCTACAAGAATCTTCAAGGTTTGAGCAAAGTATCCAGAAG
 TCCAACAAATGATTGAAGACACCTATAATAGGCTCTACAATCGTACGGTATCAAAGTCCT
 ATGATGGTAGTCATTAAACCATTGATGGACTTGCTCAGAATATCCTTACGTCCTCACC
 AAAAGAATGCATTCAACGAATTGTCGAGGAAAACAGTCTACTAGCTCATGAAGTTG
 GTTCAGGTAACACACTTACCATGCTGGGCAGGATTCAAACACTGAAAGAACTCGGAATGG
 TACATAAAACCACTTTATGTGGTGCGCTAGTCTGACTGCTCAGTTGGTCAAGAAATCA
 TGAAATTTCCTACCAAGAAAGTCTATGTGACTACTAAGAAAGACTTGCACAGGCCA
 AACGCAAGCAGTTGTGTCCTGATTATTACAGGGACTATGATGCCATTGTCATTGGGG
 ATTCAACAATTGAGAAGATACCGATGAGTCGTGAAAACAGGTACCTATATCAATGACA
 AACCTGAGCAACTCCGAGAAATCAAGCTAGGAAGTACAGTATTACACGGTGAAAGAAG
 CGGAACGTTGATTAAGGGATTAGAACACCACTGGAGAAACTCCAAAAGACTAGAGCGAG
 ATACCTTATTGAGTTGAAAACCTTGGAAATTGATTTCTTTGTGGATGAGGCTCATC
 ACTTCAGAAATATCCGTCATACTGGACTTGGGAATGTAGCTGGAAATCACCAACACAA
 CTTCTAAAAGAACGTGGATATGGAGATGAAGGTGAGACAAGTACAGGCAGAGCATGGAG
 ATAGAAATGTCGTTTGCACAGGAACACCAGTTCTAATCTTACTATTAGTGAACCTTCA
 CCATGATGGATTACATTCAACCTGATGTTGAAACGATACCTGGTATCAAATTGACT
 CCTGGGTTGGGCTTGGGAATATCGAAAACCTCATGGAACTAGCCCCGACAGGGAGATA
 AGTACCAACCAAGAAACGGTCAAGAAATTGTCACACCTCTGAACTCATGCGAATCT
 ACAAGGAAACTGCCATATTGACACCTCAGACATGCTGATTACAGTACCGGAAGCTA
 AGATTATTGCGGTGAAAGCGAGTTACGCAAGCTCAGAAATACTATTGGAAAGAGCTGG
 TAAAGCGTTGAGACGCTATCAAGTCAGCTAGTGTGATCCAAGTAGAGATAACATGCTTA
 AAATCACAGGAGAACGCCAGAAAACACTGACTATTGATATGCGGGTGTGACCCCTACTTACT
 CCTTATCGGATAATCGAAAATCTCAAGTGTGATGAGCAGTCTCATGGCTCTACGGAAAAGGGGGAA
 ATGGAGCTGGAGACAAACGCACTCAGATGATTCTCAGATAATTGGAACCCCTAAAAGTA
 AGGAAGAAGGGTTGATGCTACAATGAACCTAAGGACTTGTGTCGATCGAGGGATAC
 CAAAAGAAGAAATTGCGTTGTCATGATGCCAATACTGATGAGAAGAAAACCTCTGT
 CACGCAAGGTCATAGTGGAGAAGTACGGATTCTCATGGCTCTACGGAAAAGGGGGAA
 CAGGATTAAACGTCCAATCTCGATGAAAGCTGCCACTATTAGACGTTCCCTGGAGGC
 CCTCAGACATTGTCAGCGAAATGGACGACTAATTGACAAGGAAACATGCCACCGAGG
 TAGATATTATCACTATTAACCTAAAGGGAGCTTGTGACAATTACCTCTGGCAGACGCAGG
 AGAATAAGCTAAAGTATATCACCAGATAATGACCTCAGGATCTGTGAGATCAGCTG
 AAGACATTGATGAAACACCAGGCCCTCAGAGCTTAAAGGACTTGGCAACTGGGAACC
 CTTATCTCAAACCTCAAATGGAGTTGAAAATGAACTGACAGTTTAGAGAAATCAAAC
 GAGCCTTAATGCTCAAAGACGAGTATGCCCATACCATTGCTATAGCGAGAAGCACC
 TCCCTATTATGGAAAACCGTTGAGTCATGCAATATGATAAAAGATAATTGCCATCTTGGCAA
 CCAAGTCGCAAGATTGTCATGCGATTGACAATCAAGCAATGGATAATCGTGTGAG
 CTGGGGACTATCTGCAGAACCTATTACCTATAACCGCTCAGAGACCAAGGAAGTCAGGA
 CACTTGCCAGCTTAGAGGATTGATTAAAATGACTACAGGAGGTGCTAGTGAGCCT
 TACAGAAACCATTTCTTAATGATTGAGGTGATAACCGTATACTGTCGCCCTTGATT
 TGAATCAGACGTTGGGAACTTCAACGGATTAGTAATGCCATTGACCATATTATAGATG
 ACCAAGAAAAGACGCAAGGCTGGTAAGGATTAAAAGATAAAGCTACGAGTAGGCAAAG
 TAGAAGTTGATAAAAGTCTTCCAAGGAAGAGGACTATCAGCTGTAAAGGCTAAGTATG
 ATGTTTAGCTCCCTGGTGAAGAGATTGAAGAGATAGATGCAGCTTGG
 CCAAGTTAGTGAAGATAAACACCCCCAAAAGAAGCAACAAATGCACTCGAGATA

SEQ ID. NO. 7002

STRAIN H36B
 GGAGGGAAATGAATCAAGAAGTCTTACTACAAATGAT
 GAGGCCACTATTCTCGTGATAGAGCCTGCTTGAGGCAATTATATT
 ACCAAGCAGAGCATTGATGAGGAGTGGGATAGTCTTATTCACTGTT
 ATGACCAATAGGCAAGAAATAAAATAAGTCTGTCAGTACTCACTTGA
 GACAGATGTTCAGCTTGTCCAGGCTAGTCCTATGATACTGCTCATG
 ATCTATTGACCTATAACACAAGTTTCCGCCAAAGTGGCTTCAAAAACCA
 GATAAAACTATCGCCGCTGAAAAAAACTTGGTGATAGAAGTGGCCTTGT
 CAATCTGCCACTCGTTCAATTATTGGATTCCAATGGACACTACCAAA
 CCATATGCCGGATTCACTCTACAAAGAGTAGGGAGCTAATTGGTC
 AATGTTGATCGTGTGCTAATAATTAGCGGATCGTATTAGTCGAGATA
 TGAACAGTTCTCTTAACCTACGAGCCTGAGCTTGAAGAAACTAGAGCTGATG
 AAGACTGTTCTAGAAAATGAAGAAAAGTGTGATGAGCACAACAAAGTGT
 CATCAAGCAATATCTTTCGAGAAGAGGGCTCTGTTATTGCTAGTT
 GGATGTTAGATTGTCACTAGATGTTCAAATAGGAAAACCGTCATC
 TGCCAGCTTATGAAGAGTTACCTACGACGTTAAATTGAGATTCTAAC
 TATTGGACCAAAATCGAAATGAACGTTCCAAGTCCAAAGTTAGACCG

SEQUENCE LISTING

AGGTGATTTGACACAGAGATGGAAATGACACCAGTCTTGATGGCGAGG
 ATTACTTACTTATCTGAAGCTGATGGCAGTCCTATGAGCTGAAACGA
 ACGCTGACTCAGTCGAAGAAAAGGAATTAGAAAAAATTGGACAAGCCAT
 TAGGATAGAAAATCAAGAAAAATTGACTCAGCTASGKATTGTTTATCTC
 AGTTGACCCGAGTCGGTATTATTGKATGCAGCAGGTCGTyyT
 CGTTTAwAwAATGCAGACCTTGCCTTCACTAGGTGGTTATCCAAAGCCTC
 GGTAACTCAACTAGCCCTTGCACAGAACTACTCCAAATGGGACTAAGTC
 ATGAAAAGGTTGAATTTCCTTGGTAGCCAGCTTCCATTGAAGAGCTG
 CGACAAGTTGCCTACGCCCTTTACACCAAGAACTCAGCAGAGAAGATGC
 GGAGCAATTGAAAAAGATAAAGGTAAATCAGCCAGATTAACTCTCAGAG
 ATTGGAAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAAGTAGTTGATGAA
 GAATTCGCGAAAATCCACTGGTCAGAGAGTATTGGACACTTATCCTCT
 GGGGTCAATTGGTTCTATAAGGGACAGGACTTTGAGGTCAATGCGGTCA
 GCGATGCTCGA-TGAAACGGTTGATTCCGATTGAGTTAGTCATGACTTT
 TCGGATATCATTGAACAAAATCCAGTTTATGTGAGGACCTGGGAGA
 AGTCAGTCAGGCACCTTCATCAGCCAAAGGCAGAACACAAAAGAGTTAG
 AAGAAGCGGACCAAGAATTAAACCTATTCTCATTTCTGAAGAGGAGCTA
 GTTCAGAGTATTGGACTATTGGAACCCAGATGATTCAAGAAAATGGTCATAA
 CGATACTGATCTTGAAGAACAGATAATCAAATTCTGAAGAGGAAGTCG
 TCGAAACAATTCCAGAGATTCCAGTAACGGACTTTATTCCAGAAGAT
 TTGACGGACTTTATCCTAAGACTGCTAGAGATAAGGTTGAGACAAACAT
 TGTGGCCATTGGTGGTAAAAAATCTAGAAGTAGAGCACCGCAATGCTT
 CACCAAGTGAACAAGAAACTCCTTGCCAAAGTATGCTAGGCTGGGGTGGACTA
 GCAATGAATTGGTGTGACTATAATCCAAAATTCTAAGGAACGAGA
 AGAAGTCAGAGCCTAGTCACAGATAAAGAGTATTGGATATGAAACAGT
 CCTCCCTGACAGCCTATTACACAGACCCATCCGTATCCGTAGATGTGG
 GATAAGTTGAAAGAGATGGCTTACAGGTGGCAAATCTAGATCCTTC
 CATGGGAACAGGGAATTCTTGCCTATGCCAAACACTTAAGAGAAA
 AGAGTGAGTTGATGGCTAGAGTTAGATACTATTACAGGAGCTATTGCC
 AAACACCTTCATCCAAATAGTCATATTGAAATTAAAGGATTGAGACGGT
 GGCTTTAACGACAATAGTTGATTGGTATTCAAATGTGCCCTTG
 CCAATATAACGAAATTGGGATAATAGGTACGATAGGCCTTACATGATTCA
 GACTACTTGTGAAAGACTATGGCTTACAGGTGGCTATGCTAGATGGGACAAGT
 AGCGATTATCTTCCACAGGAACATGGATAAGCGAACAGAAAACATCT
 TACAAGATAATTGAGACAACGTGAAATTCTTGGTGGGGTTCGACTGCCT
 GACTCTGCCCTTAAGGCCATTGCAAGAACGAGTGTGACAACGGGATATGTT
 ATTCTTCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTAGCCT
 TTTCAGGTTCCATTGCTATGACAAGGATAGTCGATTGGCTCAATCCT
 TATTGGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTCA
 GAATTAAACGGAGGAACACTTCTGTTAAGGGGACTAGTGATGACTTGA
 TTGCAAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATT
 GATAAGAATGAGGTCAATTAAACCCAGATGTGTTGACAAACAGTCAA
 TGATACCTCATTCCAGCTGAAATGAGGGAAAATCTAGGTCAAGTACAGTT
 TTGGTTATCAGGGGTCTACAGTTACTATCGAGATAACAAAGGCATTGCA
 GTCGGAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

SEQ ID. NO. 7003

STRAIN 18RS21

GnAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGA
 GCCACTATTCTCGTGTAGAGCCTTGCTTGAGGCATTTTATATTACCA
 AGCAGAGCATTGATGAGGAGTGGGATAGTCTTATTGATCAGTTATG
 CCAATAGGCAAAATAATAAGTCTGTTCAAGTACTTCACCTTGAGACA
 GATGTTTCAGCTTGTCCAGGCTAGTCCTTATGATACTGCTCATGATCT
 ATTGACCTATAACACAAGTTTCCGGCAAAGTGGTCTTCAGGATA
 AACTATCGCCCTGAAAAAAACTTGGGTGATAGAAGTGGCCTTGTCAAT
 CTGGCCACTCGTTTCAATTATTGGATTCCAATGGACACTACCAAACC
 ATCGCCGATTCACTCTACAAAGAGTAGGGAGCTAATTGGTCAATG
 TGTATCGTGTGGCTAATAATTAGCGGATCGTATTAGTCGAGATATTGAA
 CAGTTCTTAAACTTACGAGCCTGAGCCTGAAACTAGAGCTGATGAAAC
 TGTCTAGAAAATGAAGAAAAGTGGATGAGCAGACAAACAGTGGTCA
 AAGCAATATCTTTCAGAGAAGAGGGCTCTGGTTATTGCTAGTTGGAT
 GTAGATTGCTCAACTAGATGTTCAATAGGAAAACAGTCATCTGCC
 AGCTTATGAAGAGTTATCCTACGACGTAATTGAGATTCTAACATATT
 TTGACCAAATTGAAATGAACGTTCCAAAGTCCCAAGTGGTAGACGAGGT

SEQUENCE LISTING

GATTTGACACAGAGATGAAATGACACCAGTCTTGATGGCGAGGAATT
 ACTTACTTATCTCGAAGCTGATGGCAGTCCTATGAGCTGAAACGAACGC
 TGACTACAGt cGAAGAAAAGGAATTAGAAAAAAATGGACAAGCCATTAGG
 ATAGAAAATCAAGAAAATGACTCAGCTAGGGATTGATTTATCTCAGTT
 TGACCCAGACGGAGTCGGTATTGATGCGAGGTCGTTTCTGTT
 TAAAAATGAGACCTTGTCTTACTAGGTGGTTATCCAAAGCCTCGGTA
 ACTCAACTAGCCTTGCAGAGAACTACTCCAAATGGGACTAAGTCATGA
 AAAGGTTGAATTTCCTTGGTAGCCAGCTTCCATTGAAGAGCTGCGAC
 AAGTTGCCTACGCCTTTTACACCAAGAACTCAGCAGAGAAGATGCGGAG
 CAATTGAAAAGATAAAGGTAATCAGCCAGATTAACTCTCAGAGATTG
 GAAAAGCAAGCTAGAGAAAGCTGAGGAAAAGAAGTAGTTGATGAAGAAT
 TCGCGAAAATCCACTGGTCAGAGAGTATTGGACACTTATCCTCTGGGG
 TCATTGGTTCTATAAGGGACAGGACTTGGAGGTCAATGCGTCAGCGA
 TGCTCGATTGAACGGTTGATTGGAGTTAGTCATGACTTTTCGg
 ATATCATTGAACAAAATCCAGTTCATTGAGGACCTGGGAAGAAGTC
 AGTCAGGCACTTCATCAGGAAAGGCAAGAACACAGAGTTAGAAGA
 AGCGGACCAAGAATTAAACCTATTCTCATTTCTGAAAGAGGAGCCAGTTC
 AGAGTATTGGACTATTGGAACCAAGTAGATTCAAGGAAATGGTCATAACGAT
 ACTGATCTTGAAGAAACAGATAATCAAATTCTGAAAGAGGAAGTCGTCGA
 AACAAATTCCAGAGATTCCAGTAACGGACTTTTATTTCAGAAGATTG
 CGGACTTTATCTAAGACTGCTAGAGATAAGGTTGAGACAAACATTG
 GCCATTCTGTTGGTAAAAAAATCTAGAAGTAGAGCACCGCAATGCTTCACC
 AAGTGAACAAGAACTCCTGCAAGTAGTGTAGGGTGGACTAGCCA
 ATGAATTTTTGATGACTATAATCCAAAATTCTAAGGAAAGAGAA
 CTGAAAGAGCCTAGTCAGAGATAAAAGAGTATTGGATATGAAACAGTCCTC
 CTCAGACGCTTATTACACAGACCCATCCCTGATCGTCAGATGTGGATA
 AGTGGAAAGAGATGGCTTACAGGGCAAAATCTAGATCCTCCATG
 GGAACAGGGAAATTCTTGCCTATGCCAAAACACTTAAGAGAAAAGAG
 TGAGTTGATGGCTAGAGTTAGATACTATTACAGGAGCTATTGCCAAAC
 ACCTTCATCCAAATAGTCATATTGAAATTAAAGGGATTGAGACGGTGGCT
 TTTAACGACAATAGTTGATTTGGTATTCAAATGTGCCCTTGCCAA
 TATACGAATTGCGATAATAGGTACGATAGGCCTACATGATTGACT
 ACTTTGTCAAAAGTCACTGATTTGCTTATGATGGTGGAAAGTAGCG
 ATTATCTCTTACAGGAATATGGATAAGCGAACAGAAAACATCTTACA
 AGATATTCTGAGACAACTGAATTCTTGGTGGGTTGACTGCTGACT
 CTGCTTTAAGGCCATTGAGGAACGAGTGTCAACACGGATATGTTATT
 TTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTAGCCTTT
 AGGTTCCATTGCTATGACAAGGATAGTCGATTGGCTCAATCCTTATT
 TTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTAGGAAT
 TTTAACGGAGAACACTTCTGTTAAGGGGACTAGTGATGACTTGATTG
 AAGTGTGAAACAGCTAAATCACGTTAAGGCCAAGAGAGATTGATA
 GAAATGAGGTATCATTAAACCCAGATGTGGTGGACAAACAGTCATGAT
 ACCTCCATTCCAGCTGAATGAGGAAATCTAGTCAGTACAGTTTGG
 TTATCAGGGTCTACAGTTACTATCGAGATAACAAAGGATTGAGTCG
 GAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

SEQ ID. NO. 7004

STRAIN H36B frame: 1

GGKMNQEVLLQMMRATIPRDRALLEAFLYYQAEHFDEEWDSLHMQFTNRQEINKSVQL
 HFETDVSASFQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPSEKNLVIEVALFNLATRFQ
 LLDNSNGHYQTISPDSLLQKSQRGANLVNVYRVANNLADRIISRDIEQFLTYEPELETRADE
 TVLENEETVDEHKTSVHQATISFREEGLSVRIASLDVDSLSQLDVQIGKTSHLPAYEELS
 LRRKFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEELLYLEADGSPYELKRLTT
 VEEKELEKIGQAIRIENQEKLQLXIXLSQFDPDRVGILLXAAGRXLXNADLASLGGYP
 KASVTQOLALATELLQMGLSHEKVEFFFGSQLSIEELRQVAYAFLHQELSREDAEOFKDK
 GNQPDILTLRDWKSKEKAEGKEVVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS
 DARLNGLIRIELVNDFSDIIIEQNPVLYVRTWEVSQALHQPKAEQTELEEADQELNLFS
 FLEEEELVQSIGLLEPDDSENGHNDTLEEDDNQIPEEEVETIPEIPVTDFYFPEDLTDF
 YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
 EREELKSLVTDKKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPSMGTGNNF
 AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFTVAFNDNSFDLVISNPVFA
 NIRIADNRYDRPYMIHDYFVKKSDDLHDDGGQVAIISSTGTMDKRTENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPYFDG
 EYNSQLGTYEVRFNGGTLVKGTSDLIASVETALNHVKAPREIDRNEVIINPDVLTK

SEQUENCE LISTING

QVNNTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID. NO. 7005

STRAIN 18RS21 frame: 1

XGKMNQEVLQMMRATIPRDRALLEAFLYQAEHFDEEDSLIHQFMTNRQEINKSVQL
 HFETDVSASFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
 LLDNSNGHYQTISPDSSLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
 TVLENEETVDEHKTSVHQAISFREEGSLVIASLDVDSLQLDVQIGKTSHPAYEELSLRR
 KFEILTYFDQIRNERSKVPFSRRGDFTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
 VEEKELEKIGQAIRIENQEKLQLGIDLSQFDPDRVGILLDAAGRFRLKNAIDLALLGGYP
 KASVTQLALATELLQMGLSHEKVEFFFGSQLSIEELRQVAYAFLHQELSREDAEQFEKDK
 GNQPDLTLDWKSKEAEGKEVVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS
 DARLNGLIRIELVNDFSDIIEQNPVLYVRTWEEVSQLHQPKAEQTELEEADQELNLFS
 FLEEEPVQSIQGLLEPDDSENGHNDTLEETDNQIPEEEVVETIPEIPVTDYFPEDLTDF
 YPKTARDKVTNIVAIRLVKNLEVERHNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGFTGGKILDPSMGTGNFF
 AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFTVAFNDNSFDLVISNPVFA
 NIRIADNRYDRPYMIHDYFVKKSLDLHDGGQVAIISSTGTMKDRTENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPYFDG
 EYNSQVLGTYEVRFNGGTLVKGTSDLIASVETALNHVKAPREIDRNEVIINPDVLTK
 QVNNTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID. NO. 7006

STRAIN 2603 frame: 1

GGKMNQEVLQMMRATIPRDRALLEAFLYQAEHFDEEDSLIHQFMTNRQEINKSVQL
 HFETDVSASFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
 LLDNSNGHYQTISPDSSLQKSRGANLVNVYRVANNLADRISRDIEQFLTYEPELETRADE
 TVLENEETVDEHKTSVHQAISFREEGSLVIASLDVDSLQLDVQIGKTSHPAYEELSLRR
 KFEILTYFDQIRNERSKVPFSRRGDFTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
 VEEKELEKIGQAIRIENQEKLQLGIDLSQFDPDRVGILLDAAGRFRLKNAIDLALLGGYP
 KASVTQLALATELLQMGLSHEKVEFFFGSQLSIEELRQVAYAFLHQELSREDAEQFEKDK
 GNQPDLTLDWKSKEAEGKEVVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS
 DARLNGLIRIELVNDFSDIIEQNPVLYVRTWEEVSQLHQPKAEQTELEEADQELNLFS
 FLEEEPVQSIQGLLEPDDSENGHNDTLEETDNQIPEEEVVETIPEIPVTDYFPEDLTDF
 YPKTARDKVTNIVAIRLVKNLEVERHNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGFTGGKILDPSMGTGNFF
 AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFTVAFNDNSFDLVISNPVFA
 NIRIADNRYDRPYMIHDYFVKKSLDLHDGGQVAIISSTGTMKDRTENILQDIRETTEFL
 GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPYFDG
 EYNSQVLGTYEVRFNGGTLVKGTSDLIASVETALNHVKAPREIDRNEVIINPDVLTK
 QVNNTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID NO. 7101

STRAIN 2603

ATGAAAAAGAAAAATTATTTGAAAAGTAGTGTCTGGTTAGTCGCTGGACTTCTATT
 ATGTTCTCAAGCGTGTGCGGGACCAAGTCGGTGTCCAAGTTATAGGCGTCATGACTTT
 CATGGTGCACCTGACAATACTGGAACAGCAAATATGCCGTATGGAAAAGTTGCTAATGCT
 GGTACTGCTGCTCAATTAGATGTTATGGATGACGCTAAAAAGATTCAAACAAACT
 AACCTTAATGGTAAAGCATTAGGGTCAAGCAGGGCATATGGTGGAGCAAGTCCAGCC
 AACTCTGGGCTCTTCAAGATGAACCAACTGTCAAAAATTAAATGCAATGAATGTTGAG
 TATGGCACATTGGTAACCATGAATTGATGAAGGGTGGCAGAAATATAATCGTATCGTT
 ACTGGTAAAGGGCTCCAGATTCTAATATAATAATTACGAAATCATAACCCACAT
 GAAGCTGCAAACAAAGAAATTGAGTGGCAAATGTTATTGATAAAAGTTAACAAACAAATT
 CCTTACAATTGGAAGCCTACGCTATAAAATATTCTGTAAATAACAAAAGTGTGAAC
 GTTGGCTTATCGGGATTGTACCAAAAGACATCCCAAACCTGTCTTACGTAAGGATAT
 GAACAATATGAATTAGATGAAGCTGAAACAATCGTAAATACGCCAAGAATTACAA
 GCTAAAAATGTCAAAGCTATTGAGTCTCGCACATGTACCTGCAACAAGTAAAATGAT
 ATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCATCAACTCTCCCTGAAAAT
 AGCGTAGATATTGCTTGGACACAATCATCAATATAACAAATGGTCTTGGTGTAAA
 ACTCGTATTGACAAGCGCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTTA
 GATACTGATAACACAAGATTGAGTGGACCCCTTCAGCTAAAGTAATTGAGTGGCTCCT
 GGTAAAAAAACAGGTAGTGGCAGATTCAAGCCATTGTTGACCAAGCTAATACATCGTT
 AAACAAGTAACAGAAGCTAAAATTGGTACTGCGCAGGTAAAGTGTCAATTACGCGTTCT
 GTTGTATCAAGATAATGTTAGTCGGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATT

SEQUENCE LISTING

GCTCGAAAAAGCTGGCCAGATATCGATTTGCCATGACAAATAATGGTGGCATTGCTGCT
 GACTTACTCATCAAACCAGATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTAACCT
 TTTGGTAATATCTTACAAGTCGTCGAAATTACTGGTAGAGATCTTATAAAGCACTCAAC
 GAACAATACGACCAAAAACAAAATTCTCCTCAAAATAGCTGGTCTGCATACTTAC
 ACAGATAATAAAGAGGGCGGGAGAACACCAATTAAAGCTGGTAAAGCTTATAAATCA
 AATGGTGGAGGAATCAATCTGATGCAAATACAAATTAGTTATCAATGACTTTTATTC
 GGTGGTGGTGTGGCTTGCAGAGCTTCAGAAATGCGACTTCTAGGAGCATTAAACCC
 GATACAGAGGTATTATGGCTATATCAGTGGTAGAAAAAGCTGGTAAAAGTGAGC
 GTTCAAATAATAACCTAAATCTATGTCAGTGAAGATGGTTAATGAAACTATTACA
 CAAATGATGGTACACATAGCATTAAAGAAACTTTATAGATCGACAAGGAATATT
 GTAGCACAAGAGATTGTATCAGACACTTAAACCAACAAATCTACAAAAATC
 AACCTGTAACATACAATTCAACAAACATTACACCAATTACAGCTATAACCTATG
 AGAAATTATGGCAAACCATCAAACACTGTAACAAACATTACCAACAAAC
 AACTCTGAATATGGACAATCATTGCTTATGTCGTGTTGGACTTATAGGAATT
 GCTTAAATACAAAGAAAAACATATGAAA

SEQ ID NO. 7102

STRAIN 090

AAGTCGGTGTCCAAGTTATAGCGTCAATGACTTTCATGGTGCACCTGAC
 AATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGCAC
 TGCTGCTCAATTAGATGCTTATATGGATGATGCTAAAAAGATTCAAAC
 AAACTAACCTAAATGGTGAAGCATTAGAGTTCAGCTGGTGTATGGTT
 GGAGCAAGTCCAGCTAACTCAGGGCTTCTCAAGATGAACCAACCGTTAA
 AACATTAAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAAAT
 TTGATGAAGGTTGGCAGAATACAATCGTACTGTTACTGGAAAGGCCCCCT
 GCTCAGATTCTAATAAATAATTACGAAATCATACCCACACGAAGC
 TGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAAGTTAACAAAC
 AAATCCCTTACAATTGAAACCTTACGCTATTAAAAATATTCTGTAAAT
 AACAAAAGTGTGAACGTTGGCTTATCGGAATCGTTACCAAAGACATCCC
 AAACCTTGCTTACGTTAAATTATGAAACAATATGAAATTAGATGAAG
 CTGAAACAATCGTTAAATACGCCAAGAATTACAAGCTAAAATGTCAG
 GCTATTGTTAGTCCCTGCTCATGTAACCTGCAACAAGCAAGGATGATATTGC
 TGAAGGTGAAGCAGCAGAAATGATGAAAAAGCTCAACTCTCCCTG
 AAAATAGCGTAGATATTGCTTGTGGACACAATCATCAATATAAAAT
 GGTCTTGTGGTAAACCTCGCATTGACAAGCGCTCTCTCAAGGAAAGC
 CTATGCTGACGTACGTGGTCTCTAGATACTGATAACACAAGATTCTATTG
 AAACCCCTTCACTAAAGTAGTTGCAAGTTGCTCTGGTAAAAAAACAGGT
 AGTGCCTGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACA
 AGTAACAGAAGCTAAATTGGTACTGCCGAGGTAGTGGCATGATTACGC
 GTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCATCACAGAG
 GCTCAACTAGCAATTGCTGAAAAGCTGGCCAGATATCGATTGGCCAT
 GACAAATAATGGTGGCATTGCTGACTTACTCATCAAACAGATGGAA
 CAATCACCTGGGGAGCTGCAACCGAGTTCAACCTTGGTATATCTTA
 CAAGTCGTCGAAATTACTGGTAGAGATCTTATAAGCACTAACGAACA
 ATACGACCAAAACAAATTCTCCTCAAAAGCTGGTCTGCATAACA
 CTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCAATTAAAGTTGTA
 AAAGCTTATAAAATCAAATGGTGAAGAAATCAATCTGATGCAAATACAA
 ATTGTTATCAATGACTTTTATTGCGTGGTGTGGCATGGCTTGCAAGCT
 TCAGAAATGCCAAACTCTAGGAGCATTAAATCCGATAACAGAGGTATT
 ATGGCCTATATCACTGATTAGAAAAGCTGGTAAAAAGTGAGCGTTCC
 AAATAATAAACCTAAACCTATGTCAGTGAAGATGGTAAATGAAACTA
 TTACACAAATGAGGTACACATAGGATTATAAGAAACTTTATTAGAT
 CGACAAGGAAATTGTTAGCACAAGAGATTGTATCAGACACTTAAACCA
 AACAAACATCAAATCTACAAAATCACCCCTGTAACACTAACATTCAACAAA
 AACAAATTACACCAATTACAGCTATTAAACCTATGAGAAATTATGGCAAAC
 CCATCAAACCTCCACTACTGTAACAAACATGAAATGCAATGAATGT

SEQ ID NO. 7103

STRAIN A909

GCCTCAATGACTTTCATGGTGCaCTTGACAATACTGGAACAGCAAATATG
 CCTGACGGAAAAGTTACTAATGCTGGCACTGCTGCTCAATTAGATGCTTA
 TATGGATGATGCTAAAAGATTCAAACAAACTAACCTAATGGTAAA
 GCATTAGAGTCAAGCTGGTGTATGGTGGAGAAGTCCAGCTAACTCA
 GGGCTTCTCAAGATGAACCAACCGTAAACACATTAAATGCAATGAATGT

SEQUENCE LISTING

TGAGTATGGCACATTAGGTAAACCATGAATTGATGAAGGTTGGCAGAAT
 ACAATCGTATCGTTACTGGAAAGGCCCTGCTCCaGATTCTAATATAAAT
 AATATTACGAAATCATAACCCACACGAAGCTGCAAAACAAGAAATTGTAGT
 GGCACACGTTATTGATAAAGTTAACAAACATCCCTACATTGGAAAC
 CTTACACTATTAAAATATTCTGTAAATAAACAAAGTGTGAACGTTGGC
 TTTATCGGAATCGTTACCAAAGACATCCAAACCTTGTCTTACGTAAAAA
 TTATGAACAATATGAATTAGATGAAGCTGAAACAATCGTAAATACG
 CCAAAGAATTACAAGCTAAAATGTCAAGGCTATTGATGCTTGTCTCAT
 GTACCTGCAACAAGCAAGGATGATATTGCTGAAGGTGAAGCAGCAGAAAT
 GATGAAAAAAGTCAATCAACTCTTCCCTGAAAATAGCGTAGATATTGTCT
 TTGCTGGACACAATCATCAATACAAATGGTCTTGTGTTAAAACCTCGT
 ATTGTACAAGCGCTCTCAAGGAAAAGCCTATGCTGATGACGTGGTGT
 CCTAGATACTGATAACACAAGATTCTCATGGAAACCCCTTCAGCTAAAGTAA
 TTGCGAGTTGCTCTGTGAAAAAAACAGGTAGTGGCGATATTCAAGCCATT
 GTGACCAAGCTAATACTATCGTTAACAAAGTAACAGAAAGCTAAAATTGG
 TACTGCCGAGGTAAGTGGCATGATTACCGTTCTGTTGATCAAGATAATG
 TTAGTCGGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATTGCTCGA
 AAAAGCTGGCAGATATCGATTTGCCATGACAAATAATGGTGGCATTCC
 TGCTGACTTACTCATCAAACCAAGATGGAACAATCACCTGGGAGCTGCAC
 AAGCAGTCAACCTTTGTAATATCTTACAAGTCGAAATTACTGGT
 AGAGATCTTATAAAGCACTCAACGAACAATACGACAAAAACAAAATT
 CTTCTTCAAATAGCTGGCTGCGATACACTTACACAGATAATAAGAGG
 GCGGGGAAGAAACACCATTTAAAGTTGTAAGGCTTATAATCAAATGGT
 GAGGAAATCAATCCTGATGCAAATACAAATTAGTTATCAATGACTTTT
 ATTGGTGGTGGTGTGATGGCTTGCAAGCTTCAGAAATGCCAACCTCTAG
 GAGCCATTAATCCGATACAGAGGTATTGCTTACACTGATTAA
 GAAAAAGCTGGTAAAAAGTGGCTTACAGATAATAAAACCTAAATCTA
 TGTCACTATGAAGATGGTTAATGAAACTATTACACAAATGATGGTACAT
 ATAGCATTATTAAGAACTTTATTTAGATGACAAGGAAATTGTTAGCA
 CAAGAGATTGATCAGACACTTAAACCAACAAATCAAATCTACAAA
 AATCAACCCCTGTAACTACAAATTGACAAACAAATTACACCAATTACAG
 CTATTAACCCATGAGAAATTATGGCAAACCATCAAACCTCCACTACTGTA
 AAATCAAAACAA

SEQ ID NO. 7104

STRAIN H36B

CCAAGTCGGTGTCCAAGTTAGGCCTCAATGACTTCAATGGTGCACCTTG
 ACAATACTGGAACAGCAAATATGCCCTGACGGAAAAGTTACTAATGCTGGC
 ACTGCTGCTCAATTAGATGCTTATGGATGATGCTCAAAAGATTTCAA
 ACAAAACTAACCCATAATGGTGAAGCATTAGGTTCAAGCTGGTGTGATATGG
 TTGGAGCAAGTCCAGCTAATCAGGGCTTCAAGATGAACCAACCGTT
 AAAACATTAAATGCAATGAATGTTGAGTATGGCACATTAGGTAAACCATGA
 ATTGATGAAGGTTGGCAGAATACATGTTACGTGAAAGGCC
 CTGCTCCAGATTCTAAATAATATTACGAAATCATACCCACAGAA
 GCTGAAAACAAGAAATTGAGTGGCAAACGTTATTGATAAAGTTAACAA
 ACAAACTCCCTACAATTGAAACCTTACACTATTAAATATTCTGTAA
 ATAACAAAAGTGTGAACGTTGGCTTATGGAATCGTTACCAAAGACATC
 CCAAACCTTGTCTTACGAAAAATTGAAACAAATGAAATTGTTAGATGA
 AGCTGAAACAATCGTAAATACGCCAAGAATTACAAGCTAAAATGTCA
 AGGCTATTGATGCTTGTCTGATGCTACCTGCAACAGCAAGGATGATATT
 GCTGAGGTGAAGCAGCAGAAATGATGAGGAAAGTCAATCAACTCTTCCC
 TGAAAATAGCGTAGATATTGCTTGTGACACAAATCATCAATATAACAA
 ATGGTCTTGGTAAACTCGTATTGATGAAAGCGCTCTCAAGGAAA
 GCCTATGCTGATGTCAGTGGCTCTAGATACTGATAACACAAGATTCT
 TGAAAACCCCTCAGCTAAAGTAATTGCAAGTGTGCTCTGGTAAAAACAG
 GTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTAAA
 CAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAGTGGCATGATTAC
 GCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAG
 AGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCAGATATCGATTGGC
 ATGACAAATAATGGTGGCATTGCTGACTTACTCATCAAACCCAGATGG
 AACAAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTGGTAAATATCT
 TACAAGTCGTCGAAATTACTGGTAGAGGATCTTATAAAGCACTCAACGAA
 CAATACGACCAAAAACAAATTCTCCCTCAAATAGCTGGTCTGCGATA
 CACTTACACAGATAATAAGAGGGCGGGAGAAACACCATTAAAGTTG

SEQUENCE LISTING

TAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATAC
 AAAATTAGTTATCAATGACTTTTATTCCGGTGGTGGTATGGCTTGCAAG
 CTTCAGAAATGCCAAACTCTAGGAGCCATTAAATCCGATACAGAGGTAT
 TTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGGCGTT
 CCAAATAATAAACCTAAATCTATGTCACTATGAAGATGGTAAATGAAAC
 TATTACACAAAATGATGGTACATATAGCATTAAAGAAACTTATTAG
 ATCGACAAGGAAATATTGAGCACAAGAGATTGATCAGACACTTAAAC
 CAAACAAAATCAAATCTACAAAATCAACCTGTAACACTACAATTCAA
 AAAACAATTACACCAATTACAGCTATTAACCTATGAGAAATTATGGCA
 AACCATCAAACCTCACTACTGAAATCAA

SEQ ID NO. 7105

STRAIN 18RS21

GACCAAGTCGGTGTCCAAGTTAGGCGTCAATGACTTTC
 ATGGTGCACTTGACAATACTGGAACAGCAAATATGCCTGACGGAAAAGTT
 AnTATGCTGGACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCA
 AAAAGATTTCAAACAAACTAACCTAATGGTAAAGCATTAGAGTTCAAG
 CTGGTGATATGGTGGAGCAAGTCCAGCTAACTCAGGGCTTCTCAAGAT
 GAACCAACCGTAAACATTTAATGCAATGAATGTTGAGTATGGCACATT
 AGGTAACCATGAATTGATGAAGGTTGGCAGAAATACAATCGTATCGTTA
 CTGGAAAGGCCCTGCTCCAGATTCTAAATATAAAATATTACGAAATCA
 TACCCACACGAAGCTGCAAACAAAGAAATTGATGGCAAACGTTATTGA
 TAAAGTTAACAAACAAATCCCTTACAATTGGAAACCTTACACTATTAAA
 ATATTCTGTAAACAAACAAATGGTAAAGCATTGCTTACACTATTAAA
 ACCAAAGACATCCCAAACCTGTCTTACGTTAAATGAAACATATGA
 ATTTTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAG
 CTAAAATGTCAGGCTATTGATGCTCATGTCACCTGCAACAAGC
 AAGGATGATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAGAAAGTCAA
 TCAACTCTCCCTGAAAATAGCGTAGATATTGCTTTGCTGGACACAATC
 ATCAATATACAAATGGTCTTGGTAAAACCTGTTACGCTACAGCGCTC
 TCTCAAGGAAAAGCCTATGCTGATGTCAGTGGTGTCTAGATACTGATAC
 ACAAGATTTCATGAAACCCCTTCAGCTAAAGTAATTGCGATTGCTCCTG
 GTAAAAAAACAGGTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAAT
 ACTATCGTTAAACAAAGTAACAGAAAGCTAAAATTGGTACTGCCGAGGTAAG
 TGGCATGATTACGCGTTCTGTTGATCAAGATAATTGTTAGTCCGGTAGGCA
 GCCTCATCACAGAGGCTCAACTAGCAATTGCTGAAAAAGCTGGCCAGAT
 ATCGATTTGCCATGACAAAATGGTGGCATTGCTGCTGACTTACTCAT
 CAAACCAGATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTT
 TTGGTAATATCTTACAAGCTCGAAATTACTGGTAGAGATCTTATAAA
 GCACATCAACGAAACAATACGACCAAAACAAAATTCTTCTTCAAATAGC
 TGGCTGCGATACACTTACACAGATAATAAGAGGGCGGGGAAGAAACAC
 CATTAAAGTGTAAACGTTATAAAATCAAATGGTGAGGAAATCAATCCT
 GATGCAAATGAAACAAATTAGTTCAATGACTTTTATTGGTGGTGGTGA
 TGGCTTGCAAGCTTCAGAAATGCCAAACTCTAGGAGCCATTATCCCG
 ATACAGAGGTATTGATGGCTATATCACTGATTAGAAAAGCTGGTAA
 AAAGTGAGCGTTCAAATAATAACCTAAAATCTATGTCACATAGCATTATAAGA
 AACTTTATTAGATGACAAGGAAATTGATGGCACAAGAGATTGTATCA
 GACACTTTAACCAAACAAATCAAATCTACAAAATCAACCTGTAAC
 TACAATTACACAAAACAAATTACACCAATTACAGCTATTAACCTATGA
 GAAATTATGGCAAACCATCAAACCTCACTACTGAAATCAA

SEQ ID NO. 7106

STRAIN M732

ACCAAGTCGGTGTCCAAGTTAGGCGTCAATGACTTTCATGGTGCACCT
 GACAATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTAAAAAGATTCA
 AACAAACTAACCTTAATGGTAAAGCATTAGAGTTCAAGCTGGTATATG
 GTGGAGCAAGTCCAGCTAACTCAGGGCTTCTCAAGATGAACCAACCGT
 TAAAACATTAAATGCAATGAATGTTGAGTATGGCACATTAGGTAAACCATG
 AATTGATGAAGGTTGGCAGAAATCAATCGTATCGTTACTGGAAAGGCC
 CCTGCTCCAGATTCTAAATAAAATATTACGAAATCATACCCACACGA
 AGCTGCAAACAAAGAAATTGATGGCAAACGTTATTGATAAAAGTTAAC
 AACAAATCCCTACAATTGGAAACCTACACTATTAAAATATTCTGTA

SEQUENCE LISTING

AATAACAAAAGTGTGAACGTTGGCTTATCGGAATCGTACCAAAGACAT
 CCCAACCTTGTCTTACGAAAATTATGAACAATATGAATTAGATG
 AAGCTGAAACATCGTTAAATACGCCAAGAATTACAAGCTAAAATGTC
 AAGCTATTGTAGTCCTTGCATGTACCTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAAATGATGACAAAAAGTCATCAACTCTTC
 CTGAAAATAGCGTAGATATTGTCTTGCAGACAAATCATCAATATACA
 AATGGTCTTGGTAAACTCGTATTGTACAAGCGCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTAGATACAGATAACACAAGATTCA
 TTGAAACCCCTCAGCTAAAGTAATTGAGCTTGCCTGGTAAAAAAC
 GGTAGTGCCTGATATTCAAGCCATTGTTGACCAAGCTAAACTATCGTTAA
 ACAAGTAACAGAAGCTAAATTGGTACTGCCAGGTAAGTGCATGATTA
 CGCGTTCTGTGATCAAGATAATGTTAGTCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATTG
 CATGACAAAATATGGTGGCATTGCTGACTTACTCATCAAACAGATG
 GAACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTGGTAAATATC
 TTACAAGTCGAAATTACTGGTAGAGATCTTATAAAGCACTAACAGA
 ACAATACGACCAAAACAAAATTCTCCTCAAATAGCTGGCTGCGAT
 ACACCTACACAGATAATAAAGAGGGGGGGAGAAAACACCATTAAAGTT
 GTAAAAGCTTATAAATCAAATGGTAGGAAATCAATCCTGATGCAAATA
 CAAATTAGTTATCAATGACTTTTATTGGTGGGTGATGGCTTGCAA
 GCTTCAGAAAATGCCAACTCTAGGAGCCATTAACTCCGATACAGAGGTA
 TTTATGGCTATATCACTGATTTAGAAAAGCTGGTAAAAAGTGAGCAT
 TCCAATAATAAACCTAAATCTATGCTACTATGAAGATGGTTAATGAAA
 CTATTACACAAAATGATGGTACATATAGCATTAAAGAAAATTATTTA
 GATCGACAAGGAAATTGGTAGCACAGAGATTGATCAGACACTTTAA
 CCAACACAAATCAAAATCAACCCCTGTAACTAACATTACA
 AAAACAAATTACACCAATTACAGCTATTACCCATTGAGAAATTATGGC
 AAACCATCAAACCTCCACTACTGTAAAATCAAACAA

SEQ ID NO. 7107

STRAIN COH1

ACCAAGTCGGTGCAGTTATAGGCGTCAATGACTTTCATGGTGCACCT
 GACAATACTGGAACAGCAATATGCCTGACGGAAAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTAAAAAGATTCA
 AACAAACTAACCTAAATGGTAAAGCATTAGAGTTCAAGCTGGTGTATG
 GTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTCAAGATGAACCAACCGT
 TAAAACATTAAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
 AATTGATGAAGGTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
 CCTGCTCCAGATTCTAATATAATAATTACGAATCATACCCACACGA
 AGCTGCAAAACAAAGAAATTGAGTGGCAACAGTTATTGATAAAGTTAAC
 AACAAACTCCCTACAAATTGGAAACCTTACACTATTAAAATATCCTGTA
 AATAACAAAAGTGTGAACGTTGGCTTATCGGAATCGTTACCAAGACAT
 CCCAACCTTGTCTTACGTTAAATACGCCAAGAATTACAAGCTAAAATGTC
 AAGCTATTGTAGTCCTTGCATGTACCTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAAATGATGAAAAAGTCATCAACTCTTC
 CTGAAAATAGCGTAGATATTGTCTTGCAGACAAATCATCAATATACA
 AATGGTCTTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTAGCTAGATACTGATACACAAGATTTC
 TTGAAACCCCTCAGCTAAAGTAATTGAGCTTGCCTCTGGTAAAAAAC
 GGTAGTGCCTGATATTCAAGCCATTGTTGACCAAGCTAAACTATCGTTAA
 ACAAGTAACAGAAGCTAAATTGGTACTGCCAGGTAAGTGCATGATTA
 CGCGTTCTGTGATCAAGATAATGTTAGTCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATTG
 CATGACAAATAATGGTGGCATTGCTGACTTACTCATCAAACCCAGATG
 GAACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTGGTAAATATC
 TTACAAGTCGAAATTACTGGTAGAGATCTTATAAAGCACTAACAGA
 ACAATACGACCAAAACAAAATTCTCCTCAAATAGCTGGCTGCGAT
 ACACCTACACAGATAATAAAGAGGGGGGGAGAAAACACCATTAAAGTT
 GTAAAAGCTTATAAATCAAATGGTAGGAAATCAATCCTGATGCAAATA
 CAAATTAGTTATCAATGACTTTTATTGGTGGGTGATGGCTTGCAA
 GCTTCAGAAAATGCCAACTCTAGGAGCCATTAACTCCGATACAGAGGTA
 TTTATGGCTATATCACTGATTTAGAAAAGCTGGTAAAAAGTGAGCAT
 TCCAATAATAAACCTAAATCTATGCACTATGAAGATGGTTAATGAAA

SEQUENCE LISTING

CTATTACACAAAATGATGGTACATATAGCATTATTAAGAAACTTATTAA
 GATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAA
 CCAAACAAAATCAAATCTACAAAATCAACCCCTGTAACTACAATTACA
 AAAAACAAATTACACCAATTACAGCTATTACCCCTATGAGAAATTATGGC
 AAACCATCAAACCTCCACTACTGTAAAATCAA

SEQ ID NO. 7108

STRAIN M781

CAAGTCGGTGTCCAAGTTAGGCGTCAATGACTTCATGGTGCACCTGAA
 CAAACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGCA
 CTGCTGTCATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAA
 CAAACTAACCTTAATGGTGAAGCATTAGAGTTCAAGCTGGTGTATGGT
 TGGAGCAAGTCCAGCTAACCTGGGCTTCTTCAGATGAACCAACCGTTA
 AAACATTAAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAA
 TTGATGAAGGTTGGCAGAAATACAATCGTATCGTTACTGGAAAGGCCCC
 TGCTCCAGATCTAATATAAAATATTACGAAATCATACCCACACGAAG
 CTGCAAAACAAAGAAATTGTAGTGGCAACGTTATGATAAAGTTAACAAA
 CAAATCCCTTACAATTGAAACCTTACACTATTAAAATATTCTGTAAA
 TAACAAAAGTGTGAACGTTGGCTTATCGGAATCGTTACCAAAGACATCC
 CAAACCTTGTCTTACGTTAAATTATGAAACAATATGAATTAGATGAA
 GCTGAAACAATCGTTAAATACGCCAAGAATTACAAGCTAAAATGTCAA
 GGCTATTGTAGTCCTTGCTCATGACTCTGCAACAAAGCAAGGATGATATTG
 CTGAAAGGTGAAGCAGCAGAAATGATGAAAAAAAGTCAACTCAACTCTCCCT
 GAAAATAGCGTAGATATTGCTTGTGGACACAAATCATCAAATATAACAAA
 TGGCTTGTGGTAAACCTCGTATTGTACAAGCGCTCTCAAGGAAAAG
 CCTATGCTGATGTACGTGGTCTAGATACTGATACACAAGATTTCATT
 GAAACCCCTTCAGCTAAAGTAATTGCAAGTGTCTGGTAAACACAGG
 TAGTGGCGATATTCAAGCCATTGtTGACCAAGCTAAACTATCGTTAAC
 AAGTAACAGAAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACG
 CGTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
 GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTGCCA
 TGACAAATAATTGGCATTGCTGACTTACTCATCAAACCCAGATGGA
 ACAATCACCTGGGAGCTGCAACAGCAGTTCAACCTTTGGTAAATATCTT
 ACAAGTGTGAAAATTACTGGTAGAGATCTTATAAAGCACTAACGAAC
 AATAGCACAAAACAAAATTCTTCCTCAAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAGAGGGGGAGAAAACACCATTAAAGTTGT
 AAAAGCTTATAAATCAAATGGTAGGAAATCAATCTGATGAAATACA
 AATTAGTTATCAATGACTTTTATTGGTGGTGTGGATGGCTTGCAAGC
 TTCAGAAATGCCAACTCTAGGAGCATTAAATCCGATACAGAGTATT
 TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGAAGCATTC
 CAAATAATAAAACCTTAAACTATGTCATGAAAGATGGTTAATGAAACT
 ATTACACAAAATGATGGTACATATAGCATTATAAGAAAACCTTATTAGA
 TCGACAAGGAAATTGTAGCACAAGAGATTGTATCAGACACTTAAACC
 AAACAAAATCAAATCTACAAAATCAACCCCTGTAACTACAATTACAAA
 AAACAAATTACACCAATTACAGCTATTACCCCTATGAGAAATTATGGCAA
 ACCATCAAACCTCCACTACTGTAAAATCAA

SEQ ID NO. 7109

STRAIN CJB110

GACCAAGTCGGTGTCCAAGTTAGGCGTCAATGACTTTCATGGTGC
 ACTTGACAATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATG
 CTGGCACTGCTGTCATTAGATGCTTATATGGATGATGCTCAAAAAGAT
 TTCAAACAAACTAACCTTAATGGTGAAGCATTAGAGTTCAAGCTGGTGA
 TATGGTTGGAGCAAGTCCAGCTAACCTGGGCTTCTCAAGATGAACCAA
 CGTTAAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAC
 CATGAATTGATGAAGGTTGGCAGAATACAATCGTATCGTTACTGGAAA
 GGCCCTGCTCCAGATTCAATATAAATAATTACGAAATCATACCCAC
 ACGAAGCTGCAAAACAAGAAATTGTAGTGGCAACGTTATTGATAAAGTT
 AACAAACAAATCCCTTACAATTGAAACCTTACGCTATTAAAATATTCC
 TGTAACAAACAAAAGTGTGAACGTTGGCTTATCGGAATCGTTACCAAAG
 ACATCCCACAACTTGCTTACGTTAAATTATGACAAATATGAATTGTTA
 GATGAAGCTGAAACAATCGTTAAATACGCCAAGAATTACAAGCTAAAAA
 TGTCAGGCTATTGTAGTGTCTTGTCTCATGTACCTGCAACAAAGCAAGGATG
 ATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTC

SEQUENCE LISTING

TTCCCTGAAAATAGCGTAGATATTGTCTTGCTGGACACAATCATCAATA
 TACAAATGGCTTGTGGTAAACTCGCATTGTACAAGCGCTCTCAAG
 GAAAAGCCTATGCTGACGTACGTGGTCTTAGATACTGATAACACAAGAT
 TTCAATTGAAAACCCCTTCAGCTAAAGTAGTTGCAAGCTGGTAAAAAA
 AACAGGTAGTGCCGATATTCAAGCCATTGGTGGACCAAGCTAATACTATCG
 TTAAACAACTGAAACAGCTAAATGGTACTGCCGAGGTAGTGGCATG
 ATTACGCGTTCTGTTGATCAAGATAATGGTAGTTGCTCAGTAGGGCAGCCTCAT
 CACAGAGGCTCAACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATT
 TTGCCATGACAAATAATGGTGGCATTGTGCTGACTTACTCATCAAACCA
 GATGGAACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTGGTAA
 TATCTTACAAGTCGTGAAATTACTGGTAGAGATCTTATAAAGCACTCA
 ACCGAAACAATACGACCAAAACAAAATTCTCCTCAAATAGCTGGCTG
 CGATACACTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTAA
 AGTTGAAAAGCTTATAAATCAAATGGTAGAGAAATCAATCCTGATGCAA
 AATAACAAATTAGTTATCAATGACTTTTATTGGTGGTGGTGGTGGCTTT
 GCAAGCTTCAGAAATGCCAAACTTCTAGGAGGCCATTAACTCCCGATACAGA
 GGTATTGATGGCCTATATCACTGATTAGAAAAGCTGGTAAAAAAAGTGA
 GCGTTCACAAATAATAAACTAAATCTATGTGACTATGAAGATGGTTAA
 GAAACTATTACACAAAATGATGGTACACATAGCATTATTAAGAAACTTTA
 TTTAGATCGACAAGGAAATTGTAGCACAAGAGATTGATCAGACACTT
 TAAACCAAACAAAATCAAATCTACAAAAATCAACCCGTAACTACAATT
 CACAAAAACAAATTACACCAATTACAGCTATTAAACCTATGAGAAATTA
 TGGCAAACCATCAAACCTCCACTGTAAAATCA

SEQ ID NO. 7110

STRAIN 1169NT

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACCTTGA
 CAATACTGGAACAGCAAATATGCCTGATGGAAAAGTTGCTAATGCTGGTA
 CTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAGATTCAA
 CAAACTAACCTTAATGGTAAAGCATTAGGGTTCAAGCAGGGGATATGGT
 TGGAGCAAGTCCAGCCAACCTCTGGGCTTCTCAAGATGAACCAACTGTCA
 AAAATTAAATGCAATGAAATGGTAGATGGCACATTGGTAACCATGAA
 TTTGATGAAGGGTTGGCAGAATATAATCGTATCGTACTGGTAAAGCCC
 TGCTCCAGATTCTAATATAATTAATAATTACGAAATCATAACCCACATGAAG
 CTGCAAAACAAGAAAATTGTTAGTGGCAATGTTATTGATAAAAGTTAACAAA
 CAAATTCTTACAATTGAAAGCCTTACGCTATTAAAAATATTCTGTAAA
 TAACAAAAGTGTGAACTGGCTTATGGGATTTGTCACCAAAGACATCC
 CAAACCTGTCTACGTTAAATTAGAACATATGAATTGGATGAA
 GCTGAAACAATCGTTAAATACGCCAAGAATTACAAGCTAAAAATGTCAA
 AGCTATTGTTAGTCTCGCACATGTACTGCAACAAAGTAAAAATGATATTG
 CTGAAAGGTGAAGCAGCAGAAATGATGAAAAAAAGTCAATCAACTCTTCCCT
 GAAAATAGCGTAGATATTGTCTTGCTGGACACAATCATCAATATAACAA
 TGGCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
 CCTATGCTGATGTACGTGGTCTTAGATACTGATACACAAGATTTCATT
 GAGACCCCTCAGCTAAAGTAATTGCAAGTTGCTCTGGTAAAAAAACAGG
 TAGTGGCGATATTCAAGCATTGTTGACCAAGCTAATACTATCGTTAAC
 AAGTAACAGAAAGCTAAATTGGTACTGCCGAGGTAAAGTGTGATGATTACCG
 CGTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
 GGCTCAACTAGCAATTGCTGAAAAAGCTGGCCAGATATCGATTTGCCA
 TGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAAACCGATGG
 ACAATCACCTGGGAGCTGCACAAGCAGTCAACCTTTGGTAAATATCTT
 ACAAGTCGCAAATTACTGGTAGAGGATCTTATAAAGCAGTCAACCGAAC
 AATACGACAAAAACAAAATTCCTTCAAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTAAAGTGT
 AAAAGCTTATAAATCAAATGGTAGGAAATCAATCTGATGCAAACAA
 AATTAGTTATCAATGACTTTTATTGGTGGTGGTATGGCTTGTGCAAGC
 TTCAAGAAATGCCAAACTTCTAGGAGCATTAAACCCGATACAGAGGTATT
 TATGGCCTATATCACTGATTAGAAAAGCTGGTAAAAAAAGTGGCGTTC
 CAAATAATAAACCTAAATCTATGTCACTATGAAGATGGTTAATGAAACT
 ATTACACAAAATGATGGTACACATAGCATTAAAGAAACTTTATTAGA
 TCGACAAGGAAATATTGTAGCACAAGAGATTGATCAGACACTTTAAACC
 AAACAAAATCAAACCAAAATCAACCCGTAACTACAATTACACAA
 AAACAAATTACACCAATTACAGCTATTAAACCTATGAGAAATTATGGCAA
 ACCATCAAACCTCCACTACTGTAAAATCAA

SEQUENCE LISTING

SEQ ID NO. 7111

STRAIN JM9130013

CGGTGTCCAAGTTATAGCGTCAATGACTTCATGGTGCAGTGACAATA
 CTGGAACAGCAAATGCGTACGGAAAAGTTACTAATGCTGGCACTGCT
 GCTCAATTAGATGCTTATGGATGATGCTCAAAAAGATTCAAACAAAC
 TAACCTTAATGGTCAAAGCATTAGAGTCAAGCTGGTATATGGTGGAG
 CAAGTCCAGCTAACTCAGGGCTTCTCAAGATGAACCAACCGTTAAAC
 TTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAATTG
 TGAAGGTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCTGCTC
 CAGATTcTAATATAAATAATTACGAAATCATACCCACACGAAGCTGCA
 AAACAAGAAATTGTTAGTGCACCGTTATTGATAAAAGTTAACAAACAAAT
 CCCTTACAATTGGAAACCTTACACTATAAAATATTCTGTAAATAACA
 AAAGTGTGAACGTTGGCTTATCGGAATCGTTACCAAGACATCCAAAC
 CTTGCTTACGTAAAATTATGAAACAATATGAATTTTAGATGAAGCTGA
 AACAAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAGGCTA
 TTGTTAGTCCTTGCTCATGTAACCTGCAACAAGCAGGATGATATTGCTGAA
 GGTGAAGCAGCAGAAATGATGAAAAAGTCATCAACTCTTCCCTGAAAA
 TAGCGTAGATATTGTTCTTGCTGGACACAATCATCAATATAACAAATGGTC
 TTGTTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAGCCTAT
 GCTGATGTACGTGGTGTCTAGATACTGATAACACAAGATTTCATTGAAAC
 CCCTTCAGCTAAAGTAATTGCAAGTTGCTCTGGTAAAAACAGGTAGTG
 CCGATATTCAAGCCATTGTTGACCAAGCTAAACTATCGTTAACAGTA
 ACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACCGGTT
 TGTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
 AACTAGCAATTGCTCGAAAAGCTGGCAGATATCGATTTCGCATGACA
 AATAATGGTGGCATTGCTGACTTACTCATCAAACCAAGATGAAACAT
 CACCTGGGAGCTGCACAAGCAGTTAACCTTTGGTAATATCTTACAAG
 TCGTCGAAATTACTGGTAGAGATCTTATAAAGCACTCAACGAACAATAC
 GACCAAAACAAAATTCTCTTCAAATAGCTGGTCTGCGATAACACTTA
 CACAGATAATAAGAGGGCGGGGAAGAAAACACCATTAAAGTTGAAAG
 CTTATAAATCAAATGGTAGGAAATCAATCTGATGCAAATACAAATT
 GTTATCAATGACTTTTATCGGTGGTGTGATGGCTTGCAAGCTTCAG
 AAATGCCAAAATTCTAGGAGCCATTAACTCCGATACAGAGGTATTG
 CCTTATCACTGATTAGAAAAGCTGGTAAAAAGTGAGCCTTCAAAT
 AATAAACCTAAATCTATGTCACTATGAAAGATGGTAATGAAACTATTAC
 AAAAAATGATGGTACATATGCAATTGAGAAACTTATTAGATGAC
 AAGGAAATATTGTTAGCACAAGAGATTGTATCAGACACTTAAACCAACA
 AAATCAAAATCTACAAAATCAACCCGTAACTACAATTCAACAAAACA
 ATTACACCAATTACAGCTATTACCCATGAGAAATTATGGCAAACCAT
 CAAACTCCACTACTGTAAAATCAAA

SEQ ID NO. 7112

STRAIN 2603 frame: 1

MKKIIILKSSVGLVAGTSIMFSSVFADQVGVQVIGVNDFHGALDNTGTANMPDGKVANA
 GTAAQLDAYMDAQKDFKQTNPNGESIRVQAGDMVGASPANSGLLQDEPTVKNFNAMNVE
 YGTLGNHEFDEGLAEYNRIVTGTGKAPAPDSNINNITKSYPHEAAKQEIVVANVIDKVNQI
 PYNWKPYAIKNIPVNNKSVNFGFIGIVTKDIPNLVLRKNYEQEFLDEAETIVKYAKELQ
 AKNVKAIVVLAHVATSKNDIAEAEAAEMMKVNVNQLFPENSVDIVFAGHNQYTNGLVGK
 TRIVQALSQGKAYADVRGVLDTDTQDFIEPTPSAKVIAVAPGKKTGSADIQAIQIVDQANTIV
 KOTVEAKIGTAEVSVMITRSVDQDNVPVGSLITEAQLAIRKSWPDIDFAMTNNGGIRA
 DLLIKPDGTITWGAAQAVQPFGNILQVVEITGRDLYKALNEEQYDQKQNFFLQIAGLRYTY
 TDNKEGGEETPFKVVKAYKNSGEEINPDAKYKLVINDFLFGGGDGFASFRNAKLLGAINP
 DTEVFMDAYITDLEKAGKKVSVPNPKIYVTMVKMNETITQNDGTHSIIKKLYLDRQGNI
 VAQEIVSDTLNQTKSKSTKINPVTTIHKKQLHQFTAIPMRNYGKPSNSTVSKQLP
 NSEYQGSFLMSVFGVGLIGIALNTKKKHMK

SEQ ID NO. 7113

STRAIN 090 frame: 3

VGQVIGVNDFHGALDNTGTANMPDGKVNTAGTAAQLDAYMDAQKDFKQTNPNGESIRV
 QAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGHNHEFDEGLAEYNRIVTGTGKAPAPDS
 NINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYAIKNIPVNNKSVNFGFIGIVTK
 DIPNLVLRKNYEQEFLDEAETIVKYAKELQAKNVKAIVVLAHVATSKDDIAEAEAAEM
 MKKVNQLFPENSVDIVFAGHNQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFIE

SEQUENCE LISTING

TPSAKVVAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPV
 GSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQVVE
 ITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPDA
 KYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSPNNKPKIY
 VTMMVMNETITQNDGTHSIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKK
 QLHQFTAIPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7114

STRAIN A909 frame: 3

VNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKOTNPNGESIRVQAGDMVG
 ASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAPDSNINNITK
 SYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIIPVNNKSVNVEFIGIVTKDIPNLVL
 RKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAEMMKVNQL
 FPENSVDIVFAGHNNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFIETPSAKVI
 AVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVGSLITEA
 QLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQVVEITGRDLY
 KALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPDAKYKLVIN
 DFLFGGGDGFAFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSPNNKPKIYVTMKMVN
 ETITQNDGTYSIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKKQLHQFTA
 INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115

STRAIN H36B frame: 2

QVGQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKOTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAP
 SNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIIPVNNKSVNVEFIGIVT
 KDIIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSPNNKPKIY
 VTMMVMNETITQNDGTYSIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKK
 QLHQFTAIPMRNYGKPSNSTTVKSK

SEQ ID NO. 7116

STRAIN 18RS21 frame: 1

DQVGQVIGVNDFHGALDNTGTANMPDGKVNAGTAAQLDAYMDDAQKDFKOTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIIPVNNKSVNVEFIGIV
 TKDIIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAA
 EMMKKVNQLFPENSVDIVFAGHNNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 PVGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQV
 VEITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 DAKYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSPNNKPKIY
 VTMMVMNETITQNDGTYSIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKK
 KKQLHQFTAIPMRNYGKPSNSTTVKSK

SEQ ID NO. 7117

STRAIN M732 frame: 3

QVGQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKOTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAP
 SNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIIPVNNKSVNVEFIGIVT
 KDIIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSPNNKPKIY
 VTMMVMNETITQNDGTYSIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKK
 KQHQFTAIPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118

SEQUENCE LISTING

STRAIN COH1 frame: 3

QVGQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGTKAPAPD
 SNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIIPVNNKSVNVGFIGIVT
 KDIPLNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEAEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSILITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFSRNAKLLGAINPDTEVFMAITYDLEKAGKKVSIPNNKPKI
 YVTMCKMVNETITQNDGTHSIICKLYLDRQGNIVQAIEIVSDTLNQTKSKSTKINPVTTIH
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7119

STRAIN M781 frame: 1

QVGQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGTKAPAPD
 SNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIIPVNNKSVNVGFIGIVT
 KDIPLNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEAEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSILITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFSRNAKLLGAINPDTEVFMAITYDLEKAGKKVSIPNNKPKI
 YVTMCKMVNETITQNDGTHSIICKLYLDRQGNIVQAIEIVSDTLNQTKSKSTKINPVTTIH
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7120

STRAIN CJB110 frame: 1

DQVGQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGTKAPAP
 DSNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYAIKNIIPVNNKSVNVGFIGIV
 TKDIPLNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEAEAA
 EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDF
 IETPSAKVVAAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 PVGSILITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
 VEITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINP
 DAKYKLVINDFLFGGGDGFAFSRNAKLLGAINPDTEVFMAITYDLEKAGKKVSVPNNKPK
 YVTMCKMVNETITQNDGTHSIICKLYLDRQGNIVQAIEIVSDTLNQTKSKSTKINPVTTIH
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7121

STRAIN 1169NT frame: 1

QVGQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKNFNAMNVEYGTGLNHEFDEGLAEYNRIVTGTKAPAPD
 SNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYAIKNIIPVNNKSVNVGFIGIVT
 KDIPLNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKNDIAEAEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSILITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFSRNAKLLGAINPDTEVFMAITYDLEKAGKKVSVPNNKPKI
 YVTMCKMVNETITQNDGTHSIICKLYLDRQGNIVQAIEIVSDTLNQTKSKSTKINPVTTIH
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7122

STRAIN JM9130013 frame: 2

GVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRQ
 AGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGTKAPAPDSN
 INNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIIPVNNKSVNVGFIGIVTKD
 IIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEAEAAEMM
 KKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFIET
 PSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVG
 SLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVEI

SEQUENCE LISTING

TGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPAK
 YKLVINDFLFGGGDGFSFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSPNNKPKIYV
 TMKMKVNETITQNDGFTSIEKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKKQ
 LHQFTAINPMRNYGKPSNSTTVKSK

SEQ ID NO. 7201

STRAIN 2603

ATGAATAACCGTAAAAATCGTGCACACTTGGTCTCGCGGTGAATTCCGTGGTG
 GTAAAGAAGTTGGTGGACTCTGGATACTGGGGTGAAGCCTGACGTAGAACGCTTCAGCAG
 AAAAAATTGCTCAATTGATTAAGAAGGTGCTAACGTTTCCGTTCAACTTCTCACATG
 GAGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGCTAAAGCAGAACAGAGATTGAG
 GACAAAAAGTTGGCTCCCTCTGATACTAAAGGACCTGAAATTGCTACAGAACCTTTG
 AAGATGGTGCAGATTTCCATTCTATACACAGGTACAAAATTACGTTGCTACTAACG
 AAGGTATCAAATCAACTCAGAAGTGAATTGCTGCTGGACTTGACATCT
 TTGATGACGTTGAAGTGGTAAGCAAATTCTGTTGATGTTGAAACTAGGTCTTACTG
 TGTTGCAAAAAGATAAAAGAACACTCGTAATTGAAAGTAGTTGAGAATGATGGCCTTA
 TTGGTAAACAAAAGGTGAAACATCCCTTATACTAAAATTCCCTTCCAGCACTTGAG
 AACCGATAATGCTGATATCCGTTGGACTTGAGCAAGGACTTAACATTATTGCTATCT
 CATTGTAACGTAACGTTGCTAAATTGAAACATGCTGCTATTGTAAGAAACTGGGsm
 ATGGACACGTTAAGTTGCTAAATTGAAACAAAGGTATGATAATATTGATG
 AGATTATCGAACAGCAGATGGTATTATGATTGCTGTTGATATGGGTATCGAACGTT
 CATTGAAATGGTCCAGTTACCAAAAATGATCATTACTAAAGTTAATGCAAGCTGGTA
 AACGAGTTATTACGCAACAAATATGCTTgAAACATGACTGATAAACCCACGTGCGACTC
 GTTCAGAAGTCTGATGCTTCAATGCTGTTATTGATGGTACTGATGCTACAATGGCTT
 CAGGTGAGTCAGCTAATGGTAAACATGGCTGTTGAGTGGTACTGTTGAGAATGGCTACTATTG
 ATAAAAATGCTCAAACATTACTCAATGAGTATGGTCACTGGTAAACTCATCTGCATTCCAC
 GTAATAACAAAACGTGTTATTGATCTGCGGTTAAAGATGCAACACACTCAATGGATA
 TCAAACATTGTTGTAACAATTACTGAAACAGGTAAACAGCTCGTGCCTATTCTAAATTCC
 GTCCAGATGCGAGACATTGGCTGTTACATTGATGAAAAAGTACAACGTTATTGATGA
 TTAACGGGGTGTATCCCTGCTTGCAGACAAACAGCATCTACAGATGATATGTTG
 AGGTTGAGAACGTGTTGAGCACTTGAAAGCAGGATTGTTGAAATCAGCGATAATATCGTTA
 TCCTGCAAGGTGTTCTGTAGGTACAGGTGGAACTAACACAATGCGTCTGTTACTGTTA
 AA

SEQ ID NO. 7202

STRAIN 090

AATAAACCGTAAAAATCGTGCACACT
 TGGCCTGCGGTAGAATTCCGTGGTGAAGAAGTTGGTGAGTCTGGAT
 ACTGGGGTGAAGCCTGACGTAGAACGTTCTCAGCAGAAAAAATTGCTCAA
 TTGATTAAAGAAGGTGCTAACGTTTCCGTTCACTTCTCACATGGAGA
 TCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGCTAAAGCAGAACAGA
 TTGAGGACAAAAGTTGGCTTCCCTGTTGATGACTAAAGGACCTGAAATT
 CGTACAGAACCTTTTGAAAGATGGTCAAGATTCCATTCTACATACACAGG
 TACAGAATTACGTTGCTACTAAGCAAGGTACAAATCAACTCCAGAAG
 TGATTGCAATTGAAATGTTGCTGGTGGACTTGACATCTTGATGACGTTGAA
 GTTGGTAAGCAAATTCTGTTGATGATGGTAAACTAGGTCTACTGTTG
 TGAAAAGATAAAAGACACTCgTGAATTGAAAGTAGTTGTTGAGAATGATG
 GCCTTATTGGTAAACAAAGGTAAACATCCCTTATACTAAATTCCCT
 TTCCCAgCACTTGCAGAACCGGATAATGCTGATATCCGTTGGACTTG
 GCAAGGACTTAACCTTATGCTATCTCATTTGACGTTACTGCTAAAGATG
 TTAATGAAAGTCTGCTATTGTAAGAAAAGTGGCAATGGACATGTTAAG
 TTGTTGCTAAATTGAAACAAAGGTATGATAATTGATGAGAT
 TATCGAAGCAGCAGATGGTATTATGATTGCTGCTGGTGAATGGGTATCG
 AAGTTCCATTGAAATGGTCCAGTTACAAAAATTGATCATTACTAAA
 GTTAATGCGAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTGAAAC
 AATGACTGATAAAACCACGTGCGACTCGTCAGAAGTATCTGATGTTCTCA
 ATGCTGTTATTGATGGTACTGATGCTACAATGCTTCAAGGTGAGTCAGCT
 AATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGATAA
 AAATGCTAAACATTACTCAATGAGTATGGTGGCTTAGACTCATCTGCAT
 TCCCACGTAATAACAAAAGTGTATTGATCTGATCTGCGGTTAAAGATGCA
 ACACACTCAATGGTAAACAAACTTGTGAGCAATTACTGAAACAGGTAA
 TACAGCTCGTGCCTTCAAAATTCCGTCCAGATGCGAGACATTGGCTG
 TTACATTGATGAAAAGTACAACGTTATTGATGATTAACAGATGATATGGGGTGT
 ATCCCTGCTTGCAGACAAACAGCATCTACAGATGATATGTTGAGGT

SEQUENCE LISTING

TGCAGAACGTGAGCACTTGAAGCAGGACTTGGTAATCAGGCGATAATA
TCGTTATCGTGCAGGTGTCCTGTAGGTACAGGTGGAACAAACACAATG
CGTGTTCGTACTGTTAAA

SEQ ID NO. 7203

STRAIN A909

AATAAACCGCGAAAAATCGTGCACACACTGGTC
CTGCGGTTGAATTCCGTGGTGGTAAGAAGTTGGTGAGTCTGGATACTGG
GGTGAAGCCTGACGTAGAACGCTTCAGCAGAAAAAATTGCTCAATTGAT
TAAAGAAGGTGCTAACGTTTCCGTTCAACTTCTCACATGGAGATCATG
CTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAGAGATTGCA
GGCAAAAAAGTTGGCTCCCTGATACTAAAGGACCTGAAATTGTC
AGAACCTTTGAAGATGGTGCAGATTCCATTCAACACAGGTACAA
AATTACGTGTCGCTACTAACGAAAGGTATCAAATCAACTCCAGAAGTGATT
GCATTGAATGTTGCTGGTGGACTTGACATCTTGATGACGTTGAAAGTTGG
TAAGCAAATCCTGTTGATGTTGAAACTAGGTCCTACTGTTGTTGCAA
AAGATAAAAGACACTCGTGAATTGAAGTAGTTGAGAATGATGGCCTT
ATTGGTAAACAAAAGGTGAAACATCCCTTAACTAAATTCCCTTCCC
AGCACTTGCAGAACCGATAATGCTGATATCGTTGGACTTGAGCAAG
GACTTAACTTATTGCTATCTCATTTGACGACTGCTAAAGATGTTAAT
GAAGTTCGTGTATTGTAAGAACACTGGCAATGGACACGTTAAGTTGGT
TGCTAAAATTGAAAATCAACAAGGTATCGATAATTGATGAGGATTATCG
AACAGCAGATGGTATTATGATTGCTCGTGGTGTATGGGTATCGAAGTT
CCATTGAAATGGTCCAGTTACAAAAAATGATCATTACTAAAGTTAA
TGCAGCTGGTAAAGCAAGTTTACAGCAACAAATATGCTTGAACAAATGA
CTGATAAACACCGTGCAGCTCGTCAAGACTGATGTCATGCT
GTTATTGATGGTACTGATGCTACAATGCTTCAGGTGAGTCAGCTAATGG
TAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGATAAAAATG
CTCAAACATTACTCAATGAGTATGGTCGTTAGACTCATCTGCATTCCC
CGTAATAACAAAACGATGTTATTGCACTGCGGTTAAAGATGCAACACA
CTCAATGGATATCAAACCTGTTGTAACAAATTACTGAAACAGGTAAACAG
CTCGTGCACATTCTAAATTCCGTCAGATGCAAGACATTGGCTGTTACA
TTTGATGAAAAGTACAACGTTCAATTGATGATTAACTGGGGTGTATCCC
TGTCTTGCAAGACAAACAGCATCTACAGATGATATGTTGAGGTTGCAG
AACGTGTAGCACTGAAGCAGGATTGTTGAATCAGGCGATAATATGTT
ATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACACAATGCGTGT
TCGTAAGTGTAAA

SEQ ID NO. 7204

STRAIN H36B

AATAAACCGCGAAAAATCGTGCAC
ACTGGTCTGGGTTGAATTCCGTGGTAAGAAGTTGGTGAGTCTG
GATACTGGGGTGAAGCCTGACGTAGAACGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAGAAGGTGCTAACGTTTCCGTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
AGATTGAGGACAAAAGTTGGCTCCCTGATACTAAAGGACCTGAA
ATTGCTACAGAACTTTGTAAGATGGTCAGATTCCATTCAATACAC
AGGTACAAAATTACGTGTGCTACTAACGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCAATTGTAATGTTGCTGGGACTTGACATCTTGATGACGTT
GAAGTTGGTAAGCAAATCCATTGTTGATGTTGAAACTAGGCTTACTGTT
GTTGCAAAAGATAAACAGACTCGTGAATTGAAAGTAGTTGAGAATG
ATGGCCTTATTGTAACAAAAGGTGTAACATCCCTTAACTAAATT
CCTTCCCAGCACTTGCAGAACCGCATAATGCTGATATCGTTGGACT
TGAGCAAGGACTTAACTTATTGCTATCTCATTGACGACTGCTAAAG
ATGTTAATGAAGGTTGCTATTGTAAGAAAATGGCAATGGACACGTT
AAGTTGTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAACGACAGATGGTATTATGATTGCTCGTGGTGTATGGGTA
TCGAAGTTCCATTGAAAATGGTCCAGTTACAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATGCTTGA
AACAAATGAcTGTAAACACCGTGCAGCTCGTCAAGGATCTGATGTC
TCAATGCTGTTATTGATGGTACTGATGCTACAAATGCTTCAAGGTGAGTC
GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGA
TAAAATGCTAAACATTACTCAATGAGTATGGTCGTTAGACTCATCTG
CATCCCACGTAATAACAAAATGATGTTATTGCACTGCGGTTAAAGAT

SEQUENCE LISTING

GCAACACACTCAATGGATATCAAACCTGGTGTAAACATTACTGAAACAGG
TAATACAGCTCGTGCATTCTAAATTCCGTCAGATGCAGACATTGG
CTGTTACATTGATGAAAAAGTACAACGTTCAATTGATGATTAACGGGGT
GTTATCCCTGCTTGCAGACAAACAGCATCTACAGATGATATGTTGA
GGTTGCAGAACCTGTTGAGCACTTGAAGCAGGATTGTTGAATCAGGGATA
ATATCGTTATCGTTGCAGGTGTTCTGTAGTCAGGGAACTAACACAA
ATGCGTGGTCTGACTGTTAAA

SEQ ID NO. 7205

STRAIN 18RS21

AATAAACGCGTAAAAATCGTTGCAAC

SEQ ID NO. 7206

STRAIN M732

AATAAACGCGTAAAAATCGTTGCAAC

SEQUENCE LISTING

TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTCGCTACAATGGCTACTATTGA
 TAAAAATGCTAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAAGTATGGATATTGCTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACATTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCATTCTAAATTCCGTCAGATGCAGACATTGG
 CTGTTACATTGATGAAAAAGTCAACGTTCAATTGATGATTAACGGGGT
 GTTATCCCTGCTTGCAGACAAACCCAGCATCTACAGATGATATGTTGA
 GGTGAGAACGTTGAGCACTTGAGCAGGACTTGTGAATCAGGCAGATA
 ATATCGTTATCGTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTGTTGTTACTGTTAAA

SEQ ID NO. 7207

STRAIN COH1

AATAAACGCGTAAAAATCGTGCAC
 ACTTGGTCCTGGTAGAATTCCGTGGTGGTAAGAAGTTGGTGGTGGTCTG
 GATACTGGGGTGAAAGCCTTGACGTTAGCAGCTTCAGCAGAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTCCGTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAAGGACAAAAAGTGGCTTCCCTCCTGATACTAAAGGACCTGAA
 ATTGTCAGAACACTTTGAAGATGGTGCAGATTCCATTCTATACAAAC
 AGGTACAAAATTACGTGTTGCTACTAACGCAAGGTATCAAATCAACTCCAG
 AAGTGTGATTGCTTGTGAAATTGCTGGGACTTGACATCTTGTGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTACTGTT
 GTTGTGAAAGGACAAACAGGACTCGTGAATTGAGTAGTGTGAGAATG
 ATGGCCTTATGGTAAACAAAAGGTGAAACATCCCTTATACTAAATT
 CCTTCCCAGCACTTGCAGAACCGCATAATGCTGATATCCGTTTGgACT
 TGAGCAAGGACTTAACCTTATTGCTATCTCATTGTCAGTACTGCTAAAG
 ATGTTAATGAAGTTCGTGCTATTGTAAGAAACTGGCAATGGACACGTT
 AAGTTGTTGCTAAATTGAAACATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTGATGCTCGTGGTGGTGGT
 TCGAAGTCCATTGAAATGGTCCAGTTACAAAATGATCATTACT
 AAAGTGTGAGCTGGTAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGCTGCGACTCGTTCAAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTAACATGCTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTCGCTAACATGGCTACTATTGA
 TAAAATGCTAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAAGTATGGTATTGCTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACATTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCATTCTAAATTCCGTCAGATGCAGACATTGG
 CTGTTACATTGATGAAAAAGTACAACGTTCATGATGATTAACGGGGT
 GTTATCCCTGCTTGCAGACAAACCCAGCATCTACAGATGATATGTTGA
 GGTGAGAACGTTGAGCACTTGAGCAGGACTTGTGAATCAGGCAGATA
 ATATCGTTATCGTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTGTTGTTACTGTTAAA

SEQ ID NO. 7208

STRAIN M781

AATAAACGCGTAAAAATCGTGCAC
 ACTTGGTCCTGGTAGAATTCCGTGGTGGTAAGAAGTTGGTGGTGGTCTG
 GATACTGGGGTGAAAGCCTTGACGTTAGCAGCTTCAGCAGAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTCCGTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAAGGACAAAAAGTGGCTTCCCTCCTGATACTAAAGGACCTGAA
 ATTGTCAGAACACTTTGAAGATGGTGCAGATTCCATTCTATACAAAC
 AGGTACAAAATTACGTGTTGCTACTAACGCAAGGTATCAAATCAACTCCAG
 AAGTGTGATTGCTTGTGAGTAGTGTGGACTTGACATCTTGTGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTACTGTT
 GTTGTGAAAGGACTAAAGACACTCGTGAATTGAGTAGTGTGAGAATG
 ATGGCCTTATGTTGAAACAAAAGGTGAAACATCCCTTATACTAAATT
 CCTTCCCAGCACTTGCAGAACCGCATAATGCTGATATCCGTTTGAGCT
 TGAGCAAGGACTTAACCTTATTGCTATCTCATTGTCAGTACTGCTAAAG
 ATGTTAATGAAGTTCGTGCTATTGTAAGAAACTGGCAATGGACACGTT
 AAGTTGTTGCTAAATTGAAACATCAACAAGGTATCGATAATATTGATGA

SEQUENCE LISTING

GATTATCGAACGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTCCAGTTACAAAAAATGATCATTACT
 AAAGTTAATCGAGCTGGTAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAACTGACTGATAAAACCAACGTGCGACTCGTTCAGAAGTATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTCAGGTGAGTCA
 GCTAATGGTAAACATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAATGATGTTATTGATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACATTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCTTCTAAGTCCGTCAGATGCGAGACATTTGG
 CTGTTACATTGATGAAAAAGTACAACGTTATTGATGATTAACGGGGT
 GTTATCCCTGCTCTTGAGACAAACCCAGCATCTACAGATGATATGTTGA
 GGTTGCAGAACCGTAGCACTTGAGCAGGACTTGTGAATCAGGCAGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGAACTAACACA
 ATGCGTGTTCGTAATGTTAAA

SEQ ID NO. 7209

STRAIN CJB110

AATAAACCGTAAACCGTTGCAAC
 ACTGGTCTGCGGTTGAATTCCGTGGTGAAGAAGTTGGTGAGTCTG
 GATACTGGGGTGAAGCCTTGACGTagAAGCTTCAGCAGAAAAATTGCT
 CAATTGATTAAGAAGGCTAACGTTTCCGTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGCTAAAGCAGAAG
 AGATTGAGGACAAAAAGTTGGCTTCCCTCTGATGACTAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAGATGGTGCAGATTCCATTGATATAAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGATCAAATCAACTCCAG
 AAGTGATTGCTTGAATGTTGCTGGTGGACTTGACATCTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTGCAAAAGATAAAAGACACTCGTGAATTGAGTAGTTGAGAATG
 ATGGCCTTATGGTAAACAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTCCCAGGACTTGAGAACCGATAATGCTGATATCCGTTTTGGACT
 TGAACAAGGACTTAACATTATTGCTATCTCATTGCTACGTTACTGCTAAAG
 ATGTTAATGAAGTTGCTGTTGAGAGAAACTGGCAATGGACACGTT
 AAGTTGTTGCTAAATTGAAACATCAACAGGATGATAATTGATGA
 GATTATCGAACGAGATGGTATTATGATTGCTCGTGGTGAATGGTAA
 TCGAAGTTCCATTGAAATGGTCCAGTTACAAAAAATGATCATTACT
 AAAGTTAATGAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAACTGACTGATAAAACACGTCGACTCGTCAGAAGTATCTGATGTCT
 TCAATGCTTATTGATGGTACTGATGCTACAATGCTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAATGATGTTATTGATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACATTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCTTCTAAGTCCGTCAGATGCGAGACATTTGG
 CTGTTACATTGATGAAAAAGTACAACGTTATTGATGATTAACGGGGT
 GTTATCCCTGCTCTTGAGACAAACCCAGCATCTACAGATGATATGTTGA
 GGTTGCAGAACCGTAGCACTTGAGCAGGATTGTAATCAGGCAGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGAACTAACACA
 ATGCGTGTTCGTAATGTTAAA

SEQ ID NO. 7210

STRAIN 1169NT

AATAAACCGTAAACCGTTGCAAC
 ACTGGTCTGCGGTTGAATTCCGTGGTGAAGAAGTTGGTGAGTCTG
 GATACTGGGGTGAAGCCTTGACGTagAAGCTTCAGCAGAAAAATTGCT
 CAATTGATTAAGAAGGCTAACGTTTCCGTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGCTAAAGCAGAAG
 AGATTGAGGACAAAAAGTTGGCTTCTCCTGATGACTAAAGGACCTGAA
 ATTGCTACAGAACTTTTGAGATGGTGCAGATTCCATTGATATAAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGATCAAATCAACTCCAG
 AAGTGATTGCTTGAATGTTGCTGGACTTGACATCTTGATGACGTT
 GAAGTTGGTAAGCAAATCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTGCAAAAGATAAAAGACACTCGTGAATTGAGTAGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAGGTGTAACATCCCTTATACTAAAATT

SEQUENCE LISTING

CCTTTCCCAGCAGTGCAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACCTTATTGCTATCTCATTGCTACGTACTGCTAAAG
 ATGTTAACATGAAGTCGTCTATTGTAAGAAGAAAATGGCAATGGACACGTT
 AAGTTGTTGCTAAAATTGAAAATCAAAGGTATCGATAATATTGATGA
 GATTATCGAACGAGATGGTATTATGATTGCTCGTGGTATATGGGTA
 TCGAACAGTTCCATTGAAATGGTCCAGTTACCAAAaAATGATCATTACT
 AAAGTTAACATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTGA
 AACAAATGACTGATAAACCACGTGCGACTCGTCAGAAGTATCTGATGTC
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTCAGGTGAGTCA
 GCTAACGGTAAATACCCAGTTGAGTCAGTCGACAATGGCTACTATTGA
 TAAAAATGCTCAAACAttACTCAATGAGTATGGTGTAGACTCATCTG
 CATTCCCACGTAAACAAAATGATGTTATTGCACTGCGGTTAAAGAT
 GCAACACACTCAAATGGATATCAAACATTGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCTTCTAAATTCGTCAGATGCAGACATTTGG
 CTGTTACATTGATGAAAAGTACAACGTTCAATTGATGATGTTAACTGGGGT
 GTTATCCCTGCTTGCAGACAAACCAACGATCTACAGATGATATGTTGA
 GGGTGCAGAACGTTGAGCAAGCAGGACTTGTGAATCAGGCATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTGTTGACTGTTAAA

SEQ ID NO. 7211

STRAIN JM9130013

AATAAACCGCTAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTGGTGGTACTG
 GATACTGGGGTGAAGCCTTGACGTAGAACGCTTCAGCAGAAAAATTGCT
 CAATTGATTAAAGAAGGGCTAACGTTTCCGTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGCAAGGACAAAAGTTGGCTTCCCTCTGATACTAAAGGACCTGAA
 ATTGTCAGAACATTGTAAGATGGTTCAGATTCCATTCAATACAAAC
 AGGTACAAAATTACGTGTTGCTACTAACAGGATCAAAACTCAACTCCAG
 AAGTGTGATTGCAATTGTAAGTGTGGGACTTGACATCTTGATGACGTT
 GAAGTTGGTAAGCAAACTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGTAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGTAACAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTTCCCAGCACTGCAAGCGATAATGCTGATATCCGTTGGACT
 TGAGCAAGGACTTAACTTATTGCTATCTCATTGTTACGTACTGCTAAAG
 ATGTTAACATGAAGTCGTCTATTGTAAGAAACTGGCAATGGACATGTT
 AAGTTGTTGCTAAAATTGAAATCAAACAGGATCGATAATATTGATGA
 GATTATCGAACGAGCAGATGGTATTATGATTGCTCGTGGTATATGGGTA
 TCGAAGTTCCTTGAATGGTCCAGTTACAAAAAAATGATCATTACT
 AAAGTTAACATGCACTGGTAAGCAGTTACAGCAACAAATATGCTGTA
 AACAAATGACTGATAAACACACGTGCGACTCGTCAGAAGTATCTGATGTC
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTCAGGTGAGTCA
 GCTAACGGTAAATACCCAGTTGAGTCAGTCGACAATGGCTACTATTGA
 TAAAAATGCTAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCACGTAAACAAACTGATGTTATTGCACTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACATTGTTGACAATTACTGAAACAGG
 TAATACAGCTCGTGCCTTCTAAATCCGTCCAGATGCAGACATTTGG
 CTGTTACATTGATGAAAAGTACAACGTTATTGATGATGTTAACTGGGGT
 GTTATCCCTGCTTGCAGACAAACCAACGATCTACAGATGATATGTTGA
 GGGTGCAGAACGTTGAGCAAGCAGGACTTGTGAATCAGGCATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTGTTGACTGTTAAA

SEQ ID NO. 7212

STRAIN 2603 frame: 1

MNKRVKIVATLGPRAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHG
 DHAEQGARMATVRKAEEIAQOKVGFLLDTKGPEIRTELLEDGADFHSYTTGKLRVATKQ
 GIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTRFEVVVENDGLI
 GKQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGX
 GHVKLFAKIENQQGIDNIDEIIEAADGIMTARGDMGIEVPFEMVPVYQKMIITKVNAAGK
 AVITATNMLETMTDKPRATRSEVDVNAVIDGTDATMLSGESANGKYPVESVRTMATID
 KNAQTLLNEYGRLDSSAFPRNNKTDVIAAVKDAHSMDIKLVVTITETGNTARAISKFR
 PDADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVEGDNIVI

SEQUENCE LISTING

VAGVPVGTGGTNTMVRTVK

SEQ ID NO. 7213

STRAIN 090 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDTKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLGLTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIATFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAIISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMVRTVK

SEQ ID NO. 7214

STRAIN A909 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDTKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLGLTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIATFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAIISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
 AGVPVGTGGTNTMVRTVK

SEQ ID NO. 7215

STRAIN H36B frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDTKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLGLTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIATFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAIISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
 AGVPVGTGGTNTMVRTVK

SEQ ID NO. 7216

STRAIN 18RS21 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDTKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLGLTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIATFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAIISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
 AGVPVGTGGTNTMVRTVK

SEQ ID NO. 7217

STRAIN M732 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDTKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLGLTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIATFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLENEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAIISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
 AGVPVGTGGTNTMVRTVK

SEQ ID NO. 7218

STRAIN COH1 frame: 1

SEQUENCE LISTING

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFFDDVEVGKQILVDDGKLGTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQQLNFIATSVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219

STRAIN M781 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFFDDVEVGKQILVDDGKLGTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQQLNFIATSVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220

STRAIN CJB110 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFFDDVEVGKQILVDDGKLGTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQQLNFIATSVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221

STRAIN 1169NT frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFFDDVEVGKQILVDDGKLGTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQQLNFIATSVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7222

STRAIN JM9130013 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDKGPEIRTELFFEDGADFHSYTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFFDDVEVGKQILVDDGKLGTVFAKDKDTREFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLEQQLNFIATSVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEIIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSEVSDVNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVTITETGNTARAISKFRP
 DADILAVTFDEKVQRSLMINWGVIPVVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7301

STRAIN 2603

TTGTCTGCTATAATAGACAAAAAGGGGTGATATTTATGTATTTAGCATTAATCGGTGAT
 ATCATTAATTCAAAACAGATACTTGAACGTAAAATTTCCAACAGTCTTCAGCAACTA
 ATGACCGAACTATCTGATGTATATGGTGAAGAGAGCTGATTTCTCCATTCACTATTACAGCT
 GGTGATGAATTCAAGCTTATTGAAACCATCAAAAAGGTATTCAAATTATTGACCAT

SEQUENCE LISTING

ATTCAACTAGCTCTAACACCTGTTAATGTAAGGTCGGCCTCGTACAGGAAACATTATA
 ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCCTGCCTACTGGCATGCTCGC
 TCAGCTATTAAATCATATAACATGATAAAAATGATTATGGAACAGTCAAGTAGCTATTG
 CTTGATGATGAAAGACCAAAACCTGAAATTAAACACTAAATGCTCATTTCAGCTGGTGAT
 TTATCAAGTCAAATGGACTACAAACCATTTCAAATGCTGAGCACTTAATACTCAA
 GATAATTCAAGAACAAATTCAACATCAAAGTTAGCCAACTGGAAAATATTGAACCT
 AGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTGAAGATTACTTAAGAACGAGAAC
 CAGGCAGCCGATCTATTAGTTGCACTCAAACAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7302

STRAIN 090

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTT
 AGCATTAAATCGGTGATATCATTAAATTCAAACAGATACTTGAACGTGAAA
 CTTCCAACAGCTTTCTCAGCAACTAATGACCGAACTATCTGATGTATAT
 GGTGAAGAGCTGATTCTCATTCACTATTACAGCTGGTGATGAAATTCA
 AGCTTATTGAAACCATCAAAAAGGTATTCAAATTATTGACCATATT
 AACCTAGCTCTAAACCTGTTAATGTAAGGTCGGCCTCGGtACAGGAAAC
 ATTATAACATCCATCAATTAAATGAAAGTATCGGTGCTGATGGTCCTGC
 CTACTGGCATGCTCGCTCAGCTATTAAATCATATACTGATAAAAATGATT
 ATGGAACAGTCAAGTAGCTATTGCTTGATGATGAAGACCAAAACCTT
 GAATTAACACTAAATAGTCTCATTCACTGGTGATTTTATCAAGTC
 ATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATACTTCAGATA
 ATTATCAAGAACAAATTCAACATCAAAGTTAGCCCAACTGGAAAATATT
 GAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTGAAGATT
 CTTAACAGAACAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCACTC
 AAACAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7303

STRAIN A909

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTAT
 TTAGCATTAAATCGGTGATATCATTAAATTCAAACAGATACTTGAACGTG
 AACTTTCCAACAGCTTTCTCAGCAACTAATGACCGAACTATCTGATGTAT
 ATGGTGAAGAGCTGATTCTCATTCACTATTACAGCTGGTGATGAAATT
 CAAGCTTATTGAAACCATCAAAAAGGTATTCAAATTATTGACCATATT
 TCAACTAGCTCTAAACCTGTTAATGTAAGGTCGGCCTCGTACAGGAA
 ACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCCT
 GCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACTGATAAAAATGA
 TTATGGAACAGTCAAGTAGCTATTGCTTGATGATGAAGACCAAAAC
 TTGAATTAACACTAAATAGTCTCATTCACTGGTGATTTTATCAAGTC
 AAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATACTTCAGA
 TAATTATCAAGAACAAATTCAACATCAAAGTTAGCCCAACTGGAAAATA
 TTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTGAAGATT
 TACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCA
 TCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7304

STRAIN H36B

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTAGCATTAAATCGGTGATATCATTAAATTCAAACAGATACTTGA
 ACCTGAAACTTCCAACAGCTTTCTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTCTCATTCACTATTACAGCTGGTGAT
 GAATTCAAGCTTATTGAAACCATCAAAAAGGTATTCAAATTATTGA
 CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTCGGCCTCGGTA
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACTGATAA
 AAATGATTATGGAACAGTCAAGTAGCTATTGCTTGATGATGAAGAC
 AAAACCTGAAFTAACACTAAATAGTCTCATTCACTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTCAACATCAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTG
 AAGATTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7305

SEQUENCE LISTING

STRAIN 18RS21

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATTCAAAACAGATACTTGA
 ACGTGAACACTTCCAACAGTCTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 GAATTCAAGCTTATTGAAACCATCAAAAAAGGTATTCAAAATTATTGA
 CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCGGCCTCGGT
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 GGTCTGCCTACTGGCATGCTCGCTCAGCTATTACATACATGATAA
 AAATGATTATGGAACAGTCAAGTAGCTATTGCCTGATGATGAAGACC
 AAAACCTGAAATTAAACACTAAATAGTCTATTCAAGCTGGTGA
 AAGTCAAAATGGACTACAAACCATTTCAAATGCTGAGCACTTAACACT
 TCAAGATAATTATCAAGAACAAATTCAACATCAAAGTTAGCCCAACTGG
 AAAATATTGAAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTG
 AAGATTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
 TTGCACTCAAACAAAGGGGGAAAGCTATGATTTC

SEQ ID NO. 7306

STRAIN M732

TCTGCTATAATAGACAAAAAGGTGGTGA
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATTCAAAACAGATACTTGA
 AACGTGAACACTTCCAACAGTCTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTCAAGCTTATTGAAACATCAAAAGGTATTCAAAATTATTG
 ACCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCGGCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGCCTGCCTACTGGCATGCTCGCTCAGCTATTACATACATGATA
 AAAATGATTATGGAACAGTCAAGTAGCTATTGCCTGATGATGAAGAC
 AAAACCTGAAATTAAACACTAAATAGTCTATTCAAGCTGGTGA
 CAAGTCAAAATGGACTACAAACCATTTCAAATGCTGAGCACTTAAC
 TTCAAGATAATTATCAAGAACAAATTCAACATCAAAGTTAGCCCAACTG
 GAAAATATTGAAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCT
 GAAGATTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
 TTGCACTCAAACAAAGGGGGAAAGCTATGATTTC

SEQ ID NO. 7307

STRAIN COH1

TCTGCTATAATAGACAAAAAGGTGGTGA
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATTCAAAACAGATACTTGA
 AACGTGAACACTTCCAACAGTCTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTCAAGCTTATTGAAACATCAAAAGGTATTCAAAATTATTG
 ACCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCGGCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGCCTGCCTACTGGCATGCTCGCTCAGCTATTACATACATGATA
 AAAATGATTATGGAACAGTCAAGTAGCTATTGCCTGATGATGAAGAC
 AAAACCTGAAATTAAACACTAAATAGTCTATTCAAGCTGGTGA
 CAAGTCAAAATGGACTACAAACCATTTCAAATGCTGAGCACTTAAC
 TTCAAGATAATTATCAAGAACAAATTCAACATCAAAGTTAGCCCAACTG
 GAAAATATTGAAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCT
 GAAGATTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
 TTGCACTCAAACAAAGGGGGAAAGCTATGATTTC

SEQ ID NO. 7308

STRAIN M781

TCTGCTATAATAGACAAAAAGGTGGTGA
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATTCAAAACAGATACTTGA
 ACGTGAACACTTCCAACAGTCTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 GAATTCAAGCTTATTGAAACATCAAAAGGTATTCAAAATTATTG
 CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCGGCCTCGGT
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 GGTCTGCCTACTGGCATGCTCGCTCAGCTATTACATACATGATAA
 AAATGATTATGGAACAGTCAAGTAGCTATTGCCTGATGATGAAGACC

SEQUENCE LISTING

AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTATC
 AAGTCAAAATGGACTACAAACCATTCAAATGCTGAGCACTTAATACT
 TCAAGATAATATCAAGAACAAATTCAACATCAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTG
 AAGATTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACAAAGGGGGAGCTATGATTTC

SEQ ID NO. 7309

STRAIN CJB110

TCTGCTATAATAGACAAAAAGGTGGTGGTA
 TTTATGTATTAGCATTAAATCGGTGATATCATTAAATTCAAACAGATACT
 TGAACGTGAAACTTCCAACAGTCTTCAGCAACTAATGACCGAAGTAT
 CTGATGTATATGGTGAAGAGCTGATTCTCTATTCACTATTACAGCTGGT
 GATGAATTTCAGCTTATTGAAACCATCAAAAAGGTATTCAAATTAT
 TGACCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCGGCCTCG
 GTACAGGAAACATTAAACATCAAATTCAAATGAAAGTATCGGTGCT
 GATGGTCCCTGCCTACTGGCATGCTCGCTCAGCTATTAAATCATACATGA
 TAAAAATGATTATGGAACAGTTCAAGTAGCTATTGCCTGATGATGAAG
 ACCAAAACCTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTT
 ATCAAGTCAAATGGACTACTAACCAATTCAAATGCTTGAGCACTTAAT
 ACTTCAAGATAATTATCAAGAACAAATTCAACATCAAAGTTAGCCCAAC
 TGAAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGT
 CTGAAGATTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAA
 AAGTTGCACTCAAACAAAGGGGGAGCTATGATTTC

SEQ ID NO. 7310

STRAIN JM9130013

TCTGCTATAATAGACAAAAAGGTGGTGTATATT
 ATGTATTAGCATTAAATCGGTGATATCATTAAATTCAAACAGATACTTGA
 ACGTGAAACTTCCAACAGTCTTCAGCAACTAATGACCGAAGTATCTG
 ATGTATATGGTGAAGAGCTGATTCTCACTATTACAGCTGGTGT
 GAATTTCAGCTTATTGAAACCATCAAAAAGGTATTCAAATTATTGA
 CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCGGCCTCGGT
 CAGGAAACATTAAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCCCTGCCTACTGGCATGCTCGCTCAGCTATTAAATCATACATGATAA
 AAATGATTATGGAACAGTCAAGTAGCTATTGCCTGATGATGAAGACC
 AAAACCTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGTATTTATC
 AAGTCAAATGGACTACAAACCATTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTCAACATCAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTG
 AAGATTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACAAAGGGGGAGCTATGATTTC

SEQ ID NO. 7311

STRAIN 2603 frame: 1

LSAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITA
 GDEFQALLKPSKKVQIIDHIQLALKPVNVRFLGTTGNIITSINSNESIGADGPAYWHAR
 SAINHIHDKNDYGTQVAICLDDDEDQNLELTLSNLSISAGDFIKSKWTTNHFQMLEHLILQ
 DNYQEKFQHQKLAQLENIEPSALTKRLKASGLKIYLRTQADLLVKSCQTQKGGSYDF

SEQ ID NO. 7312

STRAIN 090 frame: 1

SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVQIIDHIQLALKPVNVRFLGTTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLELTLSNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEKFQHQKLAQLENIEPSALTKRLKASGLKIYLRTQADLLVKSCQTQKGGSYDF

SEQ ID NO. 7313

STRAIN A909 frame: 1

SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVQIIDHIQLALKPVNVRFLGTTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLELTLSNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEKFQHQKLAQLENIEPSALTKRLKASGLKIYLRTQADLLVKSCQTQKGGSYDF

SEQUENCE LISTING

SEQ ID NO. 7314

STRAIN H36B frame: 1

SAIIDKKVVIFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLETLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7315

STRAIN 18RS21 frame: 1

SAIIDKKVVIFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLETLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7316

STRAIN M732 frame: 1

SAIIDKKVVIFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLETLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7317

STRAIN COH1 frame: 1

SAIIDKKVVIFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLETLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7318

STRAIN M781 frame: 1

SAIIDKKVVIFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLETLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7319

STRAIN CJB110 frame: 1

SAIIDKKVVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISLFTITAG
 DEFQALLKPSKKVQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLETLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7320

STRAIN JM9130013 frame: 1

SAIIDKKVVIFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKKVQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLETLNSLISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQQFHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7401

STRAIN 2603

ATGAAATGCAAGTTCAAAAAAGTTTAAATCAAATATACTACATTACGGAACACTCTAT
 CTAGTCCAACTCCAATTGGTAATCTAGATGATATGACTTTCTGTGCCATTAGGATTAA
 AGAGAAGTTGATTTATTGTCAGAGGATAACAGAAATACGGGACTTTACTCAAGCAC
 TTTGATATTACTACTAAACAAATTAGTTTACAGAACACAATGCTTACGATAAAATCTCT
 GGGTTAATTGATTGTTAAAAGAAGGGAAATCTTAGCCAAGTATCTGATGCAGGAATG
 CCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
 GTTGTATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTACGCTTCAGGTTAGCT
 CCACAACCTCATATTTTATGGCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
 TTGAAACAAAGCAAGATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTC
 TCTGATACGCTAAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTAGTACGC
 GAATTGACGAAACTCTATGAAGAGTACAAAGAGGAACCATAGTCAACTTTAGAGCAT
 ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGAGATACC
 GAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAAGAATATCGCT

SEQUENCE LISTING

AATGGTGATAAAACTAATCAAGCGATAAAAAAGTAGCAAAAGAATTAACTCAATAGA
CAAGAACTCTATGCTAGTTCCATGATTTA

SEQ ID NO. 7402

STRAIN 090

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTCTG
CCATTAGGATTAAAGAGAAGTTGATTTATTTGTGCAGAGGATAACACGA
AATACGGGACTTTACTCAAGCACTTGATATTACTACTAAACAAATTAG
TTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGT
TAAAAGAAGGGAGATCTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTCTGACCCAGgACATGACCTTGTCAGGCTGCTATTGAAGGGGGAT
CCCGGTCTGATCTACCCAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTAGCTCCACACCTCATATTTTATGGCTTCTTACCGCGT
AAGAAAGGTCAACAAATACTTTTTGAAACAAAGAAAGATTACCCCTG
AACACAAATCTTTATGAGTCACCGTTAGCTCTGATACGCTAAAC
ACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTAGTACCGAATTG
ACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCACCTTCTG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATG
GTAAGAGAGATAACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403

STRAIN A909

AGTCAAAAAAGTTTAAATCAAATACACATTACGGAACACTCTATCTAG
TCCCAACTCCAATTGGTAATCTAGATGATATGACTTTCTGCCCCATTAGG
ATTTAAAGAGAAGTTGATTTATTTGTGCAGAGGATAACACGAAATACGGG
ACTTTTACTCAAGCACTTGATATTACTACTAAACAAATTAGTTTCTCAGG
AACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTTAAAGAA
GGGAATCTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTTCTGA
CCCAAGGACATGACCTTGTCAGGCTGCTATTGAAGGGGATATCCCGTTG
TATCTATACCGAGGACTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGT
TTAGCTCCACACCTCATATTTTATGGCTTCTTACACCGTAAGAAAGG
TCAACAAATACTTTCTTGTAAACAAAGCAAGATTACCCCTGAAACACAAA
TCTTTATGAGTCACCGTTGAGTCTCTGATACGCTAAACACATGAAA
GAGATTTACGGAGATCGCCAAGTTGTTTAGTACCGAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAACCATTAGTCACCTTCTAGAGCATATTG
AAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGA
GATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404

STRAIN H36B

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTCTGCCCCATTAGGATTAAAGAGAAGTTGATTTATTTGTGCAGA
GGATACGAAATACGGGACTTTACTCAAGCACTTGATATTACTACTA
AACAAATTAGTTTACGAACACAATGCTTATGATAAAATCTCTGGGTTA
ATTGATTTGTTAAAGAGAGGAGATCTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTCGACCCAGGACATGACCTTGTCAGGCTGCTATTG
AAGGGGATATCCCGGTCTGATCTATACACCGAGGACTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTAGCTCCACACCTCATATTTTATGGCTT
CTTACCGCGTAAGCAAGGTCAACAAATACTTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAACACATGAAAGAGATTATGGAGATCGCCAAGTTGTTTAGT
ACCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTAGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACTGAGCGAGTGAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405

STRAIN 18RS21

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACACATT
ACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTGATATG

SEQUENCE LISTING

ACTTTtCGTGCCTAGGATTAAAGAGAAGTTGATTTATGGCAGA
 GgATACACGAAATACGGGACTTTACTCAAGCACTTGTATTA
 AACAAATTAGTTTACGAAACACAATGCTTACGATAAAATCTGGTTA
 ATTGATTTGTTAAAGAAGGGAAATCTTAGCCAAAGTATCTGATGCAGG
 AATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
 AAGGGGATATCCCAGTTGTATCTATACCAAGGAGTAGCGCTGGTATTACT
 GCTCTCATCGCTCAGGTTAGCTCCACAACCTCATATTTTATGGCTT
 CTTACCACGTAAGAAAGGTCAACAAATAACTTCTTGAAACAAAGCAAG
 ATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTCGAGTCTGAT
 ACGCTAAAACACATGAAAGAGATTACGGAGATGCCAAGTTGTTTAGT
 ACCGGAATTGACGAAACTCTATGAAGAGTACAAAGAGGAACCATTAGTC
 AACTTTAGAGCATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
 ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACA
 AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406

STRAIN M732

GAAATGCAAGTCAAAAAAGTTTAAATCAAAT
 ATACATTACGAAACACTCTATCTAGTCCAACTCCAATTGGTAATCTAGA
 TGATATGACTTTCTGTCATTAGGTTAAAGAGAAGTTGATTTATT
 GTGCAGGAGATACGAAATACGGGACTTTACTCAAGCACTTGTATATT
 ACTACTAAACAAATTAGTTCTGCAACACAATGCTTACGATAAAATCTC
 TGGTTAATTGATTGTTAAAGAAGGGAAATCTTAGCCAAAGTATCTG
 ATGCAGGAATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCT
 GCTATTGAAGGGATATCCCAGTTGTATCTATACCAAGGAGTAGCGCTGG
 TATTACTGCTCTATCGCTTCAGGTTAGCTCCACAACCTCATATTTT
 ATGGCTTCTTACCGTAAGAAAGGTCAACAAATAACTTCTTGAAACA
 AAGCAAGATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTCGAGT
 CTCTGATACGCTAAACACATGAAAGAGATTACGGAGATGCCAAGTTG
 TTTAGTACGCAATTGACGAAACTCTATGAAGAGTACAAAGAGGAACC
 ATTAGTCAACTTTAGAGCATTGAAAAGGTCCCTCTCAAAGGTGAATG
 CTTAATTATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTA
 GCCAACAAAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407

STRAIN COH1

GAAATGCAAGTCAAAAAAGTTTAAATCAAATACATTAC
 GGAACACTCTATCTAGTCCAACTCCAATTGGTAATCTAGATGATATGAC
 TTTCTGTCATTAGGTTAAAGAGAAGTTGATTTATTGTCAGAGG
 ATACACGAAATACGGGACTTTACTCAAGCACTTGTATATTACTAA
 CAAATTAGTTCTCACGAACACAATGCTTACGATAAAATCTGGTTAAT
 TGATTTGTTAAAGAAGGGAAATCTTAGCCAAAGTATCTGATGCAGGAA
 TGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
 GGGGATATCCCAGTTGTATCTATACCAAGGAGCTAGCGCTGGTATTACTGC
 TCTCATCGCTTCAGGTTAGCTCCACAACCTCATATTTTATGGCTTCT
 TACCACGTAAGAAAGGTCAACAAATAACTTCTTGAAACAAAGCAAGAT
 TACCCGTAAACACAAATCTTTATGAGTCACCGTTCGAGTCTGTGATAC
 GCTAAACACATGAAAGAGATTACGGAGATGCCAAGTTGTTAGTAC
 GCGAATTGACGAAACTCTATGAAGAGTACAAAGAGGAACCATTAGTCAA
 CTTTAGAGCATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTAT
 TGTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAG
 ATCCACTAGTATTAGTAA

SEQ ID NO. 7408

STRAIN M781

AAATGCAAGTCAAAAAAGTTTAAATCAAATACATTACGGAACACTC
 TATCTAGTCCAACTCCAATTGGTAATCTAGATGATATGACTTTCTGTC
 CATTAGGATTAAAGAGAAGTTGATTTATTGTCAGAGGATACGAA
 ATACGGgACTTTACTCAAGCACTTGTATATTACTAAACAAATTAGT
 TTTCACGAACACAATGCTTACGATAAAATCTGGTTAATTGATTGTT
 AAAAGAAGGGAAATCTTAGCCAAAGTATCTGATGCAGGAATGCCCTCTA
 TTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
 CCAGTTGTATCTATACCAAGGAGTAGCGCTGGTATTACTGCTCTCATCGC
 TTCAAGGTTAGCTCCACAACCTCATATTTTATGGCTTCTTACACGTA

SEQUENCE LISTING

AGAAAGGTCAACAAATAACTTCTTGAAACAAAGCAAGATTACCCCTGAA
 ACACAAATCTTTATGAGTCACCGTTCGAGTcTcTGATACGCTAAAACA
 CATGAAAGAGATTTACGGAGATGCCAAGTTGTTAGTACCGGAATTGA
 CGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCACCTTGTAGAG
 CATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGG
 TAAGAGAGATACCGAGCAGTGAAGACAGTAGCCAACAAGATCCACTAG
 TATTAGTAA

A

SEQ ID NO. 7409

STRAIN CJB110

GAATGCAAGTCAAAAAAGTTTAAATCAAATACACATTACGGGACAC
 TCTATCTAGTCCAACTCCAATTGGTAATCTAGATGATATGACTTTCTCGT
 GCCATTAGGATTTAAGAGAAGTTGATTTTATTGTCAGAGGATACACCG
 AAATACGGGACTTTACTCAAGCACTTGTGATATTACTAAACAAATTA
 GTTTTCACGAACACAATGCTTACGATAAAATCTGGGTTAATTGATTG
 TTAAAAGAAGGGAGATCTTAGCCAAGTATCTGATGCAGGAATGCCCTC
 TATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGG
 TCCCGGTCGTATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATC
 GCTTCAGGTTAGCTCCACAACCTCATATTGTTATGGCTTACCGCG
 TAAGAAAGGTCAACAAATAACTTTTTGAAACAAAGAAAGATTACCCG
 AAACACAAATCTTTATGAGTCACCGTTcGAGTCTCTGATACGCTAAA
 CACATGAAAGAGATTTACGGAGATGCCAAGTTGTTAGTACCGGAATT
 GAGCAAACCTATGAAGAGTATCAAAGAGGAACCATTAGTCACCTTGT
 GGCTATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
 GGTAAGAGAGATACCGAGCAGTGAAGACAGTAGCCAACAAGATCCACT
 AGTATTAGTAA

SEQ ID NO. 7410

STRAIN 1169NT

TGCAAGTCAAAAAAGTTTAAATCAAATACACATTATGGGACACTCTAT
 CTAGTCCAACTCCAATTGGTAATCTAGATGATATGACTTTCTGTGCCAT
 TAGGATTTAAGAgAAGTTGATTTTATTGTCAGAGGATACACGAAATA
 CGGGACTTTACTCAAGCACTTGTATAATTACTAAACAAATTAGTTT
 cACGAACACAATGCTTACGATAAAATCTGGGTTAATTGATTGTTAAA
 AGAAGGGAAATCTTAGCCAAGTATCTGATGCAGGAATGCCCTTATT
 CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
 GTTGATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
 AGGTTTAGCTCCACAACCTCATATTGTTATGGCTTACACGTAAGA
 AAGGTCAACAAATAACTTTTTGAAACAAAGCAAGATTATCTGAAACA
 CAAATCTTTATGAGTCACCGTTcGAGTCTCTGATACGCTAAAACACAT
 GAAAGAGATTTACGGAGATGCCAAGTTGTTAGTACCGGAATTGAcA
 AACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCACCTTGTAGAGCAT
 ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAA
 GAGAGATAACCGAGCAGTGAAGACAGTAGCCAACAAGATCCACTAGTAT
 TAGTAA

SEQ ID NO. 7411

STRAIN JM9130013

GAAATGCAAGTCAAAAAAGTTTAAATCAAATACACATTACGGGA
 CACTCTATCTAGTCCAACTCCAATTGGTAATCTAGATGATATGACTTT
 CGGCCATTAGGATTTAAGAGAAGTTGATTTTATTGTCAGAGGATAC
 ACGAAATAACGGGACTTTACTCAAGCACTTGTGATATTACTAAACAA
 TTAGTTTCACGAACACAATGCTTACGATAAAATCTGGGTTAATTGAT
 TTGTTAAAAGAAGGGAGATCTTAGCCAAGTATCTGATGCAGGAATGCC
 CTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGG
 ATATCCGGTCTGATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTC
 ATCGCTTCAGGTTTAGCTCACAACCTCATATTGTTATGGCTTACCG
 GCGTAAGCAAGGTCAACAAATAACTTTTTGAAACAAAGAAAGATTAC
 CTGAAACACAACAAATCTTGTAGAGTCACCGTTCGAGTCTCTGATACGCTA
 AAACACATGAAAGAGATTTATGGAGATGCCAAGTTGTTAGTACCGGA
 ATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCACCTT
 TAGGGCATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
 GATGGTAAGAGAGATACTGAGCGAGTGAAGACAGTAGCCAACAAGATCC

SEQUENCE LISTING

AGTAGTATTAGTAA

SEQ ID NO. 7412

STRAIN 2603 frame: 1

MEMQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 DITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAIAEGDIPV
 VSIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVS
 DTLKHMKEIYGDRQVVLVRELTLYEEYQRTISQLLEHIEKVPLKGECLIIIVDGKRDTE
 RVKDSSQQDPLVLVKEYIANGDKTNQAIKKVAKEFNLNRQELYASFHDL

SEQ ID NO. 7413

STRAIN 090 frame: 1

EMQVQKSFKSNTHYGTLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPISIDPGHDLVKAIAEGGIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTLYEEYQRTISQLLGHIEKVPLKGECLIIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7414

STRAIN A909 frame: 2

VQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAIAEGDIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTLYEEYQRTISQLLEHIEKVPLKGECLIIIVDGKRDTER
 SSQQDPLVLV

SEQ ID NO. 7415

STRAIN H36B frame: 1

EMQVQKSFKSNTHYGTLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPISIDPGHDLVKAIAEGDIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTLYEEYQRTISQLLGHIEKVPLKGECLIIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7416

STRAIN 18RS21 frame: 1

EMQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAIAEGDIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTLYEEYQRTISQLLEHIEKVPLKGECLIIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7417

STRAIN M732 frame: 1

EMQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAIAEGDIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTLYEEYQRTISQLLEHIEKVPLKGECLIIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7418

STRAIN COH1 frame: 1

EMQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAIAEGDIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTLYEEYQRTISQLLEHIEKVPLKGECLIIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7419

STRAIN M781 frame: 3

MQVQKSFKSNIHYGTLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPISIDPGHDLVKAIAEGDIPV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTLYEEYQRTISQLLEHIEKVPLKGECLIIIVDGKRDTER

SEQUENCE LISTING

KDSSQQDPLVLV

SEQ ID NO. 7420

STRAIN CJB110 frame: 1
 EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGGIPVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKQQITFFETKKDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLIEEYQRTISQLLGHIEKVPLKGECLIIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7421

STRAIN 1169NT frame: 3
 QVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGDI
 PGASAGITALIASGLAPQPHIFYGFLPRKKQQITFFETKKDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLIEEYQRTISQLLGHIEKVPLKGECLIIIVDGKRDTER
 DSSQQDPLVLV

SEQ ID NO. 7422

STRAIN JM9130013 frame: 1
 EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDIFICAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGDI
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKQQITFFETKKDYPETQIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLIEEYQRTISQLLGHIEKVPLKGECLIIIVDGKRDTER
 VKDSSQQDPPVVLV

SEQ ID NO. 7501

STRAIN 2603

ATGAGCGTATATGTTAGTGGAAATAGGAATTATT
 TCTCTTTGGGAAAGAATTATAGCGAGCATAAACAGCATCTCTCGACTAAAAGAAGGA
 ATTCTAAACATTATATAAAATCACGACTCTATTTAGAACTTATACAGGAAGCATA
 ACTAGTGACCCAGGGTTCTGAGCAAATACAAAGATGAGACACGTAATTAAATTGCT
 TTTACCGCTTTGAAGAGGCTCTGCTTCAAGTGTAAATTAAAGCTTATCATAAT
 ATTGCTGTGTTAGGGACCTCACTAGTGTAAATTAGAAAAGCATCTGTTAC
 CAATTGAAGAAGGAGAGCGTCAGTAGATGCTAGTTATTAGAAAAGCATCTGTTAC
 CATATTGCTGATGAATTGATGGCTTATCATGATATTGAGGGAGCTCGTATGTTATTCA
 ACCGCCTGTTGCAAGTAATAATGCCGTAAATTAGGAACACAATTACTCAAGATGGC
 GATTGTGATTAGCTATTGTTGGTGGCTGTGATGAGTTAAGTGTATTTCTTAGCAGGC
 TTCACATCACTAGGAGCTATTAAACAGAAATGGCATGTCAGCCCTATTCTCTGGAAAA
 GGAATCAATTGGGTGAGGGCGCTGGTTTGTGTTCTGTCAGATCAGTCCTTAGCT
 AAATATGGAAATTATCGGTGGCTTACTACAGATGGTTATCATATAACAGCACCT
 AAGCCAACAGGTGAAGGGCGCAGGATGCAAGCAGCTAGTGACTCAAGCAGGTATT
 GACTACAGTGAGATTGACTATTAAACGGTCACGGTACAGGTACTCAAGCTAATGATAAA
 ATGGAAAAAAATATGTATGGTAAGTTTCTCGACAACGACATTGATCAGCAGTACCAAG
 GGGCAACCGGGCTACTCTAGGGGCTGCAGGTATTATCGAATTGATTAATTGTTAGCG
 GCAATAGAGGAACAGACTGTACCAAGCAACTAAAATGAGATTGGGATAGAAGGTTTCCA
 GAAAATTGCTATCATCAAAGAGAGAACCCAATAAGAAATGCTTAAATTTCG
 TTGCTTTGGGAAATAATAGTGGTCTTATGTCATCTTAGATTCACCTCTAGAA
 ACATTACCTGCTAGAGAAATCTTAAATGGCTATCTTATCATCTGTTGCTTCCATTCT
 AAGAATGAATCACTTCTATAACCTATGAAAAAGTTGCTAGTAATTCAAGACTTTGAA
 GCATTACGCTTAAAGGGCTGACCCACAAAAGTCAACCCAGCACAATTAGGAAA
 ATGGATGATTTCAAAATGGCTGCGTAAACACAGCTCAAGCAGTAAATTAGAAAGCAAT
 ATTAATCTAAAAAACAGATACTTCAAAAGTAGGAATTGATTTACAACACTTCTGGA
 CCAGTTGAGGGTGTGAAAGTATTGAAAAGCAATCACACAGAAGGATATGCACATGTT
 TCTGCTTCACGATTCCGTTACAGTAATGAATGCAGCAGCTGGTATGCTTCTATCATT
 TTTAAAATAACAGGTCTTATCTGCATTCGACAAATAGTGGAGCGCTTGATGGTATA
 CAATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTTCTGCT
 AATCAGTGGACAGACATGAGTTTATGTTGGTGGCAACAATTAAACTATGATAGTCAAATG
 TTGTCGGTTCTGATTATGTTCAAGCACAAGTCCTCTCGTCAAGCATTGGATAATTCT
 CCTATAATATTAGGTAGTAAACAATTAAATATAGCCATAAAACATTACAGATGTGATG
 ACTATTGGTAGTAAACAATTAAATATAGCCATAAAACATTACAGATGTGATG
 ATCAAAGGTTCGTTGGAAATGAGCAGGAAGAAGGCAAGTTAGTTCAAGATTATGATTCTTA
 GCGAACTTGTCTGAGTATTATAATATGCCAACCTTGCTTCTGGTAGTTGGATTTC
 TCTAATGGTGTGGTAGAAACTGGACTATACTGTTAATGAAAGTATAGAAAAGGCTAT

SEQUENCE LISTING

TATTTAGTCCTATCTTATTCGATCTCGGTGGTATCTCTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7502

STRAIN 090

ATGTTAGTGGAAATAGGAATTATTCCTCTTGGAAAGAATTAT
 AGCGAGCATAAACAGCATCTCTCGACTTAAAGAAGGAATTCTAAACA
 TTTATATAAAAATCAGCAGCTCTATTTAGAATCTTACAGGAAGCATAA
 CTAGTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATT
 AAATTGCTTTACCGCTTGAAGAGGGCTTGCTTCTTCAGGTGTTAA
 TTTAAAAGCTTATCATAATATTGCTGTTAGGGACCTCACTGGGG
 GAAAGAGTGTGGTCAAATGCCTGTATCAATTGAAGAAGGGAGCGT
 CAAGTAGATGCTAGTTATTAGAAAAGCATCTGTTACCATATTGCTGA
 TGAATTGATGCTTATCGATATTGCTGGAGCTCGTATGTTATTCAA
 CCCCTGTTCTGCAAGTAATATGCCGAATTAGGAACACAATTACTT
 CAAGATGGCGATTGTGATTAGCTATTGTTGCTGTGATGAGTTAAG
 TGATATTCTTACAGGCTTCACATCACTAGGAGCTTAAACAGAAA
 TGGCATGTCAGCCCTATTCTCTGGAAAAGGAATCAATTGGTGAGGG
 GCTGGTTTGTGTTCTGCAAAGATCAGTCCTAGCTAAATATGGAA
 AATTATCGGTGGTCTTATTACTTCAGATGGTATCATATAACAGCAC
 AGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTACT
 GCAGGTATTGACTACAGTGAGATTGACTATATTACGGTCACGGTACAG
 TACTCAAGCTAATGATAAAATGGAAAAAAATATGTTATGGTAAGTTTCC
 CGACAACAGCACATTGATCAGCAGTACCAAGGGCAAACGGGTCAACTCTA
 GGGGCTGAGGTATTATCGAATTGATTAATTGTTAGCAGGCAATAGAGGA
 ACAGACTGTACCAAGCAACTAAAATGAGATTGGGATAGAAGGTTTCCAG
 AAAATTGCTATCATCAAAGAGAGAATACCAATAAGAAATGCTTAA
 AATTGTTGCTTGTGTTGGAAATAATAGTGGTATCTTATTGTCATC
 TTTAGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTAAATGG
 CTATCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATA
 ACCTATGAAAAGTTGCTAGTAATTCAACGACTTGAAGCATTACGCTT
 TAAAGGGGCTAGACCAACCAAAACTGTCACCCAGCACAATTAGGAAAA
 TGGATGATTCTCCAAATGGTTGCCGAACAAAGCTCAAGCAGCTAATA
 GAAAGCAATTAACTAAACAAAGATAACTCTAAAGTAGGAATTGTT
 ATTACAAACACTTCTGGACCAAGTTGAGGTTGTTGAAGGTATGAAAAGC
 AAATCACAACAGAAGGATATGCACATGTTCTGCTTCACGATCCCGTT
 ACAGTAATGAATGCGCAGCAGCTGGTATGCTTCTATCATTAAAC
 AGGCTTTATCTGTCAATTGACAATAGTGAGCGCTGATGGTATAC
 AATATGCCAAGGAATGATGCGTAACGATAACTAGACTATGTGATTCTT
 GTTCTGCTAACAGTGACAGACATGAGTTTATGTGGTGGCAACAAATT
 AAACATGATAGTCAAATGTTGCTGGTCTGATTATTGTTCAAGCACAAG
 TCCCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAA
 CAATTAAATAGCCATAAAACATTCAAGATGATGACTATTGTT
 TGCTGCGCTTCAAAATTATTATCAGACTTAGGACTAACATAAAGATA
 TCAAGGTTCTGGAAATGAGCGGAAGAAGGCAGTTAGTTCAAGATT
 GATTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTC
 TGGTCAGTTGGATTTCATCTAATGGTGTGGTGAAGAACCTGGACTATA
 CTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCCTATCTTATTG
 ATCTTGGTGGTATCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7503

STRAIN A909

ATGTTAGTGGAAATAGGAATTATTCCTCTTGGAAAGAATT
 ATAGCGAGCATAAACAGCATCTCTCGACTTAAAGAAGGAATTCTAA
 CATTATATAAAAATCAGCAGCTCTATTTAGAATCTTACAGGAAGC
 AACTAGTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACG
 TAATTAAATTGCTTTACCGCTTGTAGGGCTCTGCTTCTCAGGTGTT
 AATTAAAAGCTTATCATAATTGCTGTTAGGGACCTCACTGG
 GGGAAAGAGTGTGGTCAAAATGCCCTGTTCAATTGAAAGAAGGGAG
 GTCAAGTAGATGCTAGTTATTAGAAAAGCATCTGTTACCATATTGCT
 GATGAATTGATGGCTTATCATGATATTGTTGAGCTCGTATGTTATT
 AACCGCCTGTTCTGCAAGTAATAATGCCGAATTAGGAACACAATTAC
 TTCAAGATGGCATTGTGATTAGCTATTGTTGAGCTGTGATGAGTTA
 AGTGTATTTCTTGTGGCTTCACATCACTAGGAGCTTAAACAGA
 AATGGCATGTCAGCCCTATTCTCTGGAAAAGGAATCAATTGGTGAGG

SEQUENCE LISTING

GCGCTGGTTTGTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGA
 AAAATTATCGTGGCTTATTACTTCAGATGGTATCATATAACAGCACC
 TAAGCCAACAGGTGAAGGGGGCAGATGCAAAGCAGCTAGTGACTC
 AAGCAGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACA
 GGTACTCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTT
 CCCGACAACGACATTGATCAGCAGTACCAAGGGCAAACGGGTCAACTC
 TAGGGGCTGAGGTATTATCGAATTGATTAATTGTTAGCGGCAATAGAG
 GAACAGACTGTACCACTAAAAATGAGATTGGGATAGAAGGTTTCC
 AGAAAATTTGTCTATCATCAAAAGAGAGAATAACCAATAAGAAATGCTT
 TAAATTTTCTGTTGCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCA
 TCTTAGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAT
 GGCTATCTTATCATCTGCTTCCATTCTAAAGAATGAATCACTTCTA
 TAACCTTATGAAAAGGGCTAGTAATTCAACGACTTGAAGCATTACGC
 TTTAAAGGGGCTAGCACCCAAAAGCTGCAACCCAGCACATTAGGAA
 AATGGATGATTTCCAAATGGTGGCTAACACAGCTCAAGCACTAA
 TAGAAAGCAATATTAATCTAAAAAAACAAGATACTCAAAAGTAGGAATT
 GTATTTACAACACTTCTGGACCAGTTGAGGTTGTAAGGTTGAAAA
 GCAAATCACAACAGAAGGATATGCACATGTTCTGCTTCAGGATCCCCT
 TTACAGTAATGAAATGCAGCAGCTGGTATGCTTCTATCATTAAAT
 ACAGGCTCTTATCTGTCAATTGACAATAGTGGAGCGCTTGATGGTAT
 ACAATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATT
 TTGTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGGGCAACAA
 TTAAACTATGATAGTCATAATTGTTGCGGTTCTGATTATTGTTCAGCACA
 AGTCCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTA
 AACAAATTAAATATAGCCATAAAACATTACAGATGTGACTATT
 GATGCTGCGCTTCAAATTATTATCAGACTTAGGACTAACCATAAAAGA
 TATCAAAGGTTTCGTTGGAATGAGCGGAAGAAGGAGCTTAGTCAGATT
 ATGATTTCTAGCGAACTGTCTGAGTATTATAATATGCCAACCTTGCT
 TCTGGTCAGTTGGATTTCATCTAATGGTGTGGTGAAGAAGTGGACTA
 TACTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCCTATCTTATT
 CGATCTCGTGGTATCTTTGCTATTATTGAAAAAGG

SEQ ID NO. 7504

STRAIN H36B

ATGTTAGTGAATAGGAATTATTCTTCTTGGAAAGAATTATAGCGA
 GCATAAACAGCATCTCTCGACTTAAAGAAGGAATTCTAAACATTAT
 ATAAAAATCAGACTCTATTAGAATCTTACAGGAAGCATAACTAGT
 GACCCAGAGGTTCTGAGCAATACAAGATGAGACACGTAATTAAATT
 TGCTTACCGCTTTGAGAGGCTCTGCTTCTCAGGTGTTAATTAA
 AAGCTTATCATAATTGCTGTGTTAGGGACCTCACTGGGGAAAG
 AGTGTGGTCAAATGCTTGTATCAATTGAGAAGGAGAGCGTCAAGT
 AGATGCTAGTTATTAGAAAAGCATCTGTTACCATATTGCTGATGAAT
 TGATGGTTATCATGATATTGTTGGAGCTTCGTATGTTATTCAACCGCC
 TGTTCTGCAAGTAATAATGCCGTAAATTAGGAACACAAATTCAAGA
 TGGCGATTGTGATTTAGCTATTGTTGGCTGTGATGAGTTAAGTGATA
 TTTCTTAGCAGGCTTCACATCACTAGGAGCTATTAAACAGAAATGGCA
 TGTCAGCCATTCTGGAAAAGGAATCAATTGGGTGAGGGCGCTGG
 TTTGTTGTTCTGTCAGGATCAGTCCTAGCTAAATATGGAAAAATT
 TCGGTGGCTTATTACTTCAGATGGTATCATATAACAGCACCTAAGCCA
 ACAGGTGAAGGGCGGCACAGATGCAAAGCAGCTAGTGACTCAAGCAGG
 TATTGACTACAGTGAGATTGACTATTAAACGGTCACGGTACAGGTACTC
 AAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTCCCGACA
 ACGACATTGATCAGCAGTACCAAGGGCAAACGGGTCAACTCTAGGGC
 TGCAGGTATTATCGAATTGATTAATTGTTAGCGGCAATAGAGGAACAGA
 CTGTACAGCAACTAAATGAGATTGGGATAGAAGGTTCCAGAAAAT
 TTGTTGCTATCATCAAAGAGAGATAACCAATAAGAAATGCTTAAATT
 TTGTTGCTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTATT
 ATTACACCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCTATC
 TTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACCTA
 TGAAAAGGGCTAGTAATTCAACGACTTGAAGCATTACGCTTAAAG
 GGGCTAGACCAACCCAAAAGCTGCAACCCAGCACAAATTAGGAAAATGGAT
 GATTTTCCAAATGGTGGCTAACACAGCTCAAGCACTAATAGAAAAG
 CAATATTAACTAAAAAAACAAGATACTCAAAAGTAGGAATTGTTATT
 CAACACTTCTGGACCAGTTGAGGTTGTAAGGTTATTGAAAAGCAAATC

SEQUENCE LISTING

ACAAACAGAAGGATATGCACATGTTCTGCTTCACGATTCCCGTTACAGT
 AATGAATGCAGCAGCTGGTATGCTTCTATCATTTAAAATAACAGGTC
 CTTTATCTGTCATTCGACAAATAGTGGAGCCCTGATGGTATACAATAT
 GCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTTTC
 TGCTAATCAGTGGACAGACATGAGTTATGTTGCAACAATTAAACT
 ATGATAGTCAAATGTTGCGGTTCTGATTATGTTGCAAGCACAAGTCCTC
 TCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAATT
 AAAATATAGCCATAAAACATTACAGATGTGATGACTATTGATGCTG
 CGCTTCAAAATTATTATCAGACTTAGGACTAACCATAAAAGATATCAA
 GTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTCAGATTATGATT
 CTTAGCGAACTTGTCTGAGTATTATAATATGCCAACCTTGCCTCTGGTC
 AGTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATACTGTT
 AATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATCGATCTT
 CGGTGGTATCTCTTGCTATTATGAAAAAAGG

SEQ ID NO. 7505

STRAIN 18RS21

ATGTTAGTGGATAGGAATTATTCTTGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTCGACTTAAAGAAGGAATTCTAAACATT
 ATATAAAAATCAGACTCTATTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATT
 TTTGCTTTACCGCTTTGAAGAGGGCTTCTGCTTCTCAGGGTTAATT
 AAAAGCTTATCATATAATTGCTGTGTTAGGGACCTCACTGGGGAA
 AGAGTGCTGGTCAAATGCCGTATCAATTGAAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTATTAGAAAAAGCATCTGTTACCATATTGCTGATGA
 ATTGATGGTTATCATGATATTGTTGGAGCTTCGATGTTATTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTTAGCTATTGTTGGCTGTGATGAGTTAAGTGA
 TATTCTTACCGAGGCTTCACATCACTAGGAGCTATTACAGAAATGG
 CATGTCAGCCCTATTCTGAAAAGGAATCAATTGGGTGAGGGCGCT
 GGGTTGTTGTTCTGCAAAAGATCAGTCCTAGCTAAATATGGAAAAT
 TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAC
 CAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGAACAGCA
 GGTATTGACTACAGTGAGATTGACTATTACCGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAAGGAAAAAATATGATGGTAAGTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGCAAACGGGTCAACTCTAGGG
 GCTGCAGGTATTATGAAATTGATTAATTGTTAGCGGCAATAGAGGAACA
 GACTGTACAGCAACTAAAATGAGATTGGGATAGAAGGTTTCCAGAAA
 ATTGCTCATCAAAGAGAGATAACCCAAATAGAAATGCTTAAAT
 TTTGCTTTGGGAAATAATAGTGGTGTCTTATTGTCATCTT
 AGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAAGAATGAATCACTTCTATAACC
 TATGAAAAGTTGCTAGTAATTCAACGACTTTGAAGCATTACGCTTAA
 AGGGGCTAGACCACCCAAAATGTCAACCCAGCACAAATTAGGAAAATGG
 ATGATTTTCCAAATGGTGCCTAACACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAAACAAGATACTCAAAAGTAGGAATTGATT
 TACAAACACTTCTGGACCAGTTGAGGGTGTGAAGGTATTGAAAAGCAA
 TCACAAACAGAAGGATATGCACATGTTCTGCTTCACGATTCCGTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTAAATAACAGG
 TCCTTATCTGTCATTCGACAAATAGTGGAGCCCTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTTGCAACAATTAAA
 CTATGATAGTCAAATGTTGCGGTTCTGATTATTGTTGCAAGCACAAGTCC
 TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
 TTAAAATATAGCCATAAAACATTACAGATGTGATGACTATTGATG
 TGGCCTTCAAAATTATTATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTGCTTGGAAATGAGCGGAAGAAGGCAGTTAGTCAGATTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAACCTGCTTCTGG
 TCAGTTGGATTTCATCTAATGGTGTGGTGAAGAAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATCGATC
 TCGGTGGTATCTCTTGCTATTATGAAAAAAGG

SEQ ID NO. 7506

STRAIN M732

SEQUENCE LISTING

ATGTTAGTGGAAATAGGAATTATTCCTCTTGGGAAAGAATTATAG
 CGAGCATAAACAGCATCTTCGACTAAAGAAGGAATTCTAAACATT
 TATATAAAATCAGACTCTATTTAGAATCTTATACAGGAAGCATAACT
 AGTGAACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTAA
 ATTGCTTTACCGCTTGAAGAGGCTTCTGCTCTTCAGGTGTTAATT
 TAAAGCTTACATAATATTGCTGTGTTAGGGACCTCACTGGGGA
 AAGAGTGTGCTGAAAGCCTTGTATCAATTGAAAGAAGGAGAGCGTCA
 AGTAGATGCTAGTTATTAGAAAAGCATCTGTTACCATATTGCTGATG
 AATTGATGGCTTATCATGATATTGTTAGCTTACCATATTGCTGATG
 GCCTGTTCTGCAAGTAATAATGCCGTAAATTAGGAACACAATTACTTCA
 AGATGGCGATTGTGATTAGCTATTGTTGGTGGCTGTGATGAGTTAAGTG
 ATATTTCTTAGCAGGCTTCACATCACTAGGAGCTTAATACAGAAATG
 GCATGTCAGCCATTCTCTGGAAAAGGAATCAATTGGGTGAGGGCGC
 TGGTTTGTCTTGTCAAAGATCAGTCCTAGCTAAATATGGAAAAAA
 TTATCGGGCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGCGGCACAGATGCAAAGCAGCTAGTGACTCAAGC
 AGGTATTGACTACAGTGAGATTGACTATATTACCGTCACGGTACAGGTA
 CTCAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTCCCG
 ACAACGACATTGATCAGCAGTACCAAGGGCAACGGGTCACTCTAGG
 GGCTGCAGGTATTATCGAATTGATTAATTGTTAGCGGCAATAGAGGAAC
 AGACTGTACCAGCAACTAAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTGTCATCATCAAAGAGAGAATACCAATAAGAAATGCTTTAAA
 TTTTCGTTGCTTGTGAAATAATAGTGGTGTCTTATGTCATCTT
 TAGATTACCTCTAGAACATTACCTGCTAGAGAAAATCTTAAATGGCT
 ATCTTATCATGTTGCTTCATTCTAAGAATGAACTTCACTTCTATAAC
 CTATAAAAAGTTGCTAGTAATTCAACGACTTGAAGCATTACGCTTTA
 AAGGGCTAGACCACCCAAAATGTCAACCCAGCACAATTAGAAAATG
 GATGATTTCCAAAATGGTGGCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAAAACAGATACTTCAAAAGTAGGAATTGTAT
 TTACAACACTTCTGGACAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAAACAGAAGGATATGCACATGTTCTGCTTCACGATTCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAACAG
 GTCTTCTATCTGTCAATTGACAAATAGTGGAGCGCTTGATGGTATAACAA
 TATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 ACTATGATAGTCAAATGTTGTCGGTCTGATTATTGTCAGCACAAGTC
 CTCTCTCGTCAAGCATTGATAATTCCCTATAATATTAGGTAGTAAACA
 ATTAATATAGCCATAAAACATTACAGATGTGATGACTATTGATG
 CTGCGCTTCAAAATTATTCAGACTTAGGACTAACCAATAAGATATC
 AAAGGTTTGTGGAATGAGCGGAAGAAGGCAGTTAGTCAGATTATGA
 TTTCTTAGCGAACATTGCTGAGTATTATAATATGCCAAACCTTGCTTCTG
 GTCAAGTTGGATTTCATTAATGGTGTGGTGAAGAAACTGGACTAtaCT
 GTTAAATGAAAGTATGAAAAGGGCTATTATTAGTCCTATCTTATTGAT
 CTTCGGTGGTATCTCTTGTATTATTGAAAAAAGG

SEQ ID NO. 7507

STRAIN COH1

ATGTTAGTGGAAATAGGAATTATTCCTCTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTTCGACTAAAGAAGGAATTCTAAACATT
 ATATAAAATCAGACTCTATTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTAA
 TTTGCTTTACCGCTTTGAAGAGGCTTCTGCTTCTCAGGTGTTAATT
 AAAAGCTTATCATATAATTGCTGTGTTAGGGACCTCACTTGGGGA
 AGAGTGTGCTGAAAGCCTGATCAATTGAAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTATTAGAAAAGCATCTGTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTTGGAGCTTCGATGTTATTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATTAGGAACACAATTACTTCA
 GATGGCGATTGTGATTTAGCTATTGTTGGCTGTGATGAGTTAAGTGA
 TATTCTTACGAGGCTTACACATCACTAGGAGCTTAAATACAGAAATGG
 CATGTCAGCCCTATTCTCTGGAAAAGGAATCAATTGGGTGAGGGCGCT
 GGTGTTGTTGTTCTGCAAAGATCAGTCCTAGCTAAATATGGAAAAAA
 TATCGGTGGCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTACCGTCACGGTACAGGTAC

SEQUENCE LISTING

TCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGCAAACGGGTCAACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAATTGTTAGCGGAATAGAGGAACA
 GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTCCAGAAA
 ATTTTGTCTATCATCAAAGAGAGAATACCCAAATAAGAAATGCTTAAAT
 TTTTGTCTTGTGTTGGAAATAATAGTGGTGTCTTATTGTCATCTT
 AGATTCAACCTCTAGAAACATTACCTGCTAGAGAAAATCTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTCAACGACTTTGAAGCATTACGCTTAA
 AGGGGCTAGACCACCCAAAAGTCAACCCAGCACAAATTAGGAAATGG
 ATGATTTTCCAAAATGGTGCCTGACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAACAAAGATACTTCAAAAGTAGGAATTGTATT
 TACAACACTTCTGGACCAAGTTGAGGGTGTGAAAGGTATTGAAAAGCAAA
 TCACAAACAGAAGGATATGCACATGTTCTGCTTACGATTCCGTTACA
 GTATGAATGAGCAGCTGTTCTGTTCTATCATTTTAAATAACAGG
 TCCTTATCTGTCATTCGACAAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTTGGCAACAATTAAA
 CTATGATAGTCAAATGTTGTCGGTTCTGATTATGTTCAAGCACAAGTCC
 TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
 TTAAAATATGCCATAAAACATTACAGATGTGACTATTGATGC
 TGGCCTTCAAAATTATTATCAGACTAGGACTAACCATAAAAGATATCA
 AAGGTTTCTGTTGGAATGAGCGGAAGAAGGGCAGTTAGTCAGATTATGAT
 TTCTTAGCGAATGTCGAGTATTATAATATGCCAAACCTGCTTCTGG
 TCAGTTGGATTTCATCTAATGGTGCCTGGTAAGAACTGGACTATACTG
 TTAATGAAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTGATC
 TTCGGTGGTATCTCTTGTCTTATTGAAAAAGG

SEQ ID NO. 7508

STRAIN M781

ATGTTAGTGGAAATAGGAATTATTCTCTTGGGAAAGAATTATAGC
 GAGCATAAAACAGCATCTCTCGACTTAAAGAAGGAATTCTAAACATT
 ATATAAAAATCAGACTCTATTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTAAA
 TTTGCTTTACCGTTTGAAGAGGCTCTGCTTCTCAGGTGTTAATT
 AAAAGCTTATCATAATATTGCTGTGTTAGGACCTCACTGGGGAA
 AGAGTGTGGTCAAATGCCTGTATCAATTGAAGAAGGGAGCGTCAA
 GTAGATGCTAGTTATTAGAAAAGCATCTGTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTTGGAGCTTGTATGTTATTCAACCG
 CCTGTTCTGCAAGTAATAAGCCGTAATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTGTTGGTGGCTGTGATGAGTTAAGTGA
 TATTCTTCTAGCAGGCTTACATCACTAGGAGCTTAAATACAGAAATGG
 CATGTCAGCCCTATTCTCTGGAAAAGGAATCAATTGGGTGAGGGCGCT
 GGTTTGTGTTCTGTCAGATCAGTCTTAGCTAAATATGGAAAAT
 TATCGGTGGCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAC
 CAACAGGTGAAGGGCGGACAGATTGCAAAGCAGCTAGTGAACAGCA
 GGTATTGACTACAGTGAGATTGACTATTAAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGCAAACGGGTCAACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAATTGTTAGCGGAATAGAGGAACA
 GACTGTACCAGCAACTAAAATGAGATTGGGATAGAAGGTTCCAGAAA
 ATTTTGTCTATCATCAAAGAGAGAATACCCAAATAAGAAATGCTTAAAT
 TTTCTGTTGCTTGTGAAATAATAGTGGTATCTTATTGTCATCTT
 AGATTCAACCTCTAGAAACATTACCTGCTAGAGAAAATCTAAATGGCTA
 TCTTATCATCTGTTGCTTCAATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAGTGTAGTAATTCAACGACTTTGAAGCATTACGCTTAA
 AGGGGCTAGACCACCCAAAAGTCAACCCAGCACAAATTAGGAAAATGG
 ATGATTTTCCAAAATGGTGCCTGAAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAACAAAGATACTTCAAAAGTAGGAATTGTATT
 TACAACACTTCTGGACCAAGTTGAGGGTGTGAAAGGTATTGAAAAGCAAA
 TCACAAACAGAAGGATATGCACATGTTCTGCTTACGATTCCGTTACA
 GTAATGAATGAGCAGCTGTTATGCTTCTATCATTTTAAATAACAGG
 TCCTTATCTGTCATTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTT

SEQUENCE LISTING

TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAAA
 CTATGATAGTCAAATGTTGTCGGTTCTGATTATGTTCAGCACAAGTCC
 TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTACTAAACAA
 TTAAAATATAGCCATAAAACATTACAGATGTGACTATTGATGC
 TGCCTTCAAAATTATTATCAGACTTAGGACTAACCTAAAGATATCA
 AAGTTTGGATGAGCGGAAGAAGGCAGTAGTCAGATTGAT
 TTCTAGCGAACTTGTCTGAGTATTATAATGCTAACCTTGTCTCTGG
 TCAGTTGGATTTCATCTAATGGTGTGGTAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTCAGTCATCTTATTGATC
 TTTGGTGGTATCTCTTTGCTATTATGAAAAAAGG

SEQ ID NO. 7509

STRAIN CJB110

ATGTTAGTGGAAATAGGAATTATTTCTTGGGAAAGAATTATAGC
 GAGCATAAAACAGCATCTCTCGACTTAAAGAAGGAATTCTAAACATT
 ATATAAAAATCAGACTCTATTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCCCTGAGCAATACAAAGATGAGACACGTAATTAAA
 TTTGCTTTACCGCTTTGAAGAGGCTCTGCTTCTCAGGTGTTAATT
 AAAAGCTTATCATAATATTGCTGTGTTAGGGACCTCACTGGGGAA
 AGAGTGTGGTCAAATGCCTGTATCAATTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTATTAGAAAAAGCATCTGTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGAGCTTCGTATGTTATTCAACCG
 CCTGTTCTGCAAGTAAATAAGCCGTAATTAGGAACACAATTACTTCAA
 GATGGCGATTGATTTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTCTTACAGGCTTCACATCACTAGGAGCTATTAAACAGAAATGG
 CATGTCAGCCCTATTCTCTGAAAAGGAATCAATTGGGTGAGGGCGCT
 GGTTTGTGTTCTGTCAAAGATCAGTCCTAGCTAAATATGGAAAAT
 TATCGGGTGTCTTATTACTTCAGATGTTATCATATAACAGCACCTAAC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGA
 GGTATTGACTACAGTGAGATTGACTATATTATGGTACCGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAAATATGTTGTAAGTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGCAAACAGGGTCAACTCTAGGG
 GCTCAGGTTATCGAATTGATTAATTGTTAGGGCAATAGAGGAACA
 GACTGTACCGCAACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAAA
 ATTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGTTAAAT
 TTTCGTTGCTTTGGGAAATAATAGGTTATCTTATTGTCATCTT
 AGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTAAATGGCTA
 TCTTATCATCTGTTGCTTCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAGTGTCTAGTAATTCAACGACTTTGAAGCATTACGCTTAA
 AGGGCTAGACCACCCAAACTGTCAACCCAGCACAATTAGGAAAATGG
 ATGATTTCCAAAATGGTGGCTAACACAGCTCAAGCACAATAGAA
 AGCAATTAAATAAAAACAGATACTTCAAAGTAGGATTGAGTATT
 TACACACTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 TCACAAACAGAAGGATATGCACATGTTCTGCTCACGATTCCCGTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAACAGG
 TCCTTATCTGTCATTGACAAATAGTGGAGCGCTTGATGGTACAAAT
 ATGCCAAGGAATGATGCCAACGATAATCTAGACTATGTGATTCTGTT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAAA
 CTATGATAGTCAAATGTTGTCGGTTCTGATTATGTTCAAGCACAAGTCC
 TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
 TTAAAATATAGCCATAAAACATTACAGATGTGACTATTGATGC
 TGCCTTCAAAATTATTATCAGACTTAGGACTAACCTAAAGATATCA
 AAGTTTGGATGAGCGGAAGAAGGCAGTAGTCAGATTGAT
 TTCTAGCGAACTTGTCTGAGTATTATAATGCTAACCTTGTCTCTGG
 TCAGTTGGATTTCATCTAATGGTGTGGTAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTCAGTCATCTTATTGATC
 TTTGGTGGTATCTCTTTGCTATTATGAAAAAAGG

SEQ ID NO. 7510

STRAIN 1169NT

ATGTTAGTGGAAATAGGAATTATTTCTTGGGAAAGAATTATAG
 CGAGCATAAAACAGCATCTCTCGACTTAAAGAAGGAATTCTAAACATT
 TATATAAAAATCAGACTCTATTAGAATCTTATACAGGAAGCATAACT
 AGTGACCCAGAGGTTCCCTGAGCAATACAAAGATGAGACACGTAATTAAA

SEQUENCE LISTING

ATTTGCTTTACCGCTTTGAAGAGGCCTTGCTTCTTCAGGTGTTAATT
 TAAAAGCTTATCATAATATTGCTGTGTTAGGGACCTCACTTGGGGGA
 AAGAGTGCCTGCTAAATGCCTTGTATCAATTGAAAGAAGGAGAGCGTCA
 AGTAGATGCTAGTTAGAAAAAGCATCTGTTACCATATTGCTGATG
 AATTGATGGCTTATCATGATATTGTTGGAGCTCGTATGTTATTCAACC
 GCCTGTTCTGCAAGTAATAATGCCGTAAATTAGGAACACAATTACTTC
 AGATGGCATTGTGATTAGCTATTGTTGGCTGTGATGAGTTAAGTG
 ATATTCTTCTAGCAGGCTCACATCACTAGGAGCTATTAAACAGAAATG
 GCATGTCAGCCCTATTCTCTGGAAAAGGAATCAATTGGGTGAGGGCGC
 TGGTTTGTGTTCTGCTAAAGATCAGTCCTAGCTAAATATGGAAAAAA
 TTATCGGTGGTCTTAACTTCAGATGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGAACCAAGC
 AGGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTA
 CTCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTCCC
 ACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCAACTCTAGG
 GGCTGCAGGTATTATCGAATTGATTAAATTGTTAGCGGCAATAGAGGAAC
 AGACTGTACCACTAAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTAA
 TTTTCGTTGCTTTGGTGGAAATAATAGTGGTATCTTATTGTCATCTT
 TAGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTAAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAAC
 CTATGAAAAAGTTGCTAGTAATTCAACGACTTTGAAGCATTACGCTTTA
 AAGGGGCTAGACCACCCAAAAGTGTCAACCCAGCACAATTAGGAAAATG
 GATGATTTTCCAAAATGTTGCCGTAAACAACAGCTAACAGCAATAAGA
 AAGCAATAATTAACTAAAAAAACAGATACTTCAAAAGTAGGAATTGTAT
 TTACAACACTTCTGGACCACTGGAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAACGATATGCACATGTTCTGCTTCACGATTCCCGTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTAAATAACAG
 GTCCTTATCTGCTATTGACAAATAGTGGAGCGCTTGATGGTACACAA
 TATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 ACTATGATAGTCAAATGTTGCGGTTCTGATTATTGTTGTCAGCACAAGTC
 CTCTCGTCAAGCATTGATAATTCTCTATAAATATTAGGTAGTAAACA
 ATTAAATATGCCATAAAACATTACAGATGTGATGACTATTGGTATG
 CTGCGCTTCAAAATTATTATCAGACTTAGGACTAACCATAAAGATATC
 AAAGGTTTCGTTGGAATGAGCGGAAGAAGGCAGTTAGTTGAGATTATGA
 TTTCTAGCGAACCTGCTGAGTATTATAATATGCCAACCTGCTTCTG
 GTCAGTTGGATTTCATCTAATGGTCTGGTGAAGAACCTGGACTATACT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCCATCTTATTGAT
 CTTGGTGGTATCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7511

STRAIN JM9130013

ATGTTAGTGGAAATAGGAATTATTCTCTTGGGAAAGAATTATAGCGAG
 CATAAACAGCATCTCTCGACTAAAGAAGGAATTCTAAACATTTATA
 TAAAATCAGCACTATTAGAATCTTACAGGAAGCATAACTAGTG
 ACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTAA
 GCTTTACCGCTTTGAAGAGGCCTTGCTTCTTCAGGTGTTAATTAAA
 AGCTTATCATATAATTGCTGTGTTAGGGACCTCACTTGGGGAAAGA
 GTGCTGGTCAAATGCTGTATCAATTGAAAGAAGGAGAGCGTCAAGTA
 GATGCTAGTTATTAGAAAAAGCATCTGTTACCATATTGCTGATGAAATT
 GATGGCTTATCATGATATTGTTGGAGCTTCGTTAGTTAATTCAACCGCCT
 GTTCTGCAAGTAATAATGCCGTAAATTAGGAACACAATTACTCAAGAT
 GGCAGATTGTTAGCTATTGTTGGCTGTGATGAGTTAAGTGTGAT
 TTCTTCTGAGGCTTCACATCACTAGGAGCTATTAAACAGAAATGGCAT
 GTCAGCCATTCTCTGAAAAGGAATCAATTGGGTGAGGGCGCTGGT
 TTTGTTGTTCTGCAAAGATCAGTCCTAGCTAAATATGGAAAAATTAT
 CGGTGGCTTATTACTTCAGATGGTTATCATATAACAGCACCTAACGCAA
 CAGGTGAAGGGCGGGCACAGATTGCAAAGCAGCTAGTGAACGGTACAGG
 ATTGACTACAGTGAGATTGACTATATAACGGTCACGGTACAGGTACTCA
 AGCTAATGATAAAATGGAAAAAAATGTATGGTAAGTTTCCCAGCAA
 CGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCAACTCTAGGGC
 GCAGGTATTATCGAATTGATTAAATTGTTAGCGGCAATAGAGGAACAGAC
 TGTACAGCAACTAAAATGAGATTGGGATAGAAGGTTTCCAGAAAATT

SEQUENCE LISTING

TTGTCTATCATCAAAAGAGAGAATAACCAATAAGAAATGCTTAAATTT
 TCGTTGCTTTGGTGGAAATAATAGGGTGTCTTATTGTCATCTTAGA
 TTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGGCTATCT
 TATCATCTGTTGCTTCAAGAATGAATCACTTCTATAACCTAT
 GAAAAGTTGCTAGTAAATTCAACGACTTGAAGCATTACGCTTAAAGG
 GGCCTAGACCACCCAAAACGTCAACCCAGCACAATTAGGAAATGGATG
 ATTTTCAAAATGGTGGCGTAACAAACAGCTCAAGCACTAATAGAAAGC
 AATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATTTAC
 AACACTTCTGGACCAGTGAGGTTGTTGAAGGTATTGAAAAGCAAATCA
 CAACAGAAGGATATGCACATGTTCTGCTTCAGCATTCCGTTACAGTA
 ATGAATGCAGCAGCTGGTATGCTTCTATCATTAAAATAACAGGTCC
 TTTATCTGTCATTGACAAATAGTGGAGCGCTGATGGTATAACATATG
 CCAAGGAAATGATGCGTAACGATAATCTAGACTATGTTCTTGTGTTCT
 GCTAATCAGTGGACAGACATGAGTTTATGTTGCGCAACATAAAACTA
 TGATAGTCAAATGTTGTCGGTTCTGATTATTGTTCAGCACAAGTCCCT
 CTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACAATTA
 AAATATAGCCATAAAACATTACAGATGTGACTATTTTGATGCTGC
 GCTTCAAATTATTATCAGACTTAGGACTAACCATAAAAGATATCAAAG
 GTTTCGTTGGAATGAGCGGAAGAAGGCAGTTAGTCAGATTATGATTTC
 TTAGCGAATTGCTGAGTATTATAATATGCCAACCTGCTTCTGGTCA
 GTTTGGATTTCATCTAATGGTGTGGTAAGAACTGGACTATACTGTTA
 ATGAAAGTATAGAAAAGGGCTATTATTAGTCCTATCTTATTCGATCTTC
 GGTGGTATCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7512

STRAIN 2603 frame: 1

MSVYSGIGISSLGKNYSEHKQHLDLKEGISKHLYKNHDSILESYTGSITSDPREVPEQ
 YKDETTRNFKAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGSAGQNALYQFEEGERQV
 DASLLEKASVYHIADELMAYHDIVGASYVISTACSAASNAVILGTQLLQDGCDLAICGG
 CDELSDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIIGGL
 ITSDGYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF
 FPTTTLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFPENFVYHQKR
 EYPIRNLNFSAFGGNNSGVLLSPLDSELETLPARENLKMAILSSVASISKNESLSITY
 EKVASFNFDEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
 KVGIVFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMMAAGMLSIIIFKITGPLSV
 ISTNSGALDGIQYAKEMMRNDNLDYVILVSANQWTDMFSMWWQQLNYDSQMFVGSDYCSA
 QVLSRQALDNNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLSDLGLTIKDIKGFVWNER
 KKAVENTGYYLVLVLSYSIFGGISFAIIIEKR

SEQ ID NO. 7513

STRAIN 090 frame: 3

VSGIGISSLGKNYSEHKQHLDLKEGISKHLYKNHDSILESYTGSITSDPREVPEQYKDE
 TRNFKAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGSAGQNALYQFEEGERQV
 DASLLEKASVYHIADELMAYHDIVGASYVISTACSAASNAVILGTQLLQDGCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSAFGGNNSGVLLSPLDSELETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDDEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVG
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMMAAGMLSIIIFKITGPLSV
 ISTNSGALDGIQYAKEMMRNDNLDYVILVSANQWTDMFSMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLSDLGLTIKDIKGFVWNERKKAV
 SSDYDFLANLSEYYNMPNLASQFGFSSNGAGEEELDYTVNESIEKGYYLVLVLSYSIFGGIS
 FAIIIEKR

SEQ ID NO. 7514

STRAIN A909 frame: 3

VSGIGISSLGKNYSEHKQHLDLKEGISKHLYKNHDSILESYTGSITSDPREVPEQYKDE
 TRNFKAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGSAGQNALYQFEEGERQV
 DASLLEKASVYHIADELMAYHDIVGASYVISTACSAASNAVILGTQLLQDGCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFPENFVYHQKREYPI

SEQUENCE LISTING

RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVNPQAQFRKMDDFSKMVAVTAAQALIESNINLKKQDTSKVG
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNSPIIILGSKQLKYSHKTFTDVTMIFTDAALQNLLSDLGLTIKDIKGFVWNERKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7515

STRAIN H36B frame: 3
 VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDP
 EPEQYKDE TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS
 LGGKSAGQN
 ALYQFEE
 ERQVDASL
 LEKASVYHIADELMAYHDIVGASVYV
 I
 STAC
 S
 A
 N
 N
 A
 V
 I
 L
 G
 T
 Q
 L
 L
 Q
 D
 G
 C
 D
 L
 A
 I
 C
 G
 G
 C
 D
 E
 L
 S
 D
 I
 S
 L
 A
 G
 F
 T
 S
 I
 L
 G
 A
 I
 N
 T
 E
 M
 A
 C
 Q
 P
 Y
 S
 S
 G
 K
 G
 I
 N
 L
 G
 E
 G
 A
 G
 F
 V
 V
 L
 V
 K
 D
 Q
 S
 L
 A
 K
 Y
 G
 K
 I
 I
 G
 G
 L
 I
 T
 S
 D
 GYH
 I
 T
 A
 P
 K
 P
 T
 G
 E
 G
 A
 A
 Q
 I
 A
 K
 Q
 L
 V
 T
 Q
 A
 G
 I
 D
 Y
 S
 E
 I
 D
 Y
 I
 N
 G
 H
 G
 T
 G
 T
 Q
 A
 N
 D
 K
 M
 E
 K
 N
 M
 Y
 G
 K
 F
 F
 P
 T
 T
 TL
 I
 S
 S
 T
 K
 G
 Q
 T
 G
 H
 T
 L
 G
 A
 A
 G
 I
 I
 E
 L
 I
 N
 C
 L
 A
 A
 I
 E
 E
 Q
 T
 V
 P
 A
 T
 K
 N
 E
 I
 G
 I
 E
 G
 F
 P
 E
 N
 F
 V
 Y
 H
 Q
 K
 R
 E
 Y
 P
 I
 RN
 A
 L
 N
 F
 S
 F
 A
 F
 G
 G
 N
 N
 S
 G
 V
 L
 L
 S
 S
 L
 D
 S
 P
 L
 E
 T
 L
 P
 A
 R
 E
 N
 L
 K
 M
 A
 I
 L
 S
 S
 V
 A
 I
 S
 K
 N
 E
 L
 S
 I
 T
 Y
 E
 K
 V
 A
 S
 S
 N
 F
 N
 D
 F
 E
 A
 L
 R
 F
 K
 G
 A
 R
 P
 P
 K
 T
 V
 N
 P
 A
 Q
 F
 R
 K
 M
 D
 D
 F
 S
 K
 M
 V
 A
 V
 T
 T
 A
 Q
 A
 L
 I
 E
 S
 N
 I
 N
 L
 K
 K
 Q
 D
 T
 S
 K
 V
 G
 I
 V
 F
 T
 T
 S
 L
 G
 P
 V
 E
 V
 V
 E
 G
 I
 E
 K
 Q
 I
 T
 T
 E
 G
 Y
 A
 H
 V
 S
 A
 S
 R
 F
 P
 F
 T
 V
 M
 N
 A
 A
 G
 M
 L
 S
 I
 I
 F
 K
 I
 T
 G
 P
 L
 S
 V
 I
 S
 T
 N
 S
 G
 A
 L
 D
 G
 I
 Q
 Y
 A
 K
 E
 M
 M
 R
 N
 D
 N
 L
 D
 Y
 V
 I
 L
 V
 S
 A
 N
 Q
 W
 T
 D
 M
 S
 F
 M
 W
 W
 Q
 Q
 L
 N
 Y
 D
 S
 Q
 M
 F
 V
 G
 S
 D
 Y
 C
 S
 A
 Q
 V
 L
 S
 R
 O
 Q
 A
 L
 D
 N
 S
 P
 I
 I
 L
 G
 S
 K
 Q
 L
 K
 Y
 S
 H
 K
 T
 F
 T
 D
 V
 M
 I
 T
 F
 D
 A
 A
 L
 Q
 N
 L
 L
 S
 D
 L
 G
 L
 T
 I
 K
 D
 I
 K
 G
 F
 V
 W
 N
 E
 R
 K
 A
 V
 S
 S
 D
 Y
 D
 F
 L
 A
 N
 L
 S
 E
 Y
 Y
 N
 M
 P
 N
 L
 A
 S
 G
 Q
 F
 G
 F
 S
 S
 N
 G
 A
 G
 E
 E
 L
 D
 Y
 T
 V
 N
 E
 S
 I
 E
 K
 G
 Y
 Y
 L
 V
 L
 S
 Y
 S
 I
 F
 G
 G
 I
 S
 F
 A
 I
 E
 K
 R

SEQ ID NO. 7516

STRAIN 18RS21 frame: 3
 VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDP
 EPEQYKDE TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS
 LGGKSAGQN
 ALYQFEE
 ERQVDASL
 LEKASVYHIADELMAYHDIVGASVYV
 I
 STAC
 S
 A
 N
 N
 A
 V
 I
 L
 G
 T
 Q
 L
 L
 Q
 D
 G
 C
 D
 L
 A
 I
 C
 G
 G
 C
 D
 E
 L
 S
 D
 I
 S
 L
 A
 G
 F
 T
 S
 I
 L
 G
 A
 I
 N
 T
 E
 M
 A
 C
 Q
 P
 Y
 S
 S
 G
 K
 G
 I
 N
 L
 G
 E
 G
 A
 G
 F
 V
 V
 L
 V
 K
 D
 Q
 S
 L
 A
 K
 Y
 G
 K
 I
 I
 G
 G
 L
 I
 T
 S
 D
 GYH
 I
 T
 A
 P
 K
 P
 T
 G
 E
 G
 A
 A
 Q
 I
 A
 K
 Q
 L
 V
 T
 Q
 A
 G
 I
 D
 Y
 S
 E
 I
 D
 Y
 I
 N
 G
 H
 G
 T
 G
 T
 Q
 A
 N
 D
 K
 M
 E
 K
 N
 M
 Y
 G
 K
 F
 F
 P
 T
 T
 TL
 I
 S
 S
 T
 K
 G
 Q
 T
 G
 H
 T
 L
 G
 A
 A
 G
 I
 I
 E
 L
 I
 N
 C
 L
 A
 A
 I
 E
 E
 Q
 T
 V
 P
 A
 T
 K
 N
 E
 I
 G
 I
 E
 G
 F
 P
 E
 N
 F
 V
 Y
 H
 Q
 K
 R
 E
 Y
 P
 I
 RN
 A
 L
 N
 F
 S
 F
 A
 F
 G
 G
 N
 N
 S
 G
 V
 L
 L
 S
 S
 L
 D
 S
 P
 L
 E
 T
 L
 P
 A
 R
 E
 N
 L
 K
 M
 A
 I
 L
 S
 S
 V
 A
 I
 S
 K
 N
 E
 L
 S
 I
 T
 Y
 E
 K
 V
 A
 S
 S
 N
 F
 N
 D
 F
 E
 A
 L
 R
 F
 K
 G
 A
 R
 P
 P
 K
 T
 V
 N
 P
 A
 Q
 F
 R
 K
 M
 D
 D
 F
 S
 K
 M
 V
 A
 V
 T
 T
 A
 Q
 A
 L
 I
 E
 S
 N
 I
 N
 L
 K
 K
 Q
 D
 T
 S
 K
 V
 G
 I
 V
 F
 T
 T
 S
 L
 G
 P
 V
 E
 V
 V
 E
 G
 I
 E
 K
 Q
 I
 T
 T
 E
 G
 Y
 A
 H
 V
 S
 A
 S
 R
 F
 P
 F
 T
 V
 M
 N
 A
 A
 G
 M
 L
 S
 I
 I
 F
 K
 I
 T
 G
 P
 L
 S
 V
 I
 S
 T
 N
 S
 G
 A
 L
 D
 G
 I
 Q
 Y
 A
 K
 E
 M
 M
 R
 N
 D
 N
 L
 D
 Y
 V
 I
 L
 V
 S
 A
 N
 Q
 W
 T
 D
 M
 S
 F
 M
 W
 W
 Q
 Q
 L
 N
 Y
 D
 S
 Q
 M
 F
 V
 G
 S
 D
 Y
 C
 S
 A
 Q
 V
 L
 S
 R
 O
 Q
 A
 L
 D
 N
 S
 P
 I
 I
 L
 G
 S
 K
 Q
 L
 K
 Y
 S
 H
 K
 T
 F
 T
 D
 V
 M
 I
 T
 F
 D
 A
 A
 L
 Q
 N
 L
 L
 S
 D
 L
 G
 L
 T
 I
 K
 D
 I
 K
 G
 F
 V
 W
 N
 E
 R
 K
 A
 V
 S
 S
 D
 Y
 D
 F
 L
 A
 N
 L
 S
 E
 Y
 Y
 N
 M
 P
 N
 L
 A
 S
 G
 Q
 F
 G
 F
 S
 S
 N
 G
 A
 G
 E
 E
 L
 D
 Y
 T
 V
 N
 E
 S
 I
 E
 K
 G
 Y
 Y
 L
 V
 L
 S
 Y
 S
 I
 F
 G
 G
 I
 S
 F
 A
 I
 E
 K
 R

SEQ ID NO. 7517

STRAIN M732 frame: 3
 VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDP
 EPEQYKDE TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS
 LGGKSAGQN
 ALYQFEE
 ERQVDASL
 LEKASVYHIADELMAYHDIVGASVYV
 I
 STAC
 S
 A
 N
 N
 A
 V
 I
 L
 G
 T
 Q
 L
 L
 Q
 D
 G
 C
 D
 L
 A
 I
 C
 G
 G
 C
 D
 E
 L
 S
 D
 I
 S
 L
 A
 G
 F
 T
 S
 I
 L
 G
 A
 I
 N
 T
 E
 M
 A
 C
 Q
 P
 Y
 S
 S
 G
 K
 G
 I
 N
 L
 G
 E
 G
 A
 G
 F
 V
 V
 L
 V
 K
 D
 Q
 S
 L
 A
 K
 Y
 G
 K
 I
 I
 G
 G
 L
 I
 T
 S
 D
 GYH
 I
 T
 A
 P
 K
 P
 T
 G
 E
 G
 A
 A
 Q
 I
 A
 K
 Q
 L
 V
 T
 Q
 A
 G
 I
 D
 Y
 S
 E
 I
 D
 Y
 I
 N
 G
 H
 G
 T
 G
 T
 Q
 A
 N
 D
 K
 M
 E
 K
 N
 M
 Y
 G
 K
 F
 F
 P
 T
 T
 TL
 I
 S
 S
 T
 K
 G
 Q
 T
 G
 H
 T
 L
 G
 A
 A
 G
 I
 I
 E
 L
 I
 N
 C
 L
 A
 A
 I
 E
 E
 Q
 T
 V
 P
 A
 T
 K
 N
 E
 I
 G
 I
 E
 G
 F
 P
 E
 N
 F
 V
 Y
 H
 Q
 K
 R
 E
 Y
 P
 I
 RN
 A
 L
 N
 F
 S
 F
 A
 F
 G
 G
 N
 N
 S
 G
 V
 L
 L
 S
 S
 L
 D
 S
 P
 L
 E
 T
 L
 P
 A
 R
 E
 N
 L
 K
 M
 A
 I
 L
 S
 S
 V
 A
 I
 S
 K
 N
 E
 L
 S
 I
 T
 Y
 E
 K
 V
 A
 S
 S
 N
 F
 N
 D
 F
 E
 A
 L
 R
 F
 K
 G
 A
 R
 P
 P
 K
 T
 V
 N
 P
 A
 Q
 F
 R
 K
 M
 D
 D
 F
 S
 K
 M
 V
 A
 V
 T
 T
 A
 Q
 A
 L
 I
 E
 S
 N
 I
 N
 L
 K
 K
 Q
 D
 T
 S
 K
 V
 G
 I
 V
 F
 T
 T
 S
 L
 G
 P
 V
 E
 V
 V
 E
 G
 I
 E
 K
 Q
 I
 T
 T
 E
 G
 Y
 A
 H
 V
 S
 A
 S
 R
 F
 P
 F
 T
 V
 M
 N
 A
 A
 G
 M
 L
 S
 I
 I
 F
 K
 I
 T
 G
 P
 L
 S
 V
 I
 S
 T
 N
 S
 G
 A
 L
 D
 G
 I
 Q
 Y
 A
 K
 E
 M
 M
 R
 N
 D
 N
 L
 D
 Y
 V
 I
 L
 V
 S
 A
 N
 Q
 W
 T
 D
 M
 S
 F
 M
 W
 W
 Q
 Q
 L
 N
 Y
 D
 S
 Q
 M
 F
 V
 G
 S
 D
 Y
 C
 S
 A
 Q
 V
 L
 S
 R
 O
 Q
 A
 L
 D
 N
 S
 P
 I
 I
 L
 G
 S
 K
 Q
 L
 K
 Y
 S
 H
 K
 T
 F
 T
 D
 V
 M
 I
 T
 F
 D
 A
 A
 L
 Q
 N
 L
 L
 S
 D
 L
 G
 L
 T
 I
 K
 D
 I
 K
 G
 F
 V
 W
 N
 E
 R
 K
 A
 V
 S
 S
 D
 Y
 D
 F
 L
 A
 N
 L
 S
 E
 Y
 Y
 N
 M
 P
 N
 L
 A
 S
 G
 Q
 F
 G
 F
 S
 S
 N
 G
 A
 G
 E
 E
 L
 D
 Y
 T
 V
 N
 E
 S
 I
 E
 K
 G
 Y
 Y
 L
 V
 L
 S
 Y
 S
 I
 F
 G
 G
 I
 S
 F
 A
 I
 E
 K
 R

SEQ ID NO. 7518

STRAIN COH1 frame: 3
 VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDP
 EPEQYKDE TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS
 LGGKSAGQN
 ALYQFEE
 ERQVDASL
 LEKASVYHIADELMAYHDIVGASVYV
 I
 STAC
 S
 A
 N
 N
 A
 V
 I
 L
 G
 T
 Q
 L
 L
 Q
 D
 G
 C
 D
 L
 A
 I
 C
 G
 G
 C
 D
 E
 L
 S
 D
 I
 S
 L
 A
 G
 F
 T
 S
 I
 L
 G
 A
 I
 N
 T
 E
 M
 A
 C
 Q
 P
 Y
 S
 S
 G
 K
 G
 I
 N
 L
 G
 E
 G
 A
 G
 F
 V
 V
 L
 V
 K
 D
 Q
 S
 L
 A
 K
 Y
 G
 K
 I
 I
 G
 G
 L
 I
 T
 S
 D
 GYH
 I
 T
 A
 P
 K
 P
 T
 G
 E
 G
 A
 A
 Q
 I
 A
 K
 Q
 L
 V
 T
 Q
 A
 G
 I
 D
 Y
 S
 E
 I
 D
 Y
 I
 N
 G
 H
 G
 T
 G
 T
 Q
 A
 N
 D
 K
 M
 E
 K
 N
 M
 Y
 G
 K
 F
 F
 P
 T
 T
 TL
 I
 S
 S
 T
 K
 G
 Q
 T
 G
 H
 T
 L
 G
 A
 A
 G
 I
 I
 E
 L
 I
 N
 C
 L
 A
 A
 I
 E
 E
 Q
 T
 V
 P
 A
 T
 K
 N
 E
 I
 G
 I
 E
 G
 F
 P
 E
 N
 F
 V
 Y
 H
 Q
 K
 R
 E
 Y
 P
 I
 RN
 A
 L
 N
 F
 S
 F
 A
 F
 G
 G
 N
 N
 S
 G
 V
 L
 L
 S
 S
 L
 D
 S
 P
 L
 E
 T
 L
 P
 A
 R
 E
 N
 L
 K
 M
 A
 I
 L
 S
 S
 V
 A
 I
 S
 K
 N
 E
 L
 S
 I
 T
 Y
 E
 K
 V
 A
 S
 S
 N
 F
 N
 D
 F
 E
 A
 L
 R
 F
 K
 G
 A
 R
 P
 P
 K
 T
 V
 N
 P
 A
 Q
 F
 R
 K
 M
 D
 D
 F
 S
 K
 M
 V
 A
 V
 T
 T
 A
 Q
 A
 L
 I
 E
 S
 N
 I
 N
 L
 K
 K
 Q
 D
 T
 S
 K
 V
 G
 I
 V
 F
 T
 T
 S
 L
 G
 P
 V
 E
 V
 V
 E
 G
 I
 E
 K
 Q
 I
 T
 T
 E
 G
 Y
 A
 H
 V
 S
 A
 S
 R
 F
 P
 F
 T
 V
 M
 N
 A
 A
 G
 M
 L
 S
 I
 I
 F
 K
 I
 T
 G
 P
 L
 S
 V
 I
 S
 T
 N
 S
 G
 A
 L
 D
 G
 I
 Q
 Y
 A
 K
 E
 M
 M
 R
 N
 D
 N
 L
 D
 Y
 V
 I
 L
 V
 S
 A
 N
 Q
 W
 T
 D
 M
 S
 F
 M
 W
 W
 Q
 Q
 L
 N
 Y
 D
 S
 Q
 M
 F
 V
 G
 S
 D
 Y
 C
 S
 A
 Q
 V
 L
 S
 R
 O
 Q
 A
 L
 D
 N
 S
 P
 I
 I
 L
 G
 S
 K
 Q
 L
 K
 Y
 S
 H
 K
 T
 F
 T
 D
 V
 M
 I
 T
 F
 D
 A
 A
 L
 Q
 N
 L
 L
 S
 D
 L
 G
 L
 T
 I
 K
 D
 I
 K
 G
 F
 V
 W
 N
 E
 R
 K
 A
 V
 S
 S
 D
 Y
 D
 F
 L
 A
 N
 L
 S
 E
 Y
 Y
 N
 M
 P
 N
 L
 A
 S
 G
 Q
 F
 G
 F
 S
 S
 N
 G
 A
 G
 E
 E
 L
 D
 Y
 T
 V
 N
 E
 S
 I
 E
 K
 G
 Y
 Y
 L
 V
 L
 S
 Y
 S
 I
 F
 G
 G
 I
 S
 F
 A
 I
 E
 K
 R

SEQUENCE LISTING

RNALNFSFAFGNNNSGVLLSSLDSPLETLPARENKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNPPIILGSKQLKYSHKTFTDVTMIFTDAALQNLSDLGLTIKDIKGFVWNERKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7519

STRAIN M781 frame: 3
 VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPREVPEQYKDE
 TRNFKFAFTAAFEALASSGVNLKAYHNIACVCLGTSLGGSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLDQGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITS
 GYHITAPKPTGEAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPEFVYHQKREYPI
 RNALNFSFAFGNNNSGILLSSLDSPLETLPARENKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNPPIILGSKQLKYSHKTFTDVTMIFTDAALQNLSDLGLTIKDIKGFVWNERKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7520

STRAIN CJB110 frame: 3
 VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPREVPEQYKDE
 TRNFKFAFTAAFEALASSGVNLKAYHNIACVCLGTSLGGSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLDQGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITS
 GYHITAPKPTGEAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPEFVYHQKREYPI
 RNALNFSFAFGNNNSGILLSSLDSPLETLPARENKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNPPIILGSKQLKYSHKTFTDVTMIFTDAALQNLSDLGLTIKDIKGFVWNERKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7521

STRAIN 1169NT frame: 3
 VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPREVPEQYKDE
 TRNFKFAFTAAFEALASSGVNLKAYHNIACVCLGTSLGGSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLDQGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITS
 GYHITAPKPTGEAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPEFVYHQKREYPI
 RNALNFSFAFGNNNSGILLSSLDSPLETLPARENKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNPPIILGSKQLKYSHKTFTDVTMIFTDAALQNLSDLGLTIKDIKGFVWNERKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7522

STRAIN JM9130013 frame: 3
 VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPREVPEQYKDE
 TRNFKFAFTAAFEALASSGVNLKAYHNIACVCLGTSLGGSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLDQGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITS
 GYHITAPKPTGEAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPEFVYHQKREYPI

SEQUENCE LISTING

RNALNFSFAFGGNNSGVLLSSLDSPLETLARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVNPQAQFRKMDDFSKMAVTTAQALIESNINLKQDTSKVGI
 VFTLSPVVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGCMLSIIFKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLQYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNSPILGSKQLKYSHKTFTDVTMIFTDAALQNLSDLGLTIKDFVWNERKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7601

STRAIN 2603

ATGAAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTA
 AATAATATTAAATTGGAGGTGTTAAAGGCGAAATAATTGGATTAATAGGACCCCTGGA
 GCAGGGAAATCTACCTTGATTTAAACTATGCTTGCATGGAAAAAGCAGATAAGGGAAACA
 GCTCTTGTCTGATACTCAAATGCCAGATCGTAATATTAAATCAAATTGGCTATATG
 GCTCAATCTGATGCCCTATACGAGTCTTAAACTGGCTTAGAAAATTATTATTCTTGGGA
 AAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACTCATATTCTAAAGTA
 GTAGATCTAGAAAACCAACTTGATAAATTGTCTCAGGTTACTCAGGAGGTATGAAAAGA
 CGGCTTCTCTAGCCATGCCCTACTGGAAACCCCACAGTTTAATCCTAGATGAACCT
 ACCGTTGGAATTGATCCATCCTTGAGGAGAAAATCTGGCAAGAGCTAATTAATTAAG
 GATGAAGGACATTCTATCTTATTACAAACCCACGTTATGGATGAAGCAGAATTAACAAGT
 AAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTGATACTCCATTACATTAAAA
 AAACAATTAAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7602

STRAIN 090

ATTAAAAAAACTACAAAAAGCATATGCCTCAGAAACTGTTTTAAATAAT
 ATTAATTGGAGGTGTTAAAGGCGAAATAATTGGATTAATAGGACCCCTC
 TGGAGCAGGGAAATCTACCTTGATTTAAACTATGCTTGCATGGAAAAAG
 CAGATAAGGGAAACAGCTCTTGTCTGATACTCAAATGCCAGATCGTAAT
 ATTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCCTATACGAATC
 TTTAACTGCCTTAGAAATTATTATTCTTGGAAAATGAAAGGTATTCT
 AAAAATGAAATTAAAACAGCAGATAACTCATATTCTAAAGTAGTAGAT
 CTAGAAAACCAACTTGATAAATTGTCTCAGGTTACTCAGGAGGTATGAA
 AAGACGGCTTCTCTAGCCATGCCCTACTGGAAACCCCACAGTTAA
 TCCTAGATGAACCTAACCGTTGAAATTGATCCATCCTTGAGGAGAAAATC
 TGGCAAGAGCTAATTAATTAAGGATGAAGGACGTTCTATCTTATTAC
 AACCCACGTTATGGATGAAGCAGAATTAAACAAGTAAGGTTGCACTACTAT
 TACGTGGAAACATTATTGCCTTGATACTCCATTACATTAAAAAAACAA
 TTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7603

STRAIN A909

AAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATATGCCTCA
 GAAACCGTTTAATAATTAAATTGGAGGTGTTAAAGGCGAAATAAT
 TGGATTAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTTAAACTA
 TGCTTGGCATGGAAAAGCAGATAAGGAAACAGCTCTTGTCTGATACT
 CAAATGCCAGATCATAATATTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCCTTACGAGTCTTAACTGGCTTAGAAAATTATTCTTGG
 GAAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACTCAT
 ATTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTGTCTCAGG
 TTACTCAGGAGGTATGAAAAGACGGCTTCTCTAGCCATGCCCTACTTG
 GAAAACCCACAGTTAACTCTAGATGAACCTACCGTTGAAATTGATCCA
 TCCTTGAGGAGAAAATCTGGCAAGAGCTAATTAAATTAAAGGATGAAGG
 ACGTTCTATCTTATTACAAACCCACGTTATGGATGAAGCAGAATTAAACAA
 GTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTGATACTCCA
 TTACATTAAAAAAACAATTAAATGTGAGTACTATTGAGGAAGTTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7604

STRAIN H36B

AAAAAAAGTCATGTATTTAAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTAATAATTAAATTGGAGGTGTTAAAGGCGAAAT
 AATTGGATTAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTTAA
 CTATGCTTGGCATGGAAAAGCAGATAAGGGAAaCAGCTCTTGTCTGAT

SEQUENCE LISTING

ACTCAAATGCCAGATCGTAATATTTAAATCAAATTGGCTATATGGCTCA
 ACTGATGCCCTATACGAGTCTTAACGGCTTAGAAAATTATTATTCT
 TTGGAAAATGAAAGGTATTCAAAAAACTGAATTAAACAGCAGATAACT
 CATATTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTGGCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTCTCTAGCCATGCCCTAC
 TTGGAAACCCACAGTTAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTGAGGAGAAAATCTGGCAAGAGCTAATTAATTAAGGATGA
 AGGACGTTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAATTAA
 CAAGTAAGGTTGCACTACTATTACGTGAAACATTATTGCCTTGATACT
 CCATTACATTAAAAACAAATTAAATGTGAGTACTATTGAGGAAGTTT
 CTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7605

STRAIN 18RS21

GATTAAAAAAACTACAAAAAGCATATGCCCTCAGAAACGTTTAAATAA
 TATTAATTGGAGGTGTTAAAGGCGAAATAATTGGATTAATAGGACCT
 CTGGAGCAGGAAATCTACCTTGATTAACATGCTGGCATGGAAAAAA
 GCAGATAAGGAAACAGCTTGTCTGATACTCAAATGCCAGATCGTA
 TATTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCCTATACGAGT
 CTTAACTGGCTTAGAAAATTATTATTCTTGAAAAATGAAAGGTATT
 CAAAAAACTGAATTAAACAGCAGATAACTCATATTCTAAAGTAGTGA
 TCTAGAAAACCAACTTGATAAATTGTCTCAGGTTACTCAGGAGGTATGA
 AAAGACGGCTTCTCTAGGCATGCCCTACTGGAAACCCACAGTTTA
 ATCCTAGATGAACCTACGGTTGGAATTGATCCATCCTGAGGAGAAAAT
 CTGGCAAGAGCTAATTAATTTAaGGATGAAGGACATTCTATCTTATTAA
 CAACCCACGTTATGGATGAAGCAGAATTACAAGTAAGGTTGCACTACTA
 TTACGTGAAACATTATTGCCTTGATACTCCATTACATTTAAAAAACAA
 ATTAAATGTGAGTACTATTGAGGAAGTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7606

STRAIN M732

AAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATACGCCCTCA
 GAAACTGTTTAAATAATATTAAATTGGAGGTGTTAAAGGAGAAATAAT
 TGGATTAATAGGACCCCTGGAGCAGGAAATCTACCTTGATTAACACTA
 TGCTTGGCATGGAAAAGCAGATAAGGAAACAGCTCTGTTCTGATACT
 CAAATGCCAGATCGTAATATTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCCCTACAGGACTTTAATGGCTTAGAAAATTATTCTTGTG
 GAAAATGAAAGGTATTCAAAAAACTGAATTAAACAGCAGATAACTCAT
 ATTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTGTCTCAGG
 TTACTCAGGAGGTATGAAAAGACGGCTTCTCTAGGCATGCCCTACTTG
 GAAACCCACAGTTTAATCCTAGATGAACCTACGGTTGGAATTGATCCA
 TCCTTGAGGAGAAAATCTGGCAAGAGCTAATTAAATTAAAGGATGAAGG
 ACGTTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACAA
 GTAAGGTTGCACTACTATTACGTGAAACATTATTGCCTTGATACTCCA
 TTACATTAAAAACAAATTAAATGTGAGTACTATTGAGGAAGTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7607

STRAIN COH1

AAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATACGCCCTCAGAA
 ACTGTTTAAATAATATTAAATTGGAGGTGTTAAAGGAGAAATAATTGG
 ATTAAATAGGACCCCTGGAGCAGGAAATCTACCTTGATTAACACTATGC
 TTGGCATGGAAAAGCAGATAAGGAAACAGCTCTGTTCTGATACTCAA
 ATGCCAGATCGTAATATTAAATCAAATTGGCTATATGGCTCAATCTGA
 TGCCTTACACGAGTCTTAATGGCTTAGAAAATTATTCTTGGAA
 AAATGAAAGGTATTCAAAAAACTGAATTAAACAGCAGATAACTCATATT
 TCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTGTCTCAGGTTA
 CTCAGGAGGTATGAAAAGACGGCTTCTCTAGGCATGCCCTACTGGAA
 ACCCCACAGTTTAATCCTAGATGAACCTACGGTTGGAATTGATCCATCC
 TTGAGGAGAAAATCTGGCAAGAGCTAATTAAATTAAAGGATGAAGGACG
 TTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACAGTA
 AGGTTGCACTACTATTACGTGAAACATTATTGCCTTGATACTCCATTA
 CATTTAAAAACAAATTAAATGTGAGTACTATTGAGGAAG

SEQUENCE LISTING

SEQ ID NO. 7608

STRAIN M781

```

AAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATAAC
GCCTCAGAAACTGTTTAAATAATATTAAATTGGAGGTGTTAAAGGAGA
AATAATTGGATTAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTA
AAACTATGCTGGCATGGAAAAAGCAGATAAGGGAACAGCTTGTCTT
GATACTCAAATGCCAGATCGTAATATTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCTTACACGAGTCTTAACGGCTTAGAAAATTATTAT
TCTTGAGAAAATGAAAGGTATTCAAAAAACTGAATTAAACAGCAGATA
ACTCATATTCTAAAGTAGATCTAGAAAACCAACTTGATAAATTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTCTAGCCATGCC
TACTTGGAAACCCCACAGTTAATCCTAGATGAACCTACCGTTGAAATT
GATCCATCCTTGAGGAGAAAATCTGCAAGAGCTAATTAAATTAAAGGA
TGAAGGACGTTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCCTTGAT
ACTCCATTACATTAAAAAAACAATTAAATGTGAGTACTATTGAGGAAGT
TTCTTAAAGCTGAAGGAGAA

```

SEQ ID NO. 7609

STRAIN CJB110

```

AAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATAATG
CCTCAGAAACTGTTTAAATAATATTAAATTGGAGGTGTTAAAGGCGAA
AATAATTGGATTAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTA
AACTATGCTGGCATGGAAAAAGCAGATAAGGGAACAGCTTGTCTT
ATACTCAAATGCCAGATCGTAATATTAAATCAAATTGGCTATATGGCT
CAATCTGATGCCTTACAGAATCTTAACGGCTTAGAAAATTATTAT
CTTGAGAAAATGAAAGGTATTCAAAAAACTGAATTAAACAGCAGATAA
CTCATATTCTAAAGTAGATCTAGAAAACCAACTTGATAAATTGTC
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTCTAGCCATGCC
ACTTGGAAACCCCACAGTTAATCCTAGATGAACCTACCGTTGAAATTG
ATCCATCCTTGAGGAGAAAATCTGCAAGAGCTAATTAAATTAAAGGAT
GAAGGACGTTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAATT
AACAAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCCTTGATA
CTCCATTACATTAAAAAAACAATTAAATGTGAGTACTATTGAGGAAGT
TTCTTAAAGCTGAAGGAGAA

```

SEQ ID NO. 7610

STRAIN 1169NT

```

AAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATAAC
GCCTCAGAAACTGTTTAAATAATATTAAATTGGAGGTGTTAAAGGCGA
AATAATTGGATTAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTA
AAACTATGCTGGCATGGAAAAAGCAGATAAGGGAACAGCTTGTCTT
GATACTCAAATGCCAGATCGTAATATTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCTTACAGAATCTTAACGGCTTAGAAAATTATTAT
TCTTGAGAAAATGAAAGGTATTCAAAAAACTGAATTAAACAGCAGATA
ACTCATATTCTAAAGTAGATCTAGAAAACCAACTTGATAAATTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTCTAGCCATGCC
TACTTGGAAACCCCACAGTTAATCCTAGATGAACCTACCGTTGAAATT
GATCCATCCTTGAGGAGAAAATCTGCAAGAGCTAATTAAATTAAAGGA
TGAAGGACGTTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCCTTGAT
ACTCCATTACATTAAAAAAACAATTAAATGTGAGTACTATTGAGGAAGT
TTCTTAAAGCTGAAGGAGAA

```

SEQ ID NO. 7611

STRAIN JM9130013

```

AAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATAATGCC
TCAGAAACCGTTTAAATAATATTAAATTGGAGGTGTTAAAGGCGAAAT
AATTGGATTAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTA
CTATGCTGGCATGGAAAAAGCAGATAAGGGAACAGCTTGTCTTGTAT
ACTCAAATGCCAGATCGTAATATTAAATCAAATTGGCTATATGGCTCA
ATCTGATGCCTTACAGAGTCTTAACGGCTTAGAAAATTATTCT
TTGGAAAAATGAAAGGTATTCAAAAAACTGAATTAAACAGCAGATAACT
CATATTCTAAAGTAGATCTAGAAAACCAACTTGATAAATTGTCTC

```

SEQUENCE LISTING

AGTTTACTCAGGAGGTATGAAAAGACGGCTTCCTAGCCATGCCCTAC
 TTGGAACCCACAGTTAATCCTAGATGAACCTACCGTTGAAATTGAT
 CCATCCTTGAGGAGAAAATCTGGCAAGAGCTAAATTAAAGGATGA
 AGGACGTTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAATTAA
 CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTGATACT
 CCATTACATTAAAAAAACAATTAAATGTGAGTACTATTGAGGAAGTTTT
 CTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7612

STRAIN 2603 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7613

STRAIN 090 frame: 3
 LKKLQKAYASETVLNNINLEVFKEIIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7614

STRAIN A909 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7615

STRAIN H36B frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7616

STRAIN 18RS21 frame: 1
 DLKKLQKAYASETVLNNINLEVFKEIIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7617

STRAIN M732 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7618

STRAIN COH1 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7619

STRAIN M781 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQUENCE LISTING

SEQ ID NO. 7620

STRAIN CJB110 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7621

STRAIN 1169NT frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7622

STRAIN JM9130013 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
 LVLDTQMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQQITHISKVV
 DLENQLDKFVSGYSGGMKRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLRGNIIAFDTPHLKKQFNV

SEQ ID NO. 7701

STRAIN 2603

TTGCCTATGTTGTCGTGGTTAGTTTAGAGGGTGGCGGAATGAGAGGTCTTATACT
 GCTGGAGTTTAGATGCTTTCTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTC
 TCTGCTGGTCATTGTTGGTTAATTTGATCTAGACAACGAGAGAGGGCTTGC
 TACAATAAAAGTATTATCCCACCTAAATATGAGTCTAAGGTATGGTTCAACA
 GGGATTGGTTAATAAAGATTCAACCTATTATGAAGTCTATGAAATTGGATGTATT
 GACGATGAAGCATTAAAAATCAAGTATTGATTTCAGTAGTTGCTACAGAGATGACA
 TCTGGTAAACCTGAATTTAAATGATAGTGTGTTGAACAAATGAAATTACGT
 GCTAGTTGAGATTACCGTAGTCTCAAAGATGGTGTGCTCAGGGAAAAGTACTTA
 GATGGTGGTTATCTGATAGTATTCCCGTTGATTGGCCGTTGTTAGGATTGACAAG
 TTGATTGTTGATGACTAGGCGCTCAATTATCAGAAAAAGCCTTCAAGTGGACGATTG
 TATAAAACTCTGTATAGGAAATATCTAATTGTAAGACAGCCTCGAATCGGTACCAA
 CAGTATAATAATAGTCTGAAAAGTCATGAGCCTGAAAAAACAGCGATCTATTGCA
 ATTAGACCGAGTAAGAGCTGGTATTGGCCGCTTAGAGAAGAATCCGGATAAAACTTGAT
 AGTATTATCAGCTGGTATGAAAGATGCTAAAGTGTGATGCCTGAGCTGAATAGTT
 CTAATGAAA

SEQ ID NO. 7702

STRAIN 090

CCTATGTTGTCGTGGTTAGTTAG
 AGGGTGGCGGAATGAGAGGTCTTATACTGCTGGAGTTTAGATGCTTT
 CTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGCTCTGCTGGTGC
 ATTGTTGGTGTAAATTGATCTAGACAACGAGAGAGGGCTTGC
 ACAATAAAAGTATTATCCCACCTAAATATGAGTCTAAGGTATGG
 TTTCGAACAGGAATTGGTTAATAAGATTCAACCTATTATGAAGTTCC
 TATGAAATTGGATGATTGACGATGAAGCATTAAAAATCAAGTATTG
 ATTGTTACGTTGCTACAGAGATGACATCTGGTAAACCTGAATATT
 AAAATTGATAGTGTGTTGAACAAATGAAATTTCAGTGCTAGTTGAGC
 ATTACCAAGTAGTCTCAAAGATGGTGTGATTGGCAGGGAAAAGTACTTAG
 ATGGTGGTTATCTGATAGTATTCCCGTTGATTGGCCGTTGTTAGGA
 TTTGACAAGTTGATTGTTGATGACTAGGCGCTCAATTATCAGAAAAA
 GCCTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATT
 TTGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTGAA
 AAGGTCAATGAGCCTGAAAAAACAGCGATCTATTGCAATTAGACCGAG
 TAAGAGCTTGGTATTGGCCGCTTAGAGAAGAATCCGGATAAAACTTGATA
 GTATTATCAGCTGGTATGAAAGATGCTAAAGTGTGATGCCTGAGCTG
 AATAGTTATCTAATGAAA

SEQ ID NO. 7703

STRAIN A909

CCTATGTTGTCGTGGTTAGTTAGAG
 GGTGGCGGAATGAGAGGTCTTATACTGCTGGAGTTTAGATGCTTTCT

SEQUENCE LISTING

AGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGCAT
 TGTTGGTGTAACTTGTATCTAGACAAACGAGAGAGGGCTTGCATAC
 AATAAAAGTATTTATCCACCCCTAAATATATGAGTCTAAGGTCTGGCT
 TCGAACAGGGAAATTTGTTAATAAAGATTTACCTATTATGAAGTCT
 TGAAATTGGATGTTGACGATGAAGCTTAAAAAATCAAGTATTGAT
 TTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTAA
 AATTGATAGTGTGTTGAAACAATGGAAATTTCAGTGCTAGTCAGCAT
 TACCAAGTAGTCTAAAGATGGTGTGTTGGCAGGGAAAAGTACTTAGAT
 GGTGGTTTATCTGATAGTATTCCCGTGATTTGCCCCGTGGTTAGGATT
 TGACAAGTGTGATTGTTGATGACTAGGCCGCTCAATTATCAGAAAAGC
 CTCAGTGGAACATTGTATAAAACTCTGTATAGGAAATATCCTAATTT
 GAAAGACAGCCTCGAACCGTACCAACAGTATAATAATGCCCTGAAAA
 GGTGATGAGCCTGAAAAAACAGGCCGATCTATTGCAATTAGACCAAGTA
 AGAGCTTGGTATTGGCCGCTTAGAGAAGAATCCGGATAAAACTTGATAGT
 ATTATCAGCTTGGTATGAAAGATGCTAAAGTGGGATGCCCTGAGCTGAA
 TAGTTATCTAATGAAA

SEQ ID NO. 7704

STRAIN H36B

CCTATGTTGCTGTTGGTTAGTTAG

AGGGTGGCGGAATGAGAGGTCTTACTGCTGGAGTTTAGATGCTTT
 CTAGATGCGAGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGCT
 ATTGTTGGTGTAACTTGTATCTAGACAAACGAGAGAGGGCTTGCAT
 ACAATAAAAGTATTTATCCACCCCTAAATATATGAGTCTAAGGTCTGG
 CTTCGAACAGGGAAATTGGTTAATAAAGATTTACCTATTATGAAGTTCC
 TATGAAATTGGATGTTGACGATGAAGCATTAAAAAATCAAGTATTG
 ATTTCACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTT
 AAAATTGATAGTGTGTTGAAACAATGGAAATTTCAGTGCTAGTCAGC
 ATTACCAAGTAGTCTAAAGATGGTGTGTTGGCAGGGAAAAGTACTTAG
 ATGGTGGTTTATCTGATAGTATTCCCGTGATTTGCCCCGTGGTTAGGA
 TTTGACAAGTGTGTTGATGACTAGGCCGCTCAATTATCAGAAAAAA
 GCCTTCAAGTGGACGATTGTTAATAAAACTCTGTATAGGAAATATCCTAATT
 TTGAAAGACAGCCTCGAACCGTACCAACAGTATAATAATAGCCTTGAA
 AAGGTGATGAGCCTGAAAAAACAGGCCGATCTATTGCAATTAGACCAAG
 TAAGAGCTTGGTATTGGCCGCTTAGAGAAGAATCCGGATAAAACTTGATA
 GTATTTATCAGCTTGGTATGAAAGATGCTAAAGTGGGATGCCCTGAGCTG
 AATAGTTATCTAATGAAA

SEQ ID NO. 7705

STRAIN 18RS21

CCTATGTTGCTGTTGGTTAGTTAGAGG
 GTGGCGGAATGAGAGGTCTTACTGCTGGAGTTTAGATGCTTTCTA
 GATGCAGGAATAAAATAGATGGTATCGTATCTGCTCTGCTGGTGCATT
 GTTGGTGTAACTTGTATCTAGACAAACGAGAGAGGGCTTGCATACA
 ATAAAAGTATTTATCCACCCCTAAATATATGAGTCTAAGGTCTGGTT
 CGAACAGGGAAATTGGTTAATAAAGATTTACCTATTATGAAGTTCCAT
 GAAATTGGATGTTGACGATGAAGCATTAAAAAATCAAGTATTGATT
 TTTACGTAGTGTGCTACAGAGATGACATCTGGTAAACCTGAATATTTAAA
 ATTGATAGTGTGTTGAAACAATGGAAATTTCAGTGCTAGTCAGCATT
 ACCAGTAGTCTAAAGATGGTTGATTGGCAGGGAAAAGTACTTAGATG
 GTGGTTATCTGATAGTATTCCCGTGATTTGCCCCGTGGTTAGGATT
 GACAAGTTGATGTTGATGACTAGGCCGCTCAATTATCAGAAAAAGCC
 TTCAAGTGGACGATTGTTAATAAAACTCTGTATAGGAAATATCCTAATT
 TAAAGACAGCCTCGAACCGTACCAACAGTATAATAATAGTCTTGAAAAG
 GTCATGAGCCTGAAAAAACAGGCCGATCTATTGCAATTAGACCGAGTAA
 GAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAAACTTGATAGTA
 TTTATCAGCTTGGTATGAAAGATGCTAAAGTGTGATGCCCTGAGCTGAAT
 AGTATCTAATGAAA

SEQ ID NO. 7706

STRAIN M732

CCTATGTTGCTGTTGGTTAGTTAGAGG
 GGGTGGCGGAATGAGAGGTCTTACTGCTGGAGTTTAGATGCTTTCTA
 TAGATGCAGGAATAAAATAGATGGTATCGTATCTGCTCTGCGGGTGC

SEQUENCE LISTING

TTGTTGGTGTAAAGTCTAGACAACGAGAGAGGGCTTGCATA
 CAATAAAAAGTATTATCCCACCCCTGAATATATGAGTCTAAGATCATGGC
 TTCGAACAGGAATTGGTAAATAAGATTTCACTATTATGAAGTTCCCT
 ATGAAATTGGATGTATTGACGATGAAGCATTAAAGATCAAGTATTGA
 TTTTACGTAGTGTCTACAGAGATGACATCTGGTAAACCTGAATATTAA
 AAATTGATAGTGTGAAACAAATGAAATTACGTGCTAGTTCAAGCA
 TTACCACTAGTCTAAAGATGGTTGATTGGCAGGGAAAAAGTACTTAA
 TGGTGGTTATCTGATAGTATTCCCGTTGATTTGCCGTGGTTAGGAT
 TTGACAAGTTGATTGTTGATGACTAGGCCGCTCAATTATCAGAAAAAG
 CCTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATT
 TGTAAGACAGCCTCGAACGGTACCAACAGTATAAATAGTCTTGAAA
 AGGTCAAGGCTTGTGAAACAGGGCAGTCTATTGCAATTAGACCGAGT
 AAGAGCTTGGTTATTGCCGCTTAGAGAAGAATCCGGATAAAACTTGATAG
 TATTATCAGCTTGGTATGAAATATGCTAAAGTGTGATGCCCTGAGCTGA
 ATAGTTATCTAATGAAA

SEQ ID NO. 7707

STRAIN COH1

CCTATGTTGTCGTGGTTAGTTTA
 GAGGGTGGCGGAATGAGAGGTCTTAACTGCTGGAGTTTAGATGCTTT
 TCTAGATGCAGGAATAAAAGTATGGTATCGTATCTGTCTGCCGGTG
 CATTGGTGGTGTAAATTGGTATCTAGACAACGAGAGAGGGCTTGCAG
 TACAATAAAAAGTATTATCCCACCCCTGAATATATGAGTCTAAGATCATG
 GCTCGAACAGGAATTGGTGTAAAGATTTCACTATTATGAAGTTCC
 CTATGAAATTGGATGTATTGACGATGAAGCATTAAAAAACTCAAGTATT
 GATTTTACGTAGTGTCTACAGAGATGACATCTGGTAAACCTGAATATT
 TAAATTGATAGTGTGTTGAAACAAATGAAATTACGTGCTAGTTCA
 CATTACCACTAGTCTCAAAGATGGTGTGGCAGGGAAAAAGTACTTA
 GATGGTGGTTATCTGATAGTATTCCCGTTGATTTGCCGTGGTTAGG
 ATTGACAAGTTGATTGTTGATGACTAGGCCGCTCAATTATCAGAAAAA
 AGCCTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAAT
 TTGTAAGACAGCCTCGAACGGTACCAACAGTATAAATAGTCTTGAA
 AAAGGTCAAGGCTTGTGAAACAGGGCAGTCTATTGCAATTAGACCGA
 GTAAAGAGCTTGGTTATTGCCGCTTAGAGAAGAATCCGGATAAAACTTGAT
 AGTATTATCAGCTTGGTATGAAATATGCTAAAGTGTGATGCCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7708

STRAIN M781

CCTATGTTGTCGTGGTTAGTTTA
 AGGGTGGCGGAATGAGAGGTCTTAACTGCTGGAGTTTAGATGCTTT
 CTAGATGCAGGAATAAAAGTATGGTATCGTATCTGTCTGCCGGTG
 ATTGTTGGTGTAAATTGGTATCTAGACAACGAGAGAGGGCTTGCAG
 ACAATAAAAAGTATTATCCCACCCCTGAATATATGAGTCTAAGATCATGG
 CTTCGAACAGGAATTGGTGTAAAGATTTCACTATTATGAAGTTCC
 TATGAAATTGGATGTATTGACGATGAAGCATTAAAAAACTCAAGTATTG
 ATTGTTACGTAGTGTCTACAGAGATGACATCTGGTAAACCTGAATATT
 AAAATTGATAGTGTGTTGAAACAAATGAAATTACGTGCTAGTTCA
 ATTACCACTAGTCTCAAAGATGGTGTGGCAGGGAAAAAGTACTTAG
 ATGGTGGTTATCTGATAGTATTCCCGTTGATTTGCCGTGGTTAGGAA
 TTGACAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATT
 GCCTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATT
 TTGTAAGACAGCCTCGAACGGTACCAACAGTATAAATAGTCTTGAA
 AAGGTCAAGGCTTGTGAAACAGGGCAGTCTATTGCAATTAGACCGAG
 TAAGAGCTTGGTTATTGCCGCTTAGAGAAGAATCCGGATAAAACTTGATA
 GTATTATCAGCTTGGTATGAAATATGCTAAAGTGTGATGCCCTGAGCTG
 AATAGTTATCTAATGAAA

SEQ ID NO. 7709

STRAIN CJB110

CCTATGTTGTCGTGGTTAGTTTA
 GAGGGTGGCGGAATGAGAGGTCTTAACTGCTGGAGTTTAGATGCTTT
 TCTAGATGCAGGAATAAAAGTATGGTATCGTATCTGTCTGCCGTGGT
 CATTGGTGGTGTAAATTGGTATCTAGACAACGAGAGAGGGCTTGCAG

SEQUENCE LISTING

TACAATAAAAAGTATTTATCCCACCCCTAAATATGAGTCTAAGGTCTAG
 GTTCGAACAGGGAAATTGTTAATAAAGATTACCTATTATGAAGTTC
 CTATGAAATTGGATGTTGACGATGAAGCATTAAAAATCAAGTATT
 GATTTTACGTAGTGTCTACAGAGATGACATCTGGTAAACCTGAATATT
 TAAATTGATAGTGTGTTGAACAAATGGAAATTTCAGTGTAGTTCAAG
 CATTACCAAGTCTCAAAGATGGTGTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTATCTGATAGTATTCCGTTGATTGCCCCGTGGTTAGG
 ATTTGACAAAGTGTGATGACTAGGCCCTCAATTATCAGAAAA
 AGCCTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAAT
 TTTGAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGGTATGAGCCTTGAACACAGGCGATCTATTGCAATTAGACCAG
 GTAAGAGCTGGTTATTGCCGCTTAGAGAAGAATCCGGATAAAACTTGAT
 AGTATTATCAGCTGGTATGAAAGATGCTAAAGTGTGATGCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7710

STRAIN 1169NT
 CCTATGTTGCTGTTGGTTAGTTAGAGGGTG
 GCGGAATGAGAGGTCTTATACTGCTGGAGTTAGATGCTTTCTAGAT
 GCAGGAATAAAATAGATGGTATCGTATCTGCTCTGCGGGTGCATTGTT
 TGGTGTAAATTGTTGATCTAGACAACGAGAGAGGGCTTGCGATACAATA
 AAAAGTATTATCCCACCCCTAAATATGAGTCTAAGATCATGGCTTCGA
 ACAGGGAAATTGTTAATAAAGATTCCACCTATTATGAAGTCCATGAA
 ATTGGATGTTGACGATGAAGCATTAAAAATCAAGTATTGATTGTT
 ACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTAAAATT
 GATAGTGTCTTGAACAAATGGAATTACGTGCTAGTTCAAGCATTACC
 AGTAGTCTAAAGATGGTGTGATTGGCAGGGGAAAAAGTACTTAGATGGTG
 GTTATCTGATAGTATCCCCTGATTGCCCCGTGGTTAGGATTGAC
 AAGTTGATTGTTGTGACTAGGCCCTCAATTATCAGAAAAAGCCTTC
 AAGTGGACGATTGTTGATAAAACCTGTATAGGAAATATCCTAATTGTA
 AGACAGCCTCGAACGCGATCTATTGCAATTAGCCTTGAAAAGGTC
 ATGAGCCTGAAAAAACAGGCAGTCTATTGCAATTAGCCGAGTAAAAG
 CTTGGTTATTGTCGCTTAGAGAAGAATCCGGATAAAACTTGATAGTATT
 ATCAGCTTGGTATGAAAGATGCTAAAGTGTGATGCCTGAGCTGAATAGT
 TATCTAATGAAA

SEQ ID NO. 7711

STRAIN JM9130013
 CCTATGTTGCTGTTGGTTAGTTAGAG
 GGTGGCGGAATGAGAGGTCTTATACTGCTGGAGTTAGATGCTTTCT
 AGATGCAAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCGGGTGCAT
 TGGTGGTGTAAATTGTTGATCTAGACAACGAGAGAGGGCTTGCGATAC
 AAAAAAGTATTATCCCACCCCTAAATATGAGTCTAAGGTCTGGCT
 TCGAACAGGGAAATTGTTGTAATAAAGATTCCACCTATTATGAAGTCCCTA
 TGAAATTGGATGTTGACGATGAAGCATTAAAAATCAAGTATTGAT
 TTTACCGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTAA
 AATTGATAGTGTGTTGACAAATGGAATTACGTGCTAGTTCAAGC
 TACCAAGTAGTCTAAAGATGGTTGTTGGCAGGGGAAAAAGTACTTAGAT
 GGTGGTTATTGATAGTATTCCGTTGATTGCCCCGTGGTTAGGATT
 TGACAAGTTGATTGTTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
 CTTCAAGTGGCAGATTGATAAAACTCTGTATAGGAAATATCCTAATT
 GTAAAGACAGCCTCGAACCGGTACCAACAGTATAATAATAGCCTTGAAA
 GGTATGAGCCTGAAAAAACAGGCAGTCTATTGCAATTAGACCAAGTA
 AGAGCTTGGTTATTGCCGCTTAGAGAAGAATCCGGATAAAACTTGATAGT
 ATTATCAGCTTGGTATGAAAGATGCTAAAGTGGATGCCTGAGCTGAA
 TAGTTATCTAATGAAA

SEQ ID NO. 7712

STRAIN 2603 frame: 1
 PMLSVGVLVEGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVRQRERALRY
 NKKYLSHPKYMMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDEAFKKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRKYKPNFVKTASNRYQQYNNSLKVMLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSVMPPELNSYLMK

SEQUENCE LISTING

SEQ ID NO. 7713

STRAIN 090 frame: 1
 PMLSVGLVLEGGGMRGGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWFRGPNFKDFTYYEVPMKLDVFDDAEFKKSSIDFYVVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDFKL
 IVVMTRPLNYQKKPSSGRILYKTLRKPVFKTASNRYQQYNNNSLEKVMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7714

STRAIN A909 frame: 1
 PMLSVGLVLEGGGMRGGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWLRGPNFKDFTYYEVPMKLDVFDDAEFKKSSIDFYAVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDFKL
 IVVMTRPLNYQKKPSSGRILYKTLRKPVFKTASNRYQQYNNNSLEKVMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7715

STRAIN H36B frame: 1
 PMLSVGLVLEGGGMRGGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWLRGPNFKDFTYYEVPMKLDVFDDAEFKKSSIDFYAVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDFKL
 IVVMTRPLNYQKKPSSGRILYKTLRKPVFKTASNRYQQYNNNSLEKVMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716

STRAIN 18RS21 frame: 1
 PMLSVGLVLEGGGMRGGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWFRGPNFKDFTYYEVPMKLDVFDDAEFKKSSIDFYVVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDFKL
 IVVMTRPLNYQKKPSSGRILYKTLRKPVFKTASNRYQQYNNNSLEKVMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7717

STRAIN M732 frame: 1
 PMLSVGLVLEGGGMRGGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWLRGPNFKDFTYYEVPMKLDVFDDAEFKKSSIDFYVVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDFKL
 IVVMTRPLNYQKKPSSGRILYKTLRKPVFKTASNRYQQYNNNSLEKVMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7718

STRAIN COH1 frame: 1
 PMLSVGLVLEGGGMRGGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWLRGPNFKDFTYYEVPMKLDVFDDAEFKKSSIDFYVVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDFKL
 IVVMTRPLNYQKKPSSGRILYKTLRKPVFKTASNRYQQYNNNSLEKVMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7719

STRAIN M781 frame: 1
 PMLSVGLVLEGGGMRGGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWFRGPNFKDFTYYEVPMKLDVFDDAEFKKSSIDFYVVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDFKL
 IVVMTRPLNYQKKPSSGRILYKTLRKPVFKTASNRYQQYNNNSLEKVMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7720

STRAIN CJB110 frame: 1
 PMLSVGLVLEGGGMRGGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWFRGPNFKDFTYYEVPMKLDVFDDAEFKKSSIDFYVVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDFKL
 IVVMTRPLNYQKKPSSGRILYKTLRKPVFKTASNRYQQYNNNSLEKVMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQUENCE LISTING

SEQ ID NO. 7721

STRAIN JM9130013 frame: 1
 PMLSVGLVLEGGMGRGLYTAGVLDAGIKVVDGIISVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDEAFKKSSIDFYAVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVMTRPLNYQKKPSSGRILYKTLRKYPNFVKTASNRYQQYNNSSLEKVMsLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDsIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722

STRAIN 1169NT frame: 1
 PMLSVGLVLEGGMGRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSPHPKYSMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDEAFKKSSIDFYAVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVMTRPLNYQKKPSSGRILYKTLRKYPNFVKTASNRYQQYNNSSLEKVMsLEKTGDLFAI
 RPSKSLVIVRLEKNPDKLDsIYQLGMKDAKSVMPPELNSYLMK

SEQ ID NO. 7801

STRAIN 2603

ATGAAAGTTTAGTTAGTTGATGATGAACCAAGTTGCACGTAACGAATTAATTACCTTCTT
 AATAAGTATGATTCTAACCTCGTTAGCAGAGGCGCATGATATGGCTACTGCATTAGCT
 ATTTTACTTAGAGAAACTTTGATGATGACTGTTAGATATCCATCTCAGAGATGATTCT
 GGGTTGCAATTAGCAGAGTATCAATAAAATGCCAAACCACCATTATTGATATTTGCG
 ACTGCTTATGATCAATATGCTATTCAAGGCTTTGAGCATGATGCGCGTGAATTATTGTTA
 AAACCCATTGATTTGATAGGCTAAAGCAAGCTATGGATAGAGTAAAGGAGCGCTAAGT
 ACATCTACAATTATAGAGAGCGTAACCTCCGGTCTCTCTCAAGCAACAGTATCCATTG
 ACAGTAGAAGATCGAATCTATCTGGTGTGGCGGATGATATCCTTTGATTGAAGCTATG
 CAAGGAAAATGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTACAA
 CAATGGCAAGATAAAACTACCATCATCTCAATTGTAACGGTACATCGCTTACATTGTG
 AACATTAATGCTATTAAAACGATTGAACCTTGGTTAACAAACACTTCAGTTACACCTT
 TGTAAATAAAATAACAGTTCTGTTAGCAGAGCAAATGTAACCCCTAAACAAATGTTA
 GGCATATCTACC

SEQ ID NO. 7802

STRAIN 090

AAAGTTTAGTTAGTTGATGATGAACCAAGTTGCACGTAAC
 CGAATTAAATTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 AGGCGCATGATATGGCTACTGCATTAGCTATTACTAGAGAAACTTT
 GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGTTGCAATT
 AGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTTGCG
 CTGCTTATGATCAATATGCTATTCAAGGCTTTGAGCATGATGCGCGTGA
 TATTGTTAAACCCATTGATTTGATAGGCTAAAGCAAGCTATGGATAG
 AGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 GTCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTAT
 CTGGTGTGGCGGATGATATCCTTTGATTGAAGCTATGCAAGGAAAATC
 GATTATACAACACCTGATAAAAATTATGAAATTGATGGCTCTACAAAC
 AATGGCAAGATAAAACTACCATCATCTCAATTGTAACGGTACATCGCTCT
 TACATTGTAACATTAATGCTATTAAAACGATTGAACCTTGGTTAACCA
 AACACTTCAGTTACACCTTGTAAATAAAATAACAGTTCTGTTAGCAGAG
 CAAATGTAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803

STRAIN A909

AAAGTTTAGTTAGTTGATGATGAACCAAGTTGCACGTAAC
 GAATTAAATTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 GGCATGATATGGCTACTGCATTAGCTATTACTAGAGAAACTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGTTGCAATT
 GCAGAGTATATCAATAAAATGCCAAACCACCATTATTGATATTCGCGAC
 TGCTTATGATCAATATGCTATTCAAGGCTTTGAGCATGATGCGCGTGA
 ATTGTTAAACCCATTGAGTTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 CCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGGCGGATGATATCCTTTGATTGAAGCTATGCAAGGAAAATG
 ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTACAAACA

SEQUENCE LISTING

ATGGCAAGATAAACTACCATCATCTCAATTGTACGGGTGCACCGCTCTT
 ACATTGTGAATATTAATGCTATTAAAACGATTGAACCTGGTTAACAA
 ACACCTCAGTTACACCTTGTAAATAAAACAGTCCTGTTAGCAGAGC
 AAATGTAAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7804

STRAIN H36B

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGT
 AACGAATTAAATTACCTCTTAATAAGTATGATTCTAACCTCGTTATAGC
 AGAGGCGCATGATATGGCTACTGCATTAGCTATTACTTAGAGAAACTT
 TTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGTTGCAA
 TTAGCAGAGTATATCAATAAAATGCCAAACCACCAATTATTGATATTGCG
 GACTGCTTATGATCAATATGCTATTCAAGCTTTGAGCATGATGCGCGTG
 ATTATTGTTAAACCCCTATGAGTTGATAGGCTAAAGCAAGCTATGGAT
 AGAGTAAAAGGAGCGCTAAGTACATCTACAAATTAGAGAGCGTAACCTC
 CGGCCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAAGATCGAATCT
 ATCTGGTGTGGGGATGATATCCTTTGATTGAAGCTATGCAAGGAAA
 CTGATTATAACAAACACCTGATAAAATTATGAAATTGATGGCTCTACAA
 ACAATGGCAAGATAAAACTACCATCATCTCAATTGTACGGGTGCACCGCT
 CTTACATTGTAAATTAATGCTATTAAAACGATTGAACCTGGTTAAC
 CAAACACTTCAGTTACACCTTGTAAATAAAACAGTCCTGTTAGCAG
 AGCAAATGTAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7805

STRAIN 18RS21

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAAAC
 GAATTAATTACCTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGCACATGATATGGCTACTGCATTAGCTATTACTTAGAGAAACTTTG
 ATGTGCACTGTTAGATATCCATCTCAGAGATGATTCTGGTTGCAATT
 GCAGAGTATATCAATAAAATGCCAAACCACCAATTATTGATATTGCGAC
 TGCTTATGATCAATATGCTATTCAAGCTTTGAGCATGATGCGCGTGATT
 ATTGTTAAACCCCTATGATTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAAATTATAGAGAGCGTAACCTCCG
 TCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAAGATCGAATCTAC
 TGGTGTGGGGATGATATCCTTTGATTGAAGCTATGCAAGGAAA
 ATTATAACAAACACCTGATAAAATTATGAAATTGATGGCTCTACAAACA
 ATGGCAAGATAAAACTACCATCATCTCAATTGTACGGGTACATCGCTTT
 ACATTGTAAACATTAATGCTATTAAAACGATTGAACCTGGTTAACAA
 ACACCTTCAGTTACACCTTGTAAATAAAACAGTCCTGTTAGCAGAGC
 AAATGTAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7806

STRAIN M732

AAAGTTTGTAGTTGATGATGAACCAAGTT
 GCACGTAACGAATTAAATTACCTCTTAATAAGTATGATTCTAACCTCGT
 TATAGCAGAGCGCATGATATGGCTACTGCATTAGCTATTACTTAGAG
 AAACTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGG
 TTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCAATTATTGAT
 ATTGCGCACTGCTTATGATCAATATGCTATTCAAGGCTTTGAGCAGGATG
 CGCGTGAATTGAGTAAAAGGAGCGCTAAGTACATCTACAAATTATAGAGCGT
 ATGGATAGAGTAAAAGGAGCGCTAAGTACATCTACAAATTATGAAATTGATGGCTC
 AGCTTCCGGTCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAAGATC
 GAATCTATCTGGTGTGGGGATGATATCCTTTGATTGAAGCTATGCAA
 GGAAAACGATTATAACAAACACCTGATAAAATTATGAAATTGATGGCTC
 TCTACAACAATGGCAAGATAAAACTACCATCATCTCAATTGTACGGGTAC
 ATCGCTTACATTGTAAATTAATGCTATTAAAACGATTGAACCTTGG
 TTTAACCAACACTTCAGTTACACCTTGTAAATAAAACAGTCCTGTTAGCAGAGC
 TAGCAGAGCAAATGTAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7807

STRAIN COH1

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGT
 AACGAATTAAATTACCTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
 GAGGCGCATGATATGGCTACTGCATTAGCTATTACTTAGAGAAACTTT

SEQUENCE LISTING

TGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
 TAGCAGAGTATATCAATAAAATGCCAAACCACCAATTATTGATATTGCG
 ACTGCTTATGATCAATATGCTATTCAAGGCTTTGAGCAGGATGCGCGTGA
 TTATTTGTTAAACCCATGAGTTGATAGGTTAAAGCAAGCTATGGATA
 GAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGACCGTAGCTTC
 GGCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAGAAGATCGAATCTA
 TCTGCTGTCGGGGATGATATCCTTTGATTGAAAGCTATGCAAGGAAAAC
 TGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTACAA
 CAATGGCAAGATAAAACTACCATCATCTCAATTGATGGGTACATCGCTC
 TTACATTGTGAATATTAATGCTATTAAAACGATTGAAACCTGGTTAAC
 AAACACTTCAGTTACACCTTGTAAATAACAGTTCTGTTAGCAGA
 GCAATGTAAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7808

STRAIN M781

AAAGTTTATGTTGATGATGAAACCAGTTGCACGTAAC
 GAATTAATTTACCTCTTAAAGTATGATTCTAACCTCGTTATAGCAGA
 GGCGCATGATATGGCTACTGCATTAGCTATTTACTTAGAGAAAACCTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCAATTATTGATATTGCGAC
 TGCTTATGATCAATATGCTATTCAAGGCTTTGAGCAGGATGCGCGTGA
 ATTGTTAAACCCATGAGTTGATAGGTTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGACCGTAGCTTC
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAGAAGATCGAATCTATC
 TGGTGTGGGGATGATATCCTTTGATTGAAAGCTATGCAAGGAAAAC
 ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTACAAACA
 ATGGCAAGATAAAACTACCATCATCTCAATTGATGGGTACATCGCTCTT
 ACATTGTGAATATTAATGCTATTAAAACGATTGAAACCTGGTTAAC
 AACACTTCAGTTACACCTTGTAAATAACAGTTCTGTTAGCAGAGC
 AAATGTAAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7809

STRAIN CJB110

CTTAATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGATGATATGGC
 TACTGCATTAGCTATTTTACTTAGAGAAAACCTTGTAGCACTGTTAG
 ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
 AAAATGCCAAACCACCAATTATTGATATTGCGACTGCTTATGATCAATA
 TGCTATTCAAGCTTTGAGCAGTGCCTGATTATTGTTAAACCCCT
 ATGAGTTGATAGGCTAACGCAAGnTATGGATAGAGTAAAGGAGCGCTA
 AGTACATCTAACATTATAGAGAGCGTAACCTCCGCCCTCTTCAAGCA
 ACAGTATCCATTGACAGTAGAGATnGAATCTATCTGGTGTGGGGATG
 ATATCCTTTGATTGAAAGCTATGCAAGGAAAACGATTATAACAAAC
 GATAAAAATTGAAATTGATGGCTCTTACACAAATGGCAAGATAAAAC
 ACCATCATCTCAATTGTAACGGGTGACCGCTCTTACATTGTGAATATTA
 ATGCTATTAAAACGATTGAAACCTGGTTAACCAAACACTTCAGTTACAC
 CTTGTAATAAAATAACAGTTCTGTTAGCAGAGCAAATGTAACCCCT
 AAAACAAATGTTAGG

SEQ ID NO. 7810

STRAIN 1169NT

AAAGTTTATGTTGATGATGAAACCAG
 TTGCACTAACGAAATTATCTCTTAAATAAGTATGATTCTAACCTC
 GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTATTTACTTAG
 AGAAAACCTTGTAGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTG
 GGTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCAATTATTG
 ATATTGCGACTGCTTATGATCAATATGCTATTCAAGGCTTTGAGCATGA
 TGCCTGATTATTGTTAAACCCATGAGTTGATAGGCTAAAGCAAG
 CTATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
 GTAACCTCCGCCCTCTTCAAGCAACAGTATCCATTGACAGTAGAGA
 TCGAATCTATCTGGTGTGGGGATGATATCCTTTGATTGAAAGCTATGC
 AAGGAAAACGATTATAACAAACACCTGATAAAAATTATGAAATTGATGGC
 TCTCTACAACAAATGGCAAGATAAAACTACCACATCATCTCAATTGATGG
 GCACCGCTTACATTGTAATATTGCTATTAAAACGATTGAAACCTT
 GTTTAACCAAACACTTCAGTTACACCTTGTAAATAACAGTTCT

SEQUENCE LISTING

GTTAGCAGAGCAAATGTAAAACCCCTAAACAAATGTTAGGCATATCTAC
C

SEQ ID NO. 7811

STRAIN JM9130013

AAAGTTTATGAGTTGATGATGAACCAAGT
TGCACGTAACGAATTAAATTACCTTAAATAAGTATGATTCTAACCTCG
TTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTACTTAGA
GAAACTTTATGAGTTGACTGTTAGATATCCATCTCAGAGATGATTCTGG
GTTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCATTATTGA
TATTGCGACTGTTATGATCAATATGCTATTCAAGCTTTGAGCATGAT
GCGCGTGAATTGTTAAAACCCATGAGTTGATAGGCTAAAGCAAGC
TATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
TAACTCCGGGCTCTCTCAAGCAACAGTACATTGACAGTAGAAGAT
CGAATCTATCTGGTGTGGGATGATATCCTTTGATTGAAGCTATGCA
AGGAAAACGATTATAACAAACACCTGATAAAATTATGAAATTGATGGCT
CTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTGTTACGGGTG
CACCGCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTG
GTTAACCAACACTTCAGTTACACCTTGTATAAAATAACAGTTCTG
TTAGCAGAGCAAATGTAAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7812

STRAIN 2603 frame: 1

KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIESVTSGPLFKQQYPLTVEDRIYLVSADDILLTEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813

STRAIN 090 frame: 1

KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIESVTSGPLFKQQYPLTVEDRIYLVSADDILLTEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814

STRAIN A909 frame: 1

KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIESVTSGPLFKQQYPLTVEDRIYLVSADDILLTEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815

STRAIN H36B frame: 1

KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIESVTSGPLFKQQYPLTVEDRIYLVSADDILLTEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816

STRAIN 18RS21 frame: 1

KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIESVTSGPLFKQQYPLTVEDRIYLVSADDILLTEAMQGKLIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817

STRAIN M732 frame: 1

KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG

SEQUENCE LISTING

LQLAEYINKMPKPPLLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
 STIESVASGELFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLIQTDPDKNEYIDGSLQQ
 WQDKLPSSQFVVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7818

STRAIN COH1 frame: 1
 KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
 STIESVASGELFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLIQTDPDKNEYIDGSLQQ
 WQDKLPSSQFVVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7819

STRAIN M781 frame: 1
 KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
 STIESVASGELFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLIQTDPDKNEYIDGSLQQ
 WQDKLPSSQFVVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7820

STRAIN CJB110 frame: 1
 LNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSGLQLAEYINKMPKPPLLIF
 ATAYDQYAIQAFEHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIESVTSGPLFKQQYP
 LTVEDXIYLVSAADDILLIEAMQGKLIQTDPDKNEYIDGSLQQWQDKLPSSQFVVRVHRSYI
 VNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG

SEQ ID NO. 7821

STRAIN 1169NT frame: 1
 KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
 STIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLIQTDPDKNEYIDGSLQQ
 WQDKLPSSQFVVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7822

STRAIN JM9130013 frame: 1
 KVLVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
 STIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLIQTDPDKNEYIDGSLQQ
 WQDKLPSSQFVVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7901

STRAIN 2603

ATGGGAATTGAATTAAAAATGTAAGTTATACCTATCAAGCCGGCACTCCTTTGAAGGG
 CGTGCCCTTTTGACGTCATCTGAAAATTGAAGATGCTCCCTATACCGCGTTCATGGGG
 CACACAGGTTCTGGAAAATCAACTTATGCAACTTTGAATGGTTACATATTCTACA
 AAAGGTGAGGTAATTGTCGATGATTTCTATTAAAGCAGGGACAAGAACAAAGAACATC
 AAATTATAAGGCAAAAGTTGGTTAGTTTCATTTCCAGAAAAGTCAGCTTTGAA
 GAGACAGTTAAAGGATGTTGCTTGGACCACAAATTGTTGATTCAGTGAGGATTTCGAT
 GCTGAAAGGCTGGCTGAAGAAAATTAAAGGTTAGTTGGTATCAGTGAGGATTTCGAT
 AAAATCCATTGAACTTCTGGAGGGCAGATGAGGGGGTTGCTATAGCTGGTATTTA
 GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGA
 AGAAAAGAATTAATGACTTTTAAACCTTCAAAAAAGGAATGACTATCGTCTTA
 GTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTATGTTGATGTTTAAAGCA
 GGGAAAGTAACCTTATCAGGACAACCAACAGATTTCACAAGAAGTAGAAACTTTAGAA
 AGTAAACAATTAGGAGTTCCAAAATCACCAAGTTGCTCAAAGACTATCTCATAGGGA
 TTAAATTACCTAGTTACCAATTACTATTAAACGAATTGTGGAGGCTTAAAGCATGGA

SEQ ID NO. 7902

STRAIN 090

GGAATTGAATTAAAAATGTAAGTTATACCTATCAAGCC

SEQUENCE LISTING

GGCACTCCTTTGAAGGGCGTGCCTTTGACGTCAATCTGAAAATTGA
 AGATGCTCCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTGAATGGTTACATATTCCACAAAAGGTGAGGTA
 ATTGTCGATGATTTCTATTAAAGCAGGGGACAAGAACAAAGAAATCAA
 ATTATAAGGACAAAAGTGGTTAGTTCAATTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTAAAGGATGTTGCTTTGGACCACAAAATT
 GGTTATTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAATTAAAGGTT
 AGTGGTATCAGTGAGGATTTATCGATAAAAATCCATTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTGCATACTGGTATTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTGATCCTAACGGGAAG
 AAAAGAATTAAATGACTTTTAAATCTCATAAAAAAGGAATGACTA
 TCGCTTAGTGAECTACTTAATGGACATGTTAGCGGATTATGCTGACTAT
 GTGTATGTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTCAAGAAGTAGAACACTTTAGAAAGTAACAAATTAGGAGTTCCA
 AAATCACCAAGTTGCTCAAAGACTATCTCATAACGGGATTAAATTACCT
 AGTTACCAATTACTATTACGAATTGTGGAGGCTATTAGCATGGA

SEQ ID NO. 7903

STRAIN A909

GGAAATTGAATTAAAAATGTAAGTTACCTATCAA
 GCGGGCACTCCTTTGAAGGGCGTGCCTTTGACGTCAATCTGAAAAT
 TGAAGATGCTCCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAAT
 CAACATTATGCAACTTTGAATGGTTACATATTCCACAAAAGGTGAG
 GTAATTGTCGATGATTTCTATTAAAGCAGGGGACAAGAACAAAGAAAT
 CAAATTAAAGCAAAAGTTGGTTAGTTTCAATTCCAGAAAAGTC
 AGCTTTGAAGAGACAGTTAAAGATGTTGCTTTGGACCAAAAT
 TTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAATTAAAG
 GTTAGTTGGTATCAGTGAGGATTTATCGATAAAAATCCATTGAACTTT
 CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTAGCGATGGAA
 CCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATCCTAACGG
 AAGAAAAGAATTAAATGACTCTTTAAATCTCATAAAAAAGGAATGAA
 CTATCGCTTAGTGAECTACTTAATGGACATGTTAGCGGATTATGCTGAC
 TATGTTAGTGTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAA
 GCAGATTTCAGAAGTAGAACACTTTAGAAAGTAACAAATTAGGAGTT
 CCAAATCACCAAGTTGCTCAAAGGCTATCTCATAACGGGATTAAATT
 CCTAGTTACCAATTACTATTACGAATTGTGGAGGCTATTAGCATGG
 A

SEQ ID NO. 7904

STRAIN H36B

GGAAATTGAATTAAAAATGTAAGTTAC
 CTATCAAGCCGGCACTCCTTTGAAGGGCGTGCCTTTGACGTCAATC
 TGAAAATTGAAGATGCTCCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTGAATGGTTACATATTCCACAAA
 AGGTGAGGTAATTGTCGATGATTTCTATTAAAGCAGGGGACAAGAAC
 AAGAAATCAAATTATAAGGCAAAAGTTGGTTAGTTTCAATT
 GAAAGTCAGCTTTGAAGAGACAGTTAAAGATGTTGCTTTGGACC
 ACAAAATTGGTATTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATAAGGTTAGTTGGTATCAGTGAGGATTTATCGATAAAAATCCATT
 GAACTTCTGGAGGGCAGATGAGGCGGGTGCATACTGGTATTAGC
 GATGGAACCCAAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAAATGACTCTTTAAAGATCTCATAAAAAA
 GGAATGACTATCGCTTAGTGAECTACTTAATGGACATGTTAGCGGATT
 TGCTGACTATGTGTAGTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAGCAGATTTCAGAAGTAGAACACTTTAGAAAGTAACAAATT
 GGAGTTCCAAAATCACCAAGTTGCTCAAAGGCTATCTCATAACGGGATT
 AAATTACCTAGTTACCAATTACTATTACGAATTGTGGAGGCTATT
 AGCATGGA

SEQ ID NO. 7905

STRAIN 18RS21

GGAAATTGAATTAAAAATGTAAGTTAC
 CTATCAAGCCGGCACTCCTTTGAAGGGCGTGCCTTTGACGTCAATC
 TGAAAATTGAAGATGCTCCTATACCGCGTTCATTGGGCACACAGGTTCT

SEQUENCE LISTING

GGAAAATCAACTATTATGCAACTTTGAATGGTTACATATCCTACAAA
 AGGTGAGGTAATTGTCATGATTTCTATTAAGCAGGGGACAAGAACAA
 AAGAAATCAAATTATAAGGCAAAAGTTGGTTAGTTTCAATTTC
 GAAAGTCAGCTTTGAAGAGACAGTTAAAGGATGTTGCTTTGGACC
 AAAAAATTGGTATTCTCAGATTGAGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTATTGATAAAAATCCATT
 GAACTTTCTGGAGGGCAGATGAGGCAGGGTGGCTAGCTGGTATTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAAGAAAAGAATTAAATGACTCTTTAAAATCTCATAAAAAAA
 GGAATGACTATCGTCTAGTGAACAGCTTAATGGACGATGTAGCGGATT
 TGCTGACTATGTGTATGTTAGAACAGGGAAAGTAACCTTACAGGAC
 AACCAAAACAGATTTCAGAACAGTAAACAAATTAA
 GGAGTTCCAAAATCACCAGTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTACCTAGTTACCAATTACTATTAACGAATTGTGGAGGCTATT
 AGCATGGA

SEQ ID NO. 7906

STRAIN M732

GGAATTGAATTAAAAATGTAAGTTAC
 CTATCAAGCCGGCACTCCTTTGAAGGGCGTGCCTTTGACGTCAATC
 TGAAAATTGAAGATGTTCTATACCGCGTTCATGGGACACAGGTTCT
 GAAAATCAACTATTGCAACTTTGAATGGTTACATATTCTACAAA
 AGGTGAGGTAATTGTCATGATTTCTATTAAGCAGGGGACAAGAACAA
 AAGAAATCAAATTATAAGGCAAAAGTTGGTTAGTTTCAATTTC
 GAAAGTCAGCTTTGAAGAGACAGTTAAAGGATGTTGCTTTGGACC
 ACAAAATTGGTATTCTCAGATTGAAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTATTGATAAAAATCCATT
 GAACTTTCTGGAGGGCAGATGAGGCAGGGTGGCTAGCTGGTATTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAAGAAAAGAATTAAATGACTCTTTAAAATCTCATAAAAAAA
 GGAATGACTATCGTCTAGTGAACAGCTTAATGGACGATGTAGCGGATT
 TGCTGACTATGTGTATGTTAGAACAGGGAAAGTAACCTTACAGGAC
 AACCAAAACAGATTTCAGAACAGTAAACAAATTAA
 GGAGTTCCAAAATCACCAGTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTACCTAGTTACCAATTACTATTAACGAATTGTGGAGGCTATT
 AGCATGGA

SEQ ID NO. 7907

STRAIN COH1

GGAATTGAATTAAAAATGTAAGTTACCTATCAAGCC
 GGCACCTCCTTTGAAGGGCGTGCCTTTGACGTCAATCTGAAAATTGA
 AGATGTTCTATACCGCGTTCATGGGACACAGGTTCTGAAAATCAA
 CTATTATGCAACTTTGAATGGTTACATATTCTACAAAAGGTGAGGTA
 ATTGTCATGATTTCTATTAAGCAGGGGACAAGAACAAAGAAATCAA
 ATTATAAGGCAAAAGTTGGTTAGTTTCAATTCCAGAAAAGTCAGC
 TTTTGAAGAGACAGTTAAAGGATGTTGCTTTGGACCACAAAATT
 GGTATTCTCAGATTGAAAGCTGAAAGGCTGGCTGAAGAAAATTAGGTT
 AGTGGTATCAGTGAGGATTATTGATAAAAATCCATTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTGCATAAGCTGGTATTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAAG
 AAAAGAAATTAAATGACTCTTTAAAATCTCATAAAAAGGAATGACTA
 TCGCTTCTAGTGAACAGCTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTAGAACAGGGAAAGTAACCTTACAGGACAACAAAACA
 GATTTTCAAGAACAGTAAACAAATTAGGAGTTCCCA
 AAATCACCAAGTTGCTCAAAGACTATCTCATAAGGGATTAAATTACCT
 AGTTACCAATTACTATTAACGAATTGTGGAGGCTATTAGCATGGA

SEQ ID NO. 7908

STRAIN M781

GGAATTGAATTAAAAATGTAAGTTAC
 CTATCAAGCCGGCACTCCTTTGAAGGGCGTGCCTTTGACGTCAATC
 TGAAAATTGAAGATGTTCTATACCGCGTTCATGGGACACAGGTTCT
 GAAAATCAACTATTGCAACTTTGAATGGTTACATATTCTACAAA
 AGGTGAGGTAATTGTCATGATTTCTATTAAGCAGGGGACAAGAACAA

SEQUENCE LISTING

AAGAAATCAAATTATAAGGCAAAAGTTGGTTAGTTTCAATTCCA
 GAAAGTCAGCTTTGAAGAGACAGTTAAAGGATGTTGCTTTGGACC
 ACAAAATTGGTATTCAGATTGAAAGCTGAAAGCTGGCTGAAGAAA
 AATTAAGGTTAGTGGTACAGTGAGGATTTCAGATAAAATCCATT
 GAACCTCTGGGGCAGATGAGGGGGTGCATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCACAGCTGGACTTGATC
 CTAAGGAAAGAAAAGAATTAAATGACTCTTTAAAGATCTCATAAAAAAA
 GGAATGACTATCGCTTAGTGAACCTTAATGGACGATGTAGCGGATT
 TGCTGACTATGTGTATGTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAAACTTTAGAAAGTAAACAATTA
 GGAGTCCAAAATCACCAGTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTACCTAGTTACCAATTACTATTAACGAATTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7909

STRAIN CJB110
 GGAATTGAATTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTGAAGGGCGTGCCTTTGACGTCAATC
 TGAAAATTGAAGATGCTCCTATACCGCGTCATTGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTGAATGGTTACATATTCTACAAA
 AGGTGAGGTAATTGTCGATGATTTCTATTAAAGCAGGGACAAGAAC
 AAGAAATCAAATTATAAGGCAAAAGTTGGTTAGTTCAATTTC
 GAAAGTCAGCTTTGAAGAGACAGTTAAAGGATGTTGCTTTGGACC
 AACAAATTGGTATTCAGATTGAAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTCAGATAAAATCCATT
 GAACCTCTGGAGGGCAGATGAGGCAGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCACAGCTGGACTTGATC
 CTAAGGAAAGAAAAGAATTAAATGACTCTTTAAAGATCTCATAAAAAAA
 GGAATGACTATCGCTTAGTGAACCTTAATGGACGATGTAGCGGATT
 TGCTGACTATGTGTATGTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAAACTTTAGAAAGTAAACAATTA
 GGAGTCCAAAATCACCAGTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTACCTAGTTACCAATTACTATTAACGAATTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7910

STRAIN 1169NT
 GGAATTGAATTAAAAATGTA
 GTTATACCTCAAGCCGGCACTCCTTTGAAGGGCGTGCCTTTGAC
 GTCAATCTGAAAATGAAGATGCTCCTATACCGCGTCATTGGCACAC
 AGGTTCTGGAAAATCAACTATTATGCAACTTTGAATGGTTACATATT
 CTACAAAAGGTGAGGTAATTGTCGATGATTTCTATTAAAGCAGGGAC
 AAGAACAAAGAAATCAAATTATAAGGCAAAAGTTGGTTAGTTCA
 ATTCCAGAAAAGTCAGTTGAAGAGACAGTTAAAGGATGTTGCTT
 TTGGACCACAAAATTGGTATTCAGATTGAAAGCTGAAAGGCTGGCT
 GAAGAAAATTAAGGTTAGTTGGTACAGTGAGGATTTCAGATAAAA
 TCCATTGAACTTCTGGAGGGCAGATGAGGCAGGTTGCTATAGCTGGTA
 TTTAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCACAGCTGGA
 CTTGATCCTAAGGAAAGAAAAGAATTATGACTCTTTAAAGATCTC
 TAAAAGGAATGACTATCGCTTAGTGAACCTTAATGGACGATGTAG
 CGGATTATGCTGACTATGTGTATGTTAGAAGCAGGGAAAGTAACCTTA
 TCAGGACAACCAAAACAGATTTCAAGAAGTAGAAACTTTAGAAAGTAA
 ACAATTAGGAGTTCCAAAATCACCAGTTGCTCAAAGACTATCTCATA
 AGGGATTAAATTACCTAGTTACCAATTACTATTAACGAATTGTGGAG
 GCTATTAAAGCATGGA

SEQ ID NO. 7911

STRAIN JM9130013
 GGAATTGAATTAAAAATGTAAGTT
 ATACCTATCAAGCCGGCACTCCTTTGAAGGGCGTGCCTTTGACGTT
 AATCTGAAAATGAAGATGCTCCTATACCGCATTGTCATTGGCACACAGG
 TTCTGGAAAATCAACTATTATGCAACTTTGAATGGTTACATATTCTA
 CAAAAGGTGAGGTAATTGTCGATGATTTCTATTAAAGCAGGGACAAAG
 AACAAAGAAAATCAAATTATAAGGCAAAAGTTGGTTAGTTCAATT

SEQUENCE LISTING

TCCAGAAAGTCAGCTTTGAAGAGACAGTTAAAGGATGTTGCTTTG
 GACCACAAAATTTGGTATTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
 GAAAAAATTAAAGGTTAGTTGGTATTAGTCAGGATTATTGATAAAAATCC
 ATTTGAACCTTCTGGAGGGCAGATGAGGCAGGGTCTAGCTGGTATT
 TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCACAGCTGGACTT
 GATCCTAAGGGAAGAAAAGAATTAAATGACTCTTTAAAAATCTTCATAA
 AAAAGGAATGACTATCGCTTAGTGAECTACTTATGGACGATGTAGCAG
 ATTATGCTGACTATGTGATGTTAGAAGCAGGGAAAGTAACCTTATCA
 GGACAACCAAAACAGATTTCAGAAGTAGAAACTTTAGAAAGTAAACA
 ATTAGGAGTTCCAAAATACCAAGTTGCTCAAAGACTATCTCATAAGG
 GATTAATTTACCTAGTTACCAATTACTATTAACGAATTGTGGAGGCT
 ATTAAGCATGGA

SEQ ID NO. 7912

STRAIN 2603 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVLVQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGISEDLFDKNPFEELSGGQMRRAVIAIGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7913

STRAIN 090 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVLVQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGISEDLFDKNPFEELSGGQMRRAVIAIGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7914

STRAIN 090 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVLVQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGISEDLFDKNPFEELSGGQMRRAVIAIGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7915

STRAIN H36B frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVLVQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGISEDLFDKNPFEELSGGQMRRAVIAIGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7916

STRAIN 18RS21 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVLVQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGISEDLFDKNPFEELSGGQMRRAVIAIGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7917

STRAIN M732 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVLVQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLVGISEDLFDKNPFEELSGGQMRRAVIAIGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7918

STRAIN COH1 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK

SEQUENCE LISTING

GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNGISQIEA
ERLAEEKLRILVGISEDLFDPKNPFEGLGGQMRRVIAIGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7919

STRAIN M781 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLIKEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNGISQIEA
ERLAEEKLRILVGISEDLFDPKNPFEGLGGQMRRVIAIGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7920

STRAIN CJB110 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLIKEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNGISQIEA
ERLAEEKLRILVGISEDLFDPKNPFEGLGGQMRRVIAIGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7921

STRAIN 1169NT frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLIKEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNGISQIEA
ERLAEEKLRILVGISEDLFDPKNPFEGLGGQMRRVIAIGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7922

STRAIN JM9130013 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLIKEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNGISQIEA
ERLAEEKLRILVGISEDLFDPKNPFEGLGGQMRRVIAIGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 8001

STRAIN 2603

GTGAACCACTTACTAACCTCAGTAAAGAAAATATAGCTAAATAGATTGACTTTCTT
AATGAGGCACTTAATGCAAATATTGTTGAAAGAATTAGTAGATGAACCTAAAGATTCA
AAAGAACTGGACAGTAAAGGTTGGTCCAAAAGACTCTCGAACGATAAAATCTGTAC
GATGGCCTTATCAATAAACATATAGTTCCCTAGATCGTCAGATTATAACATTATCAA
GTCATTCCATTGCTAATGTACATGTAACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
AAAAATTATAGAATATACAACACAGTGATTAGACCAATTGATACTTGTGATATT
CAACAATTTCAAAATATGAAACAGTTGATTAGACCAATTGATACTTGTGATATT
AATATTGATGACTACATTCATCATATTAAACAATA

SEQ ID NO. 8002

STRAIN H36B

AACCACTTACTAACCTCAGTAAAGAAAATATAGCT
AAAATAGATTGACTTTCTTAATGAGGCACTTAATGCAAATATTGTT
GAAAGAATTAGTAGATGAACCTAAAGAATTCTCAAAGAACTGGACAGTAAAG
GTTGGTCCAAAAGACTCTCGAACGATAAAATCTGTACGATGGCCTT
ATCAATAAACATATAGTTCCCTAGATCGTCAGATTATAACATTATCAA
AGTCATTCCATTGCTAATGTACATGTAACAGTGATTATGAAATG
GGGAGAATTCTAAAATTATAgAATATACAACACAGTGATTATGAAATG
GAGTTAATCAATGAGGATAGGCAACAATTTCAAAATATGAAACAGTTGA
TTTAGACCAATTGATACTTGTGATATTAAATATTGATGACTACATT
CATCATATTAAACAATA

SEQ ID NO. 8003

STRAIN 18RS21

AACCACTTACTAACCTCAGTAAAGAAAATATAG

SEQUENCE LISTING

CTAAAATAGATTTGACTTTCTTAATGAGGCACCTAATGCAAATATTGCTT
 TTGAAAGAATTAGTAGATGAACTAAAAATTCAAAAGAACTGGACAGTAA
 AGGTTGGTCAAAAAAGACTCTCGAACGATAAAATCTGACGATGGC
 TTATCAATAAACATATAGTTCCCTAGATCGTGCAGATTATAACATTATC
 CAAGTCATTCCATTGCTAATGTACATGTACTACTGTTTTAATACCAGA
 AAGGGAGAATTCTAAAATTATAGAATATACAACATGATTATGAAA
 TGGAGTTAATCAATGAGGATAGGCAACAATTTCAAAATATGAAACAGTT
 GATTTAGACCAATTGATACTGTTGATATTTAATATTGATGACTACAT
 TTCATCATATTTAACATA

SEQ ID NO. 8004

STRAIN 2603 frame: 1

VNHLLNLSKENIAKIDFDLNEALNANIRLKEVDELKISKELDSKGWSKKDSRTIKILYD
 GLINKHIVSLDRADYNIIQVIPFANVHVLFLIPERENSKNYRIYNYSDYEMELINEDRQ
 QFSKYETVLDQQLILVDIFNIDDYISSYLTI

SEQ ID NO. 8005

STRAIN H36B frame: 1

NHLLNLSKENIAKIDFDLNEALNANIRLKEVDELKISKELDSKGWSKKDSRTIKILYD
 GLINKHIVSLDRADYNIIQVIPFANVHVLFLIPERENSKNYRIYNYSDYEMELINEDRQ
 QFSKYETVLDQQLILVDIFNIDDYISSYLTI

SEQ ID NO. 8006

STRAIN 18RS21 frame: 1

NHLLNLSKENIAKIDFDLNEALNANIRLKEVDELKISKELDSKGWSKKDSRTIKILYD
 GLINKHIVSLDRADYNIIQVIPFANVHVLFLIPERENSKNYRIYNYSDYEMELINEDRQ
 QFSKYETVLDQQLILVDIFNIDDYISSYLTI

SEQ ID NO. 8101

STRAIN 090

AGCAAGCCTAATGTTGTTCAAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCAAAAAATCGTTAATGGGTTGGGTTCTTATTTTGTCTAG
 CTTTATTTATTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGAAATTAAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAAGAAGTTGCTAGCAAAACAACAAAAAT
 CCAGATTACGTTCAAAATATGCTCGAGCTAAGTATTATTCCTCTAAGAC
 CGCGAAATGATTACCCATTACCAAGACCTTTACCAAAA

SEQ ID NO. 8102

STRAIN A909

AGCAAGCCTAATGTTGTTCAAGTTAAA
 TATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAATCG
 TTTAATGGGTTGGGTTCTTATTTTGTCTAGCTtttATTTATTTACCCACTTATAATTT
 AGTTAAGAGTTACAGAACTTACAAGAACGTCGTCAAGAAGTTGTAACGAAAGA
 CTATCAGACATTAACAACTAGAACTGAGAACCAAGAAGTTACTAGCAAAACAACAAAAAA
 TCCAGATTACGTTCAAAATATGCTCGAGCTAAGTATTATTCCTCTAAGACCGGGCGAAT
 GATTACCCATTACCAAGACCT

SEQ ID NO. 8103

STRAIN H36B

AGCAAGCCTAATGTTGTTCAAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCAAAAAATCGTTAATGGGTTGGGTTCTTATTTTGTCTAG
 CTTTATTTATTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTCAAGAAGTTGAAATTAAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAAGAAGTTACTAGCAAAACAACAAAAAT
 CCAGATTACGTTCAAAATATGCTCGAGCTAAGTATTATTCCTCTAAGAC
 CGCGAAATGATTACCCATTACCAAGACCTTTACCAAAA

SEQ ID NO. 8104

STRAIN 18RS21

AGCAAGCCTAATGTTGTTCAAGTTAAAATCAATATATTAACGATGAGAATCTAAAAAA
 CGTTACGAAGCTGAGGAGTTACGCCGAAAAATCGTTAATGGGTTGGGTTCTTATTTT

SEQUENCE LISTING

GTCATGCTTTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACTTACAA
 GAACGTCGTAAGAAGTTGAAATTAAACGAAAGACTATCAGACATTAACATAAGAACT
 GAGAACAGAAGTTGCTAGCAAAACAACAAAAATCCAGATTACGTTCAAAAATATGCT
 CGAGCTAAGTATTATTCCTCTAAGACCGGCGAAATGATTACCCATTACCAGACCTTTA
 CCAAA

SEQ ID NO. 8105

STRAIN M732

AGCAAGCCTAATGTTGTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAATCGTTAATGGGTTGGGTTCTTATTTTGTATG
 CTTTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTAAGAAGTTGAAATTAAACGAAAGACTATCAGACAT
 TAACAAATAGAACTGAGAACCGAGAAGTTACTAGCAAAACAACAAAAAT
 CCAGATTACGTTCAAAATATGCTCGAGCGAAGTATTATTCCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTACCAAAA

SEQ ID NO. 8106

STRAIN COH1

AGCAAGCCTAATGTTGTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAATCGTTAATGGGTTGGGTTCTTATTTTGTATGCTttt
 ATTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACTTTACAAG
 AACGTCGTAAGAAGTTGAAATTAAACGAAAGACTATCAGACATTAAC
 AATAGAACTGAGAACCGAGAAGTTACTAGCAAAACAACAAAAATCCAGA
 TTACGTTCAAAATATGCTCGAGCGAAGTATTATTCCTCTAAGACCGGCG
 AAATGATTACCCATTACCAGACCTTTACCAAAA

SEQ ID NO. 8107

STRAIN M781

AGCAAGCCTAATGTTGTTCAGTT
 AAATAATCAATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCT
 AGGAGTTACGCCGAAAAATCGTTAATGGGTTGGGTTCTTATTTTGT
 ATGTTTATTTATTTACCCACTTATAATTAGTTAAGAGTTACAGAAC
 TTACAGAACGTCGTAAGAAGTTGAAATTAAACGAAAGACTATCAGA
 CTTAAACTAATAGAACTGAGAACCGAGAAGTTACTAGCAAAACAAC
 AATCCAGATTACGTTCAAAATATGCTCGAGCGAAGTATTATTCCTCTAA
 GACCGGCGAAATGATTACCCATTACCAGACCTTTACCAAAA

SEQ ID NO. 8108

STRAIN CJB110

AGCAAGCCTAATGTTGTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAATCGTTAATGGGTTGGGTTCTTATTTTGTATGCTttt
 ATTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACTTTACAAG
 AACGTCGTAAGAAGTTGAAATTAAACGAAAGACTATCAGACATTAAC
 AATAGAACTGAGAACCGAGAAGTTGCTAGCAAAACAACAAAAATCCAGA
 TTACGTTCAAAATATGCTCGAGCTAAGTATTATTCCTCTAAGACCGGCG
 AAATGATTACCCATTACCAGACCTTTACCAAAA

SEQ ID NO. 8109

STRAIN 1169NT

AGCAAGCCTAATGTTGTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAATCGTTAATGGGTTGGGTTCTTATTTTGTATG
 CTTTATTTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACTTT
 ACAAGAACGTCGTAAGAAGTTGAAATTAAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCGAGAAGTTACTAGCAAAACAACAAAAAT
 CCAGATTACGTTCAAAATATGCTCGAGCTAAGTATTATTCCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTACCAAAA

SEQ ID NO. 8110

STRAIN JM9130013

AGCAAGCCTAATGTTGTTCAGTTAAA

SEQUENCE LISTING

SYRTLQERRQEVVKLTQDYLQTLNRTEQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIY
PLPDLPLPK

SEQ ID NO. 8120

STRAIN 1169NT

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSRTLQERRQEVVKLTQDYLQTLNRTEQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLPLPK

SEQ ID NO. 8121

STRAIN JM9130013

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSRTLQERRQEVVKLTQDYLQTLNRTEQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLPLPK

SEQ ID NO. 8122

STRAIN 2603

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
ERRQEVVKLTQDYLQTLNRTEQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIYPLPDL
PK

SEQ ID NO. 8201

STRAIN 2603

ATGAAAAAAATTATTGTTAAAATGTAAGGATAAAGAAGGTTAACGCATTACACTTTAGAA
TGTGTTGGTAGCATGGTTACAATCACAGGAGCTTACTAGTTATCAAGGACTGACAAAA
TTGTTGGCTAACAGATAAGTAGTGATGTTCTTCAAGGACTGACAAAA
ActCAGCAACTAAATGCAGAATTGAGGCGCTCATCTGGAAATATTAAAGACAGAACAAA
CTTATTTACGTAAGCAAGATAAGATTGTAACCTTGGCAATCTAACAAAGATGATTC
CGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTATGGTTAGACAATTG
CAAATGAGTCAGACCAAAAGTATGGTAAAGACTTGTGTTTATTTAAGGACGGGTTAAA
AGGACATTTACTATGATTTAAAGAAGAAACTTAA

SEQ ID NO. 8202

STRAIN 090

AATTCGAAGGGCGCTCACTGGAAATATTAAAGACAGAACAAACTTTATTA
CGTAAGCAAGATAAGATTGTAACCTTGGCAAATCTAACAAAGATGATT
CCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTATGGGT
TAGACAATTGTCAAATGAGTCACCAAAAGTATGGTAAAGACTTGTGTTTT
TATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGAAGA
AACT

SEQ ID NO. 8203

STRAIN A909

CAGAATTGAAAGGCGCTCATCTGGAAATATTAAAGACAGAACAAACTTTAT
TTACGTAAGCAAGATAAGATTGTAACCTTGGCAAATCTAACAAAGATGA
TTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTATGG
GGTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAGACTTGT
TTTATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGA
AGAAACT

SEQ ID NO. 8204

STRAIN H36B

ATGCAGAATTGAAAGGCGCTCATCTGGAAATATTAAAGACAGAACAAACTT
TATTTACGTAAGCAAGATAAGATTGTAACCTTGGCAAATCTAACAAAGA
TGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTT
ATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAGACTT
GTTTTTATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGA
AGAAAGAAACT

SEQ ID NO. 8205

STRAIN 18RS21

AGAATTGAAAGGCGCTCATCTGGAAATATTAAAGACAGAACAAACTTTATT
TACGTAAGCAAGATAAGATTGTAACCTTGGCAAATCTAACAAAGATGAT
TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTATGG

SEQUENCE LISTING

GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT
TTTATTAAAGGACGGGTAAAAAGGACATTTACTATGATTTAAAGAA
GAAACT

SEQ ID NO. 8206

STRAIN M732

CAGAATTCGAAGGCGCTCACTTGGAAATTAAAGACAGAACAAACTTAT
TTACGTAAGCAAGATAAGATTGTAACCTTGGCAAATCTAATAAGATGA
TTTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTATG
GGTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT
TTTATTAAAGGACGGGTAAAAAGGACATTTACTATGATTTAAAGA
GAAACT

SEQ ID NO. 8207

STRAIN COH1

GAATTCGAAGGCGCTCACTTGGAAATTAAAGACAGAACAAACTTAT
ACGTAAGCAAGATAAGATTGTAACCTTGGCAAATCTAATAAGATGATT
TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTATGG
TTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT
TTTATTAAAGGACGGGTAAAAAGGACATTTACTATGATTTAAAGAAG
AAACT

SEQ ID NO. 8208

STRAIN M781

AGAATTCGAAGGCGCTCACTTGGAAATTAAAGACAGAACAAACTTAT
TACGTAAGCAAGATAAGATTGTAACCTTGGCAAATCTAATAAGATGAT
TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTATGG
GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT
TTTATTAAAGGACGGGTAAAAAGGACATTTACTATGATTTAAAGAAG
GAAACT

SEQ ID NO. 8209

STRAIN CJB110

GAATTCGAAGGCGCTCACTTGGAAATTAAAGACAGAACAAACTTAT
ACGTAAGCAAGATAAGATTGTAACCTTGGCAAATCTAATAAGATGATT
TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTATGG
TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAACTTGT
TTTATTAAAGGACGGGTAAAAAGGACATTTACTATGATTTAAAGAAG
AAACT

SEQ ID NO. 8210

STRAIN 1169NT

TCGAAGGCGCTCACTTGGAAATTAAAGACAGAACAAACTTATTTACGT
AAGCAAGATAAGATTGTAACCTTGGCAAATCTAATAAGATGATTTCG
TAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTATGGGTTAG
ACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAACTTGT
TTTATTAAAGGACGGGTAAAAAGGACATTTACTATGATTTAAAGAAGAAC
T

SEQ ID NO. 8211

STRAIN JM9130013

TGCAGAATTGAGGCGCTCATCTGGAAATTAAAGACAGAACAAACTT
ATTACGTAAGCAAGATAAGATTGTAACCTTGGCAAATCTAATAAGAT
GATTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTA
GGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTGT
TTTTTATTAAAGGACGGGTAAAAAGGACATTTACTATGATTTAAA
GAAGAAACT

SEQ ID NO. 8212

STRAIN 2603 frame: 1

MKNLLKCKDKVKRAFTLLECLVALVTTGALLVYQGLTKLLAQQIVVMSSSQSEWLL
TQQLNAEFEGAHLEYLRQNKLRLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNC
QMSQTKSMVKLVFYFKDGLKRTFYYDFKEET.

SEQUENCE LISTING

SEQ ID NO. 8213

STRAIN 090 frame: 3

FEGAHLEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
MVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8214

STRAIN A909 frame: 3

EFEGAHLEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8215

STRAIN H36B frame: 3

AEFEGAHLEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
KSMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8216

STRAIN 18RS21 frame: 2

EFEGAHLEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8217

STRAIN M732 frame: 3

EFEGAHLEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8218

STRAIN COH1 frame: 1

EFEGAHLEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8219

STRAIN M781 frame: 2

EFEGAHLEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8220

STRAIN CJB110 frame: 1

EFEGAHLEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8221

STRAIN 1169NT frame: 3

EGAHELEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8222

STRAIN JM9130013 frame: 2

AEFEGAHLEYLRQNKLRLRKQDKIVTFGKSINKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
KSMVKLVFYFKDGLKRTFYDFKEET

SEQ ID NO. 8301

STRAIN 2603

atggaaaaagattcattatcaaagttttattaaaatgattgttgttattttgttttaatt
 agtgttagcagctagttttatttttccacgttgcggccaaagttcgagatgataaaatccctt
 atttcaaatggtaacgttaaggcctggaaactctttatatatgcttatgataaaatccttgat
 aagcttattaaagcaaaaaatagaaaatgacaaacccaaaatataaaagcaaggcgttggat
 gttcctgtgttaagaaaactcataagacagctgttgtcgttcatggtttgcgaatagc
 aaagagaatatggcatatgggtggctgtttcataagtttaggatacaatgttcttatg
 cctgacaatattgcacatggtaaagtcatggcaggctatggctggaaacgac
 cggcagaacattatcaaatggacagaaaatgatagttgtataagaatccatcaaggccaaatt
 actttatgtgtttcaatggggagcaacagtcatgtatggcttagtggtaaaaaatta
 cctagtcaggtgttaatatcattgaagattgcgttattctatgtgtttggatgaatta
 aaatttcaggctaaagagatgtatggtttaccaggcccccactcttatatgaagttca
 acaatttctaaaatcagagcagggtttcgtatggacaagcaagtagtgcgaacaattg

SEQUENCE LISTING

aaaaagaataatttaccagcccttttattcatggtgataaggataatttggccaaca
 agtatggtttatgacaactataaaagctacagcaggtaaaaagagcttataattgtaaaa
 ggggcaaaacatgcgaaatctttgaaacagagccagaaaatatgagaaacgtatctct
 agttttgaaaaatatgaaaaa

SEQ ID NO. 8302

STRAIN 090

GCTAGTTTTATTTCACGTTGCCAAGTTCG
 AGATGATAAAATCCTTATTCAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGTTATGATAAAATCCTTGATTAAGCTATTAAAGCAAAAAATAGAA
 ATGACAAACCAAAATATAAAAGCAAGTTGCTTGGTATGTTCCGTGCTAA
 GAAACTCATAAAGACAGCTGTTGCTTCATGGTTGGCAATAGCAAAG
 AGAATATGAAGGCATATGGTGGCTGTTCATAGTTAGGATACAATGTT
 CTTATGCCTGACAATATTGCACATGGTGAAGTCATGGGAGTTGATAGG
 CTATGGCTGAAACGACCGCGAGAACATTATCaATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAATTACTTtaTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTAAAAATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGCGGTTATTCTAGTGTGTTGGGATGAATTAAAAT
 TTCAGGCTAAAGAGATGTATGGTTACCAGCCTCCACTCTTATATGAA
 GTTCAACAATTCTAAATCAGAGCAGGTTTCGTATGGACAAGCAAG
 TAGTGTGCAAAATTGAAAAAATAATTACGAGCCCTCTTATTCATG
 GTGATAAGGATAATTGGTCCAACAAGTATGGTTATGACAACATAAA
 GCTACAGCAGGTAAGAAAGAGCTTATATTGTAAGGGGCAAAACATGC
 GAAATCTTTGAAACAGAGCCAGAAAATATGAGAAACGTATCTCTAGTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8303

STRAIN A909

AATCCTTATTCAATGGTCAACGTAAGCCTGGAAACTCTTATATGCT
 TATGATAAAATCCTTGATAAGCTATTAAAGCAAAAAATAGAAATGACAAA
 CAAATATAAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAATC
 ATAAGACAGCTGTTGCTGGTTCATAAGTTAGGATACAATGTCCTATGCC
 AAGGCATATGGTGGCTGTTCATGGTGAAGTCATGGCAGTTGATAGGCTATGGCT
 TGACAACATTGCACATGGTGAAGTCATGGCAGTTGATAGGCTATGGCT
 GGAACGACCGCGAGAACATTCAAATGGACAGAAATGATAGTTGATAAG
 AATTCAAGCCAAATTACTTTATTGGTGTTCATGGGGAGCAAC
 AGTCATGATGGCTAGTGGTGAAGGAAATTACCTAGTCAGGTTGTTAATATCA
 TTGAAGAATGGGTTATTCTGGTGTGGGATGAATTAAAATTTCAGGCT
 AAAGAGATGTATGGTTACAGCAGGTTTCGTATGGACAAGCAAGTAGTGTG
 AACATTGAAAAAGAATAATTACGAGCCCTCTTATTGATGGTGTGATAAG
 GATAATTGGTCCAACAAGTATGGTTATGACAACATAAAAGCTACAGC
 AGGTAAGAAAGAGCTTATATTGTAAGGGGCAAAACATGCGAAATCTT
 TTGAAACAGAGCCAGAAAATATGAGAAACGTATCTCTAGTTTTGAAA
 AAATATGAAAAA

SEQ ID NO. 8304

STRAIN H36B

AGTTTTATTTCACGTTGCCAAGTTCGAGATGATAAAATCCTTAT
 TTCAAATGGTCAACGTAAGCCTGGAAACTCTTATATGTTATGATAAAAT
 CTTGATAAGCTATTAAAGCAAAAAATAGAAATGACAAACCAAAATATA
 AAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAATCATAAGACAGC
 TGTGTCGTTCATGGTTGCAATAGCAAAGAGAAATATGAGGCATATG
 GTGGCTGTTCATAGTTAGGATACAATGTTATGCTGACAACATT
 GCACATGGTGAAGTCATGGCAGTTGATAGGCTATGGCTGGAACGACCG
 CGAGAACATTCAAATGGACAGAAATGATAGTTGATAAGAATTGATCAA
 GCCAAATTACTTTATTGGTGTTCATGGGTGGAGCAACAGTCATGATG
 GCTAGTGGTGAAGGAAATTACCTAGTCAGGTTGTTAATATCATTGAAGGATG
 CGGGTATTCTGGTGTGGGATGAATTAAAATTTCAGGCTAAAGAGATGT
 ATGGTTTACGAGCCCTCCACTCTTATATGAGTTCAACAATTCTAAA
 ATCAGAGCAGGTTTCGTATGGACAAAGCAAGTAGTGTGCAACAAATTGAA
 AAAGAATAATTACGAGCCCTTTTATTGATGGTGTGATAAGGATAATTG
 TTCCAACAAGTATGGTTATGACAACATAAAAGCTACAGCAGGTAAGAAA
 GAGCTTATATTGTAAGGGGCAAAACATGCGAAATCTTTGAAACAGA

SEQUENCE LISTING

GCCAGAAAAATATGAGAACGTATCTCTAGTTTTGAAAAAaTATgAAA
AA

SEQ ID NO. 8305

STRAIN 18RS21

GCTAGTTTTATTCCCCACGTTGCCAAGTCGA
GATGATAATCCTTATTCAAATGGCAACGTAAGCCTGAAACTCTT
ATATGCTTATGATAAAATCCTTGTATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACAAAATAAAGCAAGTTGCTGGTATGTTCTGCTGTTAAG
AAAACCTATAAGACAGCTTGTGTTCATGGTTGCGAATAGCAAAGA
GAATATGAAGGCATATGGTGGCTGTTCATAGTTAGGATAACAATGTC
TTATGCCGACAATGGCACATGGTAAAGTCATGGCAGTTGATAGGC
TATGGCTGGAACGACCGCAGAACATTATCAAATGGCACAGAAATGATAGT
TGATAAGAACATGGCTAGTGGTGGAAATACTTATTGGTGGCTAATGGG
GAGCAACAGTCATGATGGCTAGTGGTGGAAATACTTACCTAGTCAGGTTGTT
AATATCATTGAAGATTGGCTTATTCTAGTGGTGGATgAATTAAAATT
TCAGGCTAAAGAGATGTATGGTTACCCAGCTCCACTCTTATATGAAG
TTCAACAATTCTAAAATCAGAGCAGGTTTCTGATGGACAAgCAAGT
AGTGTGCAACAATTGAAATAATTACAGCCCTCTTATTGATGG
TGATAAGGATAATTGTTCCAACAAGTATGGTTATGACAACATAAAG
CTACAGCAGGTAAAGAAAGAGCTTATATTGAAAAGGGGAAACATGCG
AAATCTTTGAAcAGAGCCAGAAAATATGAGAACAGTATCTCTAGTTT
TTGAAAAAATATGAAAAA

SEQ ID NO. 8306

STRAIN M732

GCTAGTTTTATTCCCCACGTTGCCAAGTCGA
GATGATAATCCTTATTCAAATGGCAACGTAAGCCTGAAACTCTT
ATATGCTTATGATAAAATCCTTGTATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACAAAATAAAGCAAGTTGCTGGTATGTTCTGCTGCTAAG
AAAACCTATAAGACAGTTGCTGCTCATGGTTGCGAATAGCAAAGA
GAATATGAAGGCATATGGTGGCTGTTCATAGTTAGGATAACAATGTC
TTATGCCGACAACATTGACATGGTAAAGTCATGGCAGTTGATAGGC
TATGGCTGGAACGACCGCAGAACATTATCAAATGGCACAGAAATGATAGT
GGATAAGAACATGGCTAGTGGTGGAAATACTTATTGGTGGCTAATGGG
GAGCAACAGTCATGATGGCTAGTGGTGGAAATACTTACCTAGTCAGGTTGTT
AATATCATTGAAGATTGGCTTATTCTAGTGGTGGATGAATTAAAATT
TCAGGCTAAAGAGATGTATGGTTACCCAGCTCCACTCTTATATGAAG
TTCAACAATTCTAAAATCAGAGCAGGTTTCTGATGGACAAgCAAGT
AGTGTGCAACAATTGAAATAATTACAGCCCTCTTATTGATGG
TGATAAGGATAATTGTTCCAACAAGTATGGTTATGACAACATAAAG
CTACAGCAGGTAAAGAAAGAGCTTATATTGAAAAGGGGAAACATGCG
AAATCTTTGAAACAGAGCCAGAAAATATGAGAACAGTATCTCTAGTTT
TTGAAAAAATATGAAAAA

SEQ ID NO. 8307

STRAIN COH1

GCTAGTTTTATTCCCCACGTTGCCAAGTC
GAGATGATAAAATCCTTATTCAAATGGCAACGTAAGCCTGAAACTCT
TTATATGCTTATGATAAAATCCTTGTATAAGCTATTAAAGCAAAAAATAGA
AATGAAACAAAATAAAGCAAGTTGCTGGTATGTTCTGCTGCTA
AGAAAACCTATAAGACAGTTGCTGCTCATGGTTGCGAATAGCAA
GAGAATATGAAGGCATATGGTGGCTGTTCATAGTTAGGATAACAATGT
TCTTATGCCGACAACATTGACATGGTAAAGTCATGGCAGTTGATAG
GCTATGGCTGGAACGACCGCAGAACATTATCAAATGGCACAGAAATGATA
GTGGATAAGAACATGGCTAGTGGTGGAAATACTTACCTAGTCAGGTTG
TTAATATCATTGAAGATTGGCTTATTCTAGTGGTGGATgAATTAAA
TTTCAGGCTAAACAGATGTATGGTTACCCAGCCTCCACTCTTATATGA
AGTTTCAACAATTCTAAAATCAGAGCAGGTTTCTGATGGACAAAGCAA
GTAGTGTGCAACAATTGAAAAGAATAATTACAGCCCTCTTATTGATGG
GGTGATAAGGATAATTGTTCCAACAAAGTATGGTTATGACAACATAA
AGCTACAGCAGGTAAAGAAAGAGCTTATATTGAAAAGGGGAAACATG
CGAAATCTTTGAAcAGAGCCAGAAAATATGAGAACAGTATCTCTAGT

SEQUENCE LISTING

TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8308

STRAIN M781

GCTAGTTTTATTTTCCACGTTGCCAAGTTCG
 AGATGATAAATCCTTATTCAAATGGCAACGTAAGCCTGGAAACTCTT
 TATATGTTATGATAAATCCTTGATAAGCTATTAAGCAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
 GAAAACCTATAAGACAGTTGCTTGGTATGTTCTGCTGCTGCTAA
 AGAATATGAAGGCATATGGTGGCTTCTATAAGTTAGGATACAATGTT
 CTTATGCTGACAACATTGACATGGTAAAGTCATGGCAGTTGATAGG
 CTATGGCTGAGACGACCGAGAACATTATAAATGGACAGAAATGATAG
 TGATAAGAAATCCATCAAGCCAAATTaCTTATGGTGGTATGTTCAATGGGT
 GGAGCAACAGTCATGTTGCTTCTAGTGGTAAAGATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGTTATTcTAGTGTGTTGGGATgAATTAAAAT
 TTCAGGcTAAAGAGATGATGGTTTACCAAGCCTCCACTcTTATGAA
 GTTTCAcAATTcTAAATCAGAGCAGGTTTCTGATGGACAGCAAG
 TAgtGTCGAACAATTGAAAAGAATAATTACAGCCCTcTTTATTGATG
 GTGATAAGGATAATTGGTCCAACAAAGTATGGTTATGAACTATAAA
 GCTACAGCAGGTAAGAAAGAGCTTATATTGAAAGGGGCAAAACATGC
 GAAATCTTTGAAaCAGAGCCAGAAAATATGAGAAACGTATCTAGTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8309

STRAIN CJB110

GCTAGTTTTATTTTCCACGTTGCCAAGTTCGAG
 ATGATAAATCCTTATTCAAATGGCAACGTAAGCCTGGAAACTCTTAA
 TATGTTATGATAAATCCTTGATAAGCTATTAAGCAAAAATAGAAAT
 GACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGA
 AAACTCATAAGACAGCTGTTGCTGTTCATGGTTTGGCAATAGCAAAGAG
 AATATGAAGGCATATGGTGGCTGTTCTATAAGTTAGGATACAATGTTcT
 TATGCTGACAATATTGCACTGGTAAAGTCATGGCAGTTGATAGGCT
 ATGGCTGGAACAGACCGAGAACATTATAAATGGACAGAAATGATAGTT
 GATAAGAATCCATCAAGCCAAATTACTTATTGGTGGTCAATGGGTGG
 AGCAACAGTCATGGCTAGTGGTGGGAAATTACCTAGTCAGGTTGTTA
 ATATCATTGAAGATTGCGTTATTcTAGTGTGTTGGGATgAATTAAAATT
 CAGGCTAAAGAGATGATGGTTTACCAAGCCTCCACTCTTATATGAACT
 TTCACAAATTCTAAATCAGAGCAGGTTTCTGATGGACAAAGCAAGTA
 gTGTGCAACAATTGAAAAGAATAATTACAGCCCTcTTTATTGATGGT
 GATAAGGATAATTGGTCCAACAAAGTATGGTTATGACAACCTATAAAGC
 TACAGCAGGTAAGAAAGAGCTTATATTGAAAGGGGCAAAACATGC
 AATCTTTGAAACAGAGCCAGAAAATATGAGAAACGTATCTAGTTT
 TTGAAAAAATATGAAAAA

SEQ ID NO. 8310

STRAIN 1169NT

GCTAGTTTTATTTTCCACGTTGCCAAGTTCGA
 GATGATAAATCCTTATTCAAATGGCAACGTAAGCCTGGAAACTCTT
 ATATGTTATGATAAATCCTTGATAAGCTATTAAGCAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAG
 AAAACTCATAAGACAGCTGTTGCTGTTCATGGTTTGGCAATAGCAAAGA
 gAATATGAAGGCATATGGTGGCTGTTCTATAAGTTAGGATACAATGTTc
 TTATACCTGACAATATTGCACTGGTAAAGTCATGGCAGTTGATAGGC
 TATGGCTGGAACAGACCGAGAACATTATAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTATTGGTGGTCAATGGGTG
 GAGCAACAGTCATGTTGCTAGTGGTGGGAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTgCGGTTATTcTAGTGTGTTGGGATgAATTAAAATT
 TCAGGCTAAAGAGATGATGGTTaCCAGCCTCCACTcTTTATATGAAAG
 TTCAACAATTCTAAAATCAGAGCAGGTTTCTGATGGACAAAGCAAGT
 AGTGTAGAACAATTGAAAAGAATAATTACAGCCCTCTTATTGATGG
 TGATAAGGATAATTGGTCCAACAAAGTATGGTTATGACAACCTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTATATTGAAAGGGGCAAAACATGC
 AAATCTTTGAAaCAGAGCCAGAAAATATGAGAAACGTATCTAGTT
 TTTGAAAAAATATGAAAAA

SEQUENCE LISTING

SEQ ID NO. 8311

STRAIN JM9130013

GCTAGTTTTTATTTCACGTTGCCAAGTCG
 AGATGATAAAATCCTTATTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAAATCCTTGATAAGCTATTAAAGCAAAAATAGAA
 ATGAAACACAAATATAAAGCAAGTGTGCTGGTATGTTCTGCTGTTAA
 GAAAACATCATAAGACAGCTGTTGCTCATGGTTTGCAGATAGCAAAG
 AGAATATGAAGGCATATGGTGGCTGTTCATAAAGTTAGGATACAATGTT
 CTTATGCCTGACAATATTGCACATGGTAAAGTCATGGCAGTTGATAGG
 CTATGGCTGAAACGACCGCGAGAACATTATCaATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTAAAGATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATGGGGTTATTcTAGTGGTGGGATgAAATTAAAAT
 TTCAGGCTAAAGAGATGTATGGTTTACAGCCTCCCCTTATATGAA
 GTTCAACAAATTCTAAATCAGAGCAGGTTTGTATGGACAAGCAAG
 TAGTGTGCAACAATTGAAAAGATAATTACAGCCCTTTTATTGATG
 GTGATAAGGATAATTGGTCAACAAGTATGGTTATGACAACATAAA
 GCTACAGCAGGTAAGAAAGAGCTTATATTGAAAGGGGAAACATGC
 GAAATCTTTGAAACAGAGCCAGAAAATATGAGAAACGTATCTCTAGTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8312

STRAIN 2603 frame: 1

MKKTRLSKFIKMIIVVILFLISVAASFYFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF
 KLLKQKIEMTNQNIKQVAWVPAVKKTHKTAVVVHGFA NSKENMKAYGWL
 PDNIAHGESHGQLIGYGVNDRENI IKWTEMI
 VDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNI
 IEDCGYSSVWDELKFQ
 PSQVNNI
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKNNL
 P
 KNNL
 P
 L
 F
 I
 H
 G
 D
 K
 D
 N
 F
 V
 P
 T
 S
 M
 V
 Y
 D
 N
 Y
 K
 A
 T
 A
 G
 K
 K
 E
 L
 Y
 I
 V
 K
 G
 A
 H
 K
 A
 S
 F
 T
 E
 P
 E
 K
 Y
 E
 K
 R
 I
 S
 S
 F
 L
 K
 K
 Y
 E
 K

SEQ ID NO. 8313

STRAIN 090 frame: 1

ASFYFFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF
 DKL
 KLL
 KQKIEMTNQNIKQVAWVPA
 AKKTHKTAVVVHGFA NSKENMKAYGWL
 PDNIAHGESHGQLIGYGVNDRENI
 IKWTEMI
 VDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNI
 IEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKNNL
 P
 L
 F
 I
 H
 G
 D
 K
 D
 N
 F
 V
 P
 T
 S
 M
 V
 Y
 D
 N
 Y
 K
 A
 T
 A
 G
 K
 K
 E
 L
 Y
 I
 V
 K
 G
 A
 H
 K
 A
 S
 F
 T
 E
 P
 E
 K
 Y
 E
 K
 R
 I
 S
 S
 F
 L
 K
 K
 Y
 E
 K

SEQ ID NO. 8314

STRAIN A909 frame: 3

SFISNGQRKPGNSLYAYDKSF
 DKL
 KLL
 KQKIEMTNQNIKQVAWVPA
 AKKTHKTAVVVHGFA NSKENMKAYGWL
 PDNIAHGESHGQLIGYGVNDRENI
 IKWTEMI
 VDKN
 SSS
 QITLFGVSMGGATVMMASGEKLPSQVNNI
 IEDCGYSGVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKNNL
 P
 L
 F
 I
 H
 G
 D
 K
 D
 N
 F
 V
 P
 T
 S
 M
 V
 Y
 D
 N
 Y
 K
 A
 T
 A
 G
 K
 K
 E
 L
 Y
 I
 V
 K
 G
 A
 H
 K
 A
 S
 F
 T
 E
 P
 E
 K
 Y
 E
 K
 R
 I
 S
 S
 F
 L
 K
 K
 Y
 E
 K

SEQ ID NO. 8315

STRAIN H36B frame: 1

SFYFFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF
 DKL
 KLL
 KQKIEMTNQNIKQVAWVPA
 AKKTHKTAVVVHGFA NSKENMKAYGWL
 PDNIAHGESHGQLIGYGVNDRENI
 IKWTEMI
 VDKN
 SSS
 QITLFGVSMGGATVMMASGEKLPSQVNNI
 IEDCGYSGVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKNNL
 P
 L
 F
 I
 H
 G
 D
 K
 D
 N
 F
 V
 P
 T
 S
 M
 V
 Y
 D
 N
 Y
 K
 A
 T
 A
 G
 K
 K
 E
 L
 Y
 I
 V
 K
 G
 A
 H
 K
 A
 S
 F
 T
 E
 P
 E
 K
 Y
 E
 K
 R
 I
 S
 S
 F
 L
 K
 K
 Y
 E
 K

SEQ ID NO. 8316

STRAIN 18RS21 frame: 1

ASFYFFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF
 DKL
 KLL
 KQKIEMTNQNIKQVAWVPA
 AKKTHKTAVVVHGFA NSKENMKAYGWL
 PDNIAHGESHGQLIGYGVNDRENI
 IKWTEMI
 VDKN
 SSS
 QITLFGVSMGGATVMMASGEKLPSQVNNI
 IEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKNNL
 P
 L
 F
 I
 H
 G
 D
 K
 D
 N
 F
 V
 P
 T
 S
 M
 V
 Y
 D
 N
 Y
 K
 A
 T
 A
 G
 K
 K
 E
 L
 Y
 I
 V
 K
 G
 A
 H
 K
 A
 S
 F
 T
 E
 P
 E
 K
 Y
 E
 K
 R
 I
 S
 S
 F
 L
 K
 K
 Y
 E
 K

SEQ ID NO. 8317

SEQUENCE LISTING

STRAIN M732 frame: 1
 ASFYFFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF DKL KQKIE MTN QNI KQVAWYVPA
 AKKTHKT VVVVHGFANSKENMKAYGWL FHKL GYNVL MPD NI AHGE SHGQ LIGY GWNDREN
 II KWTE MIV DKNPSS QIT LFGV SMMGAT VMMAS GEKL PSQV VN II EDCG YSSV WDEL KFQ
 AKEMYGLPAFPPLL YE VSTISKIRAGFSYQASSVEQLKKNL P ALFI HGD KDNF VPTSMV
 YDNYKATAGKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8318

STRAIN COH1 frame: 1
 ASFYFFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF DKL KQKIE MTN QNI KQVAWYVPA
 AKKTHKT VVVVHGFANSKENMKAYGWL FHKL GYNVL MPD NI AHGE SHGQ LIGY GWNDREN
 II KWTE MIV DKNPSS QIT LFGV SMMGAT VMMAS GEKL PSQV VN II EDCG YSSV WDEL KFQ
 AKEMYGLPAFPPLL YE VSTISKIRAGFSYQASSVEQLKKNL P ALFI HGD KDNF VPTSMV
 YDNYKATAGKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8319

STRAIN M781 frame: 1
 ASFYFFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF DKL KQKIE MTN QNI KQVAWYVPA
 AKKTHKT VVVVHGFANSKENMKAYGWL FHKL GYNVL MPD NI AHGE SHGQ LIGY GWNDREN
 II KWTE MIV DKNPSS QIT LFGV SMMGAT VMMAS GEKL PSQV VN II EDCG YSSV WDEL KFQ
 AKEMYGLPAFPPLL YE VSTISKIRAGFSYQASSVEQLKKNL P ALFI HGD KDNF VPTSMV
 YDNYKATAGKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8320

STRAIN CJB110 frame: 1
 ASFYFFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF DKL KQKIE MTN QNI KQVAWYVPA
 AKKTHKTAVVVHGFANSKENMKAYGWL FHKL GYNVL MPD NI AHGE SHGQ LIGY GWNDREN
 II KWTE MIV DKNPSS QIT LFGV SMMGAT VMMAS GEKL PSQV VN II EDCG YSSV WDEL KFQ
 AKEMYGLPAFPPLL YE VSTISKIRAGFSYQASSVEQLKKNL P ALFI HGD KDNF VPTSMV
 YDNYKATAGKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8321

STRAIN 1169NT frame: 1
 ASFYFFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF DKL KQKIE MTN QNI KQVAWYVPA
 AKKTHKTAVVVHGFANSKENMKAYGWL FHKL GYNVL MPD NI AHGE SHGQ LIGY GWNDREN
 II KWTE MIV DKNPSS QIT LFGV SMMGAT VMMAS GEKL PSQV VN II EDCG YSSV WDEL KFQ
 AKEMYGLPAFPPLL YE VSTISKIRAGFSYQASSVEQLKKNL P ALFI HGD KDNF VPTSMV
 YDNYKATAGKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8322

STRAIN JM9130013 frame: 1
 ASFYFFFHVAQVRDDKSFI SNGQRKPGNSLYAYDKSF DKL KQKIE MTN QNI KQVAWYVPA
 VKKTHKTAVVVHGFANSKENMKAYGWL FHKL GYNVL MPD NI AHGE SHGQ LIGY GWNDREN
 II KWTE MIV DKNPSS QIT LFGV SMMGAT VMMAS GEKL PSQV VN II EDCG YSSV WDEL KFQ
 AKEMYGLPAFPPLL YE VSTISKIRAGFSYQASSVEQLKKNL P ALFI HGD KDNF VPTSMV
 YDNYKATAGKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8401

STRAIN 2603

ATGATGAAAGTTTACGGCTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAC
 AATATGGAATGTTAGCGACTGTCACTATCAATATCAAAAAGAATCATAGCATTAAATTG
 ATGCCAGCCATTGATTTTTAATGCAATCAATTGATTTAGAACCTCAAGATTGGACCGT
 ATCGTAGTAGCAGAGGGTCCAGGATCTTACGGCTTACGTGTAGCTGTTGCTACAGCA
 AAAATGCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCTGTACGCTTA
 ACAAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGATGCACGACGTAATAAT
 GTTATGTTGGTTCTATCAAATGGTACTGTTAAACCAAGACTGTACACTCTCTT
 GAAGAAGTCTACAAGAGGTGGGAATAAGCCAATGTCATTTGTCGGAGAGGTTGCA
 GCATTTTTGATCAGATTAAGAAAGCCTTACCCACATGCTAAAATTACAGAAAACCTTACCT
 TGTGCACTGAGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATGCGTT
 GTTCCACGATACTTAAACGTTGAGGAAAATTGGTTAAAAACCACTGTGAA
 AGAATACAGAAGAATATTAAGAGAGTT

SEQ ID NO. 8402

STRAIN 090

SEQUENCE LISTING

AAAGTTTACGCTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
 AAACAATATGGAATGTTAGCGACTGTCACTaTCAATATCAAAAAGAAC
 ATAGCATTAAATTGATGCCAGCCATTGATTTTAATGCAATCAATTGAT
 TTAGAACCTCAAGATTGGACCGTATCGTAGTGGCAGAGGGTCCAGGATC
 TTATACGGGCTTACGTAGCTGGCTACAGCAAAATGCTAGCTTATA
 CGCTTAAGATTGACTTAGTTGGAGTATCTAGCTGTACGCTTAACAAAT
 GGATTTCAGAAAATGATTGTTGGTACCACTTATAGATGACAGACGTAA
 CAATGTTTATGTTGGTTCTATCAAATGGTACTGTAAACCAgACT
 GTCACACTTCTCTGAAGAAGTCTTACAAGAGGTGGGAATAAGCCAAT
 GTTCATTTGTCGGAGAGGTTGCAGCATTGATCAGATTAAgAAAGC
 CTTACACATGCTAAAATTACAGAAACTTACCTTGTGCAGTGGCAATTG
 GGGCAGAAAAGACAAAATGAAAGCGTTAATGTAGATGCGTTGTTCCA
 CGATACTTAAACGAGTTGAAGCTGAGGAAAATTGGTTAAAAACCACTG
 TGAAACGAAT

SEQ ID NO. 8403

STRAIN A909

AAAGTTTACGCTTGATACTTCAAGCAAAGCACTATCAG
 TGGCTGACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATATC
 AAAAGAACATAGCATTAAATTGATGCCAGCCATTGATTTTAATGCA
 ATCAATTGATTTAGAACCTCAAGATTGGACCGTATCGTAGTGGCAGAG
 GTCCAGGATCTTACGGGCTTACGTAGCTGGCTACAGCAAAATG
 CTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCTGTACGC
 TTTAACAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGATG
 CACGACGTAACAATGTTATGTTGGTTCTATCAAATGGAGATACTGTT
 AAACCAAGACTGTCACACTCTCTGAAGAAGTCTTACAAGAGGTGGGA
 TAAAGCCAATGTTCATTGTCGGAGGGTTGCAGCATTGTTGACCAGA
 tTAAGAAAGTTTACCATGCTAAAATTACAGAAACTTACCTTGTGCA
 GtGGCAATTGGCGCAAAGGACAAAATGAAAGCGTTAATGTAGATG
 GTTGTCCACGATACTTAAACGAGTTGAAGCTGAGGAAAATTGGTTAA
 GAAACCACTGTGAAACGAAT

SEQ ID NO. 8404

STRAIN H36B

AAAGTTTACGCTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATAT
 CAAAAGAACATAGCATTAAATTGATGCCAGCCATTGATTTTAATGCA
 ATCAATTGATTTAGAACCTCAAGATTGGACCGTATCGTAGTGGCAGAG
 GTTCCAGGATCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCTGTACCG
 CTTAACAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGAT
 GCACGACGTAACAATGTTATGTTGGTTCTATCAAATGGAGATACTGTT
 TAAACCAAGACTGTCACACTCTCTGAAGAAGTCTTACAAGAGGTGGGA
 ATAAAGCCAATGTTCAATTGTCGGAGAGGTGCAGCATTGTTGACCAG
 ATTAAGAAAAGTTTACCATGCTAAAATTACAGAAACTTACCTTGTGCA
 AGTGGCAATTGGCGCAAAGGACAAAATGAAAGCGTTAATGTAGATG
 CGTTGTCCACGATACTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8405

STRAIN 18RS21

AAAGTTTACGCTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATAT
 CAAAAGAACATAGCATTAAATTGATGCCAGCCATTGATTTTAATGCA
 ATCAATTGATTTAGAACCTCAAGATTGGACCGTATCGTAGTGGCAGAG
 GTTCCAGGATCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCTGTACCG
 CTTAACAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGAT
 GCACGACGTAATAATGTTATGTTGGTTCTATCAAATGGGAGATACTGTT
 TAAACCAAGACTGTCACACTCTCTGAAGAAGTCTTACAAGAGGTGGGA
 ATAAAGCCAATGTTCAATTGTCGGAGAGGTGCAGCATTGTTGATCAg
 ATTAAGAAAGCCTTACCATGCTAAAATTACAGAAACTTACCTTGTGCA
 AGTAGCAATTGGCGCAAAGGACAAAATGAAAGCGTTAATGTAGATG
 CGTTGTCCACGATACTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA

SEQUENCE LISTING

AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8406

STRAIN M732

AAAGTTTACGCTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATAT
CAAAAAGAACATAGCATTAAATTGATGCCAGCATTGATTTTAATGC
AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTACGGGCTTACGTGTAGCTGCTACAGCAAAAT
GCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTAAACAAATGGATTTTACGAAAATGATTTATTGGTACCACTTATAGAT
GCACGACGTAACATGTTATGTTGGTTCTATCAAAATGGTGTACTGT
TAAACCAGACTGTCACACTCTTGTGAAAGAAGTCTTACAAGAGGTGGGA
ATAAAAGCCAATGTTACATTGTGAGGAGGTTGCAGCATTGATCAG
ATTAAGAAAGCTTACCATGCTAAATTACAGAAAATTACCTTGTG
AGTAGCAATTGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGAn
CGTTGTTCCACGATACTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8407

STRAIN COH1

AAAGTTTACGCTTGATACTTCAAGCAAAGCAC
TATCAGTGGCTGTACTAAACAATATGGAATGTTAGCGACTGTCACTATC
AATATCAAAAAGAACATAGCATTAAATTGATGCCAGCATTGATTTTT
AATGCAATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAG
CAGAGGGTCCAGGATCTTACGGGCTTACGTGTAGCTGCTACAGCA
AAAATGCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
GTACGCTTAAACAAATGGATTTTACGAAAATGATTTATTGGTACCACTTA
TAGATGCACGACGTAACATGTTATGTTGGTTCTATCAAAATGGTGT
ACTGTTAAACCAAGACTGTCACACTCTTGTGAAAGAAGTCTTACAAGAGGT
GGGAATAAAAGCCAATGTCATTGGTGGAGGTTGCAGCATTGTTG
ATCAGATTAAGAAAGCCTTACCATGCTAAATTACAGAAAATTACCT
TGTGAGTAGCAATTGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGT
AGATGCGTTGTTCCACGATACTAAAACGTGTTGAAGCTGAGGAAAATT
GGTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8408

STRAIN M781

AAAGTTTACGCTTGATACTTCAAGCAAAGCACTA
TCAGTGGCTGTACTAAACAATATGGAATGTTAGCGACTGTCACTATCAA
TATCAAAAAGAACATAGCATTAAATTGATGCCAGCATTGATTTTTAA
TGCATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTATCA
GAGGGTCCAGGATCTTACGGGCTTACGTGTAGCTGCTACAGCAA
AATGCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGT
ACGCTTAAACAAATGGATTTTACGAAAATGATTTATTGGTACCACTTATA
GATGCACGACGTAACATGTTATGTTGGTTCTATCAAAATGGTGTAC
TGTAAACCAAGACTGTCACACTCTTGTGAAAGAAGTCTTACAAGAGGTGG
GGAATAAAAGCCAATGTCATTGGTGGAGGTTGCAGCATTGAT
CAGATTAAGAAAGCCTTACCATGCTAAATTACAGAAAATTACCTTG
TGCAGTAGCAATTGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAG
ATGCGTTGTTCCACGATACTAAAACGTGTTGAAGCTGAGGAAAATTGG
TTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8409

STRAIN CJB110

AAAGTTTACGCTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATAT
CAAAAAGAACATAGCATTAAATTGATGCCAGCATTGATTTTTAATGC
AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTGGCAGAG
GGTCCAGGATCTTACGGGCTTACGTGTAGCTGCTACAGCAAAAT
GCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTAAACAAATGGATTTTACGAAAATGATTTGGTGGTACCACTTATAGAT
GCACGACGTAACATGTTATGTTGGTTCTATCAAAATGGTGTACTGT
TAAACCAGACTGTCACACTCTTGTGAAAGACTTACAAGAGGTGGGA

SEQUENCE LISTING

ATAAAGCCAATGTTCATTTGTCGGAGAGGTTGCAGCATTTCgATCAG
 ATTAAGAAAGCCTTACACATGCTAAATTACAGAAACTTACCTTGTGC
 AGTGGCAATTGGCGCAAAGGACAAAAAATGAAAGCGTTAATGTAgATG
 CGTTTGTCCACGATACTAAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8410

STRAIN 1169NT
 AAAGTTTAGCCTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATAT
 CAAAAAGAACATAGCATTAAATTGATGCCAGCCATTGATTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTACGTAGTAGCAGAG
 GGTCCAGGATCTTACGGGTTACGTGTAGCTGCTACAGCAAAAT
 GCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTAACAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGAT
 GCACGACGTAACAAATGTTATGTTGGTTCTATCAAATGGTGTACTGT
 TAAACACGACTGTCACACTCTTGAAGAAGTCTTACAAGAGGTGGGA
 ATAAAGCCAATGTCATTTGTCGGAGAGGTTGCAGCATTTGTTGACCAG
 ATTAAGAAAGCTTACACATGCTAAATTACAGAAACTTACCTTGTGC
 AGTGGCAATTGGCGCAAAGGACAAAAAATGAAAGCGTTAATGTAgATG
 CGTTTGTCCACGATACTAAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8411

STRAIN JM9130013
 AAAGTTTAGCCTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATAT
 CAAAAAGAACATAGCATTAAATTGATGCCAGCCATTGATTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTACGTAGTAGCAGAG
 GGTCCAGGATCTTACGGGTTACGTGTAGCTGTTGCTACAGCAAAAT
 gCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTAACAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGAT
 GCACGACGTAACAAATGTTATGTTGGTTCTATCAAATGGAGATACTGT
 TAAACACGACTGTCACACTCTTGAAGAAGTCTTACAAGAGGTGGGA
 ATAAAGCCAATGTCATTTGTCGGAGAGGTTGCAGCATTTGTTGACCAG
 ATTAAGAAAGCTTACACATGCTAAATTACAGAAACTTACCTTGTGC
 AGTGGCAATTGGCGCAAAGGACAAAAAATGAAAGCGTTAATGTAgATG
 CGTTTGTCCACGATACTAAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8412

STRAIN 2603 frame: 1
 MMKVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDR
 IVVAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNN
 VYVGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPC
 CAVAIGRKQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8413

STRAIN 090 frame: 1
 KVLAFTDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETN

SEQ ID NO. 8414

STRAIN A909 frame: 1
 KVLAFTDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
 VAIGRKQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETN

SEQ ID NO. 8415

STRAIN H36B frame: 1
 KVLAFTDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV

SEQUENCE LISTING

VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFVQIKKVLPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8416

STRAIN 18RS21 frame: 1
 KVLA FDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRI
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFVQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8417

STRAIN M732 frame: 1
 KVLA FDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRI
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFVQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVXXFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8418

STRAIN COH1 frame: 1
 KVLA FDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRI
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFVQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8419

STRAIN M781 frame: 1
 KVLA FDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRI
 VSEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFVQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8420

STRAIN CJB110 frame: 1
 KVLA FDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRI
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFVQIKKALPHAKITETLPCA
 VAIGRKGQKMKESNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8421

STRAIN 1169NT frame: 1
 KVLA FDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRI
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFVQIKKALPHAKITETLPCA
 VAIGRKGQKMKESNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8422

STRAIN JM9130013 frame: 1
 KVLA FDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRI
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFVQIKKVLPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8501

STRAIN 2603

atgagtaaacacaaaatttaggaatttagtaaaaaaggagcaattatcagggctctca
 gtggcactattgttagtaatagggtggcttttatgggtacaatctcaacctaataagagt
 gcagtaaaaactaactacaaaggttttatgttagagaaggaaagtgtttcgccact
 cttttgacaggaaaagctaaaggctaatcaagaacaggactgttatgtgctaataaaa
 ggttaatcgagcaactgtcacagttaaagtgggtgataaaatcacagctgtcagcagtt
 gttcaatatgataacaacaactgcacaaggcgcactacgtcaatcgtcaattaaat
 aaagttagcgcgtcagattaatactaaagacaacaggaaatgtttccagctatggaaatca
 agtcatatgttatcttcatcatcacaaggacaaggactcaatcgtactatgtggcgcacg
 aatcgtctacagaaaaattatcaaagtcaagctaatcgttcatacaaccaacaacttcaa

SEQUENCE LISTING

gatttgaatgatgcttatgcagatgcacaggcagaagtaataagcacaaaaagcattg
 aatgatacttttattacaagtgcgtatcaggcacagtgttgaagttaatgtatatt
 gatccagcttcaaaaactactgtcaagtaacttgcgtatgtcaactgaagtaactccaa
 gtacaaggaaacatgcgtatgttgcataatgttggaaaagaccaggctgttaaa
 ataaatctaaaggctatccgtacaaggatgggaaaatttcatatatctcaat
 tatccagaaggcagaagcaacaacaatgactctaatacgcgtctatgttgcgttatt
 aaatataaagttagatattactagccctctcgatgcattaaaacaagggtttaccgtatca
 gttgaagtagttatggagataagcaccttattgtccctacaagttctgtatca
 gataataaacactttgttgggtatacaatgatctatgttggaaaatttccaaaggta
 gtcaaaaattgtttaagctgtatgcataagacacaagaattttatcaggttggaaa
 caaatcgtgttactatccaagtaaaaccttcaaggatggcaaaaaattgataatatt
 gaatcaatcgtatcttaactctaataagaaatcagaggtaaa

SEQ ID NO. 8502

STRAIN 090

TTTTTATGGGTACAATCTAACCTAATAAGAGTGCAGTAAAAACTAACTA
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTACAGTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCTACG
 ACACGTCTAATCGTCAATTAAATAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAAGTGTATCTTCTTC
 ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCACGAACTCGTC
 TACAGCAAAATTATCAAAGCTAAGCTTACATACAACCAACAACCT
 CAAGATTGAAATGATGTTATGCAGATGCACAGGAGAAGTAAATAAAC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGTATTGATCCAGCTTCAAAACTAGTCAAGTA
 CTTGTCATGTAGCAACTGAAGGTAACCTCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAGACCAGGCTGTTAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCATATATCTCA
 AATTATCCAGAAGCAGAACAAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAATTATAAATAAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAACAAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCTACAAGTTCTGTGATAAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATGTTAAATTCCAAAGTTGAAGTCAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTCAGGTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAAACCTTCAAGGATGGGAAAA
 AATTGATAATATTGAATCAATCGATCTTAACCTAATAAGAAATCAGAGG

SEQ ID NO. 8503

STRAIN A909

TTTTTATGGGTACAATCTAACCTAATAAGAGTGCAGTAAAAACTAA
 CTACAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTT
 TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGATGCT
 AATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCAC
 AGCTGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCT
 ACGACACTGCTAATCGTCAATTAAATAAGTAGCGCGTCAGATTAATAAT
 CTAAGACAAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTC
 ATCATCATCACAAGGACAAGGGCTCAATCGACTAGTGGTGCACGAACTC
 GTCTACAGCAAAATTATCAAAGCTAATGCTTACATACAACCAACAA
 CTTCAAGATTGAAATGATGTTATGCAGATGCACAGGAGAAGTAAATAA
 AGCACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGA
 CAGTTGTTGAAGTTAATAGTGTATTGATCCAGCTTCAAAACTAGTC
 GTACTTGTCCATGTAGCAACTGAGGGTAAACTCCAAGTACAAGGAACGAT
 GAGTGAGTATGATTGGCTAATGTTAAAAAGACCAGTGTGTTAAAATAA
 AATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTTCATATATC
 TCAAATTATCCAGAAGCAGAACAAACAATGACTCTAATAACGGCTC
 TAGTGCTGTAATTATAAATAAAAGTAGATATTACTAGCCCTCTCGATG
 CATAAAAACAAGGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAG
 CACCTTATTGTTCTACAAGTTCTGTGACAACAAAGATAATAAACACTT
 TGTTGGGTATACAATGATTCTAATGTTAAATTCCAAAGTTGAAGTC
 AAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTCAGGTTGAAA
 GCAGGACAAATCGTGGTTACTAATCCAAGCAAAACCTTCAAGGATGGGCA
 AAAATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAG

SEQUENCE LISTING

AGGTGAAA

SEQ ID NO. 8504

STRAIN H36B

TTTTTATGGTACAATCTAACCTAATAAGAGTCAGTAAAAACTAATTA
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTATTTGATGCTAAT
 AAAGGTAACTCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTCATATGATACAACAACAGCACAAGCAGCCTACCG
 ACAC TGCTAATCGTCAATTAAATAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
 CAAGATTTGAATGATGCTTATGAGATGCAAGCAGGAGAAGTAAATAAGC
 ACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGGTAAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTA
 CTTGTCATGTAGCAACTGAAGGTAACCTCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAGGACAGGCTGTTAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCTATATCTCA
 AATTATCCAGAACAGCAAACAATGACTCTAATAACGGCTCTAG
 TGCTGAAATTATAAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAACACAAGGTTTACTGATCGAGTGAAGTAGTTAATGGAGATAAGC
 CCTTATTGTCCTACAAGTCTGTGACAAACAAAGATAATAAAACACTTGT
 TTGGGTATAACATGATTCTAATCGTAAATTCCAAAGGTTGAAGTC
 TTGGTAAAGCTGATGCTAAGACACAAGGAAATTTCAGGTTGAAAGCA
 GGACAAATCGTAGTTACTAATCCAAGTAAAGCTTCAAGGATGGGCAAA
 AATTGATAATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TG

SEQ ID NO. 8505

STRAIN 18RS21

TTTTTATGGTACAATCTAACCTAATAAGAGTCAGTAAAAACTAACTA
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTATTTGATGCTAAT
 AAAGGTAACTCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTCATATGATACAACAACAGCACAAGCAGCCTACCG
 ACAC TGCTAATCGTCAATTAAATAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCAGCTATGGAATCAAGTGATCAATCTTC
 ATCATCACAAGGACAAGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
 CAAGATTTGAATGATGCTTATGAGATGCAAGCAGGAGAAGTAAATAAGC
 ACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGGTAAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTA
 CTTGTCATGTAGCAACTGAAGGTAACCTCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAGGACAGGCTGTTAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCTATATCTCA
 AATTATCCAGAACAGCAAACAATGACTCTAATAACGGCTCTAG
 TGCTGAAATTATAAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAACACAAGGTTTACCGTATCGAGTGAAGTAGTTAATGGAGATAAGC
 CCTTATTGTCCTACAAGTCTGTGATAAAACAAAGATAATAAAACACTTGT
 TTGGGTATAACATGATTCTAATCGTAAATTCCAAAGGTTGAAGTC
 TTGGTAAAGCTGATGCTAAGACACAAGGAAATTTCAGGTTGAAAGCA
 GGACAAATCGGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAA
 AATTGATAATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAG

SEQ ID NO. 8506

STRAIN M732

TTTTTATGGTACAATCTAACCTAATAAGAGTCAGTAAAAACTAATTA
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTATTTGATGCTAAT
 AAAGGTAACTCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTCATATGATACAACAACAGCACAAGCAGCCTACCG
 ACAC TGCTAATCGTCAATTAAATAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGGAGTTCCAGCTATGGAATCAAGTGATCAATCTTCATC

SEQUENCE LISTING

ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
 CAAGATTGAAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGTATTGATCCAGCTTCAAAAACAGTCAAGTA
 CTTGTCCATGTGCAACTGAAGGTAACCTCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAGATCAGGCTGTTAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCATATATCTCA
 AATATCCAGAACGACAAGCAACAAACATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAACAAGGTTTACCGTATCAGTTAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCTACAAGTCTGTGATAAACAAAGATAATAAACACTTTGT
 TTGGGTATAATGATTCTAATCGTAAATTTCCAAGGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTCAGGTTGAAAGCA
 GGACAATCGTGGTTACTAATCCAAGCAAAACCTTCAAGGATGGGAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8507

STRAIN COH1

TTTTTATGGGTACAATCTCACCTAATAAGAGTCAGTAAAAAC
 TAATTACAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTC
 TTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGAT
 GCTAATAAAGGTAATCGAGCAACTGTGTACAGTTAAAGTGGGTGATAAAAT
 CACAGCTGGTCAGCAGTTAGTCAATATGATACAAACACTGCACAAGCAG
 CCTACGACACTGCTAATCGTCATAAATAAAAGTAGCGCGTCAGATTAAT
 AATCTAAAGACAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATC
 TTCATCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCACGA
 ATCGTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAA
 CAACTTCAGGATTGAAATGATGTTATGCAGATGCACAGGCAGAAGTAAA
 TAAAGCACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAG
 GGACAGTTGTTGAAGTTAATAGTGTATTGATCCAGCTTCAAAAACAGT
 CAAGTACTTGTCCATGTGCAACTGAAGGTTAAACTCCAAGTACAAGGAAC
 GATGAGTGGAGTATGATTGGCTAATGTTAAAAAGATCAGGCTGTTAAA
 TAAAATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCATAT
 ATCTCAAATTATCCAGAACGACAAGCAACAAATGACTCTAATAACGG
 CTCTAGTGTGTTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCG
 ATGCATTAAAACAAGGTTTACCGTATCAGTTAAGTAGTTAATGGAGAT
 AAGCACCTTATTGTCCTACAAGTCTGTGATAAACAAAGATAATAACCA
 CTTGTTGGTATAATGATTCTAATGTTAAATTTCCAAGGTTGAAG
 TCAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTCAGGTTG
 AAAGCAGGACAATCGTGGTTACTAATCCAAGCAAAACCTTCAAGGATGG
 GCAAAAAATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAAT
 CAGAGGTGAA

SEQ ID NO. 8507

STRAIN M781

TTTTTATGGGTACAATCTCACCTAATAAGAGTCAGTAAAAACTAATTA
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTCAATATGATACAAACACTGCACAAGCAGCCTACG
 ACACTGCTAATCGTCATAAATAAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
 CAAGATTGAAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGTATTGATCCAGCTTCAAAAACAGTCAAGTA
 CTTGTCCATGTGCAACTGAAGGTTAAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAGATCAGGCTGTTAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCATATATCTCA
 AATTATCCAGAACGACAAGCAACAAACATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT

SEQUENCE LISTING

TAAAACAAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCTACAAGTCTGTGATAAAACAAAGATAATAAACACTTTGT
 TTGGGTATACATGATTCTAATCGTAAAATTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTATCAGGTTGAAAGCA
 GCACAAATCGGGTTACTAATCCAAGCAAAACCTTCAGGATGGGAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8508

STRAIN CJB110

TTTTTATGGGTACAATCTAACCTAATAAGAGTCAGTAAAAACTAACTA
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTCATATGATAACAACACTGCACAAGCAGCCTACG
 ACACTGCTAATCGTCAATTAAATAAAAGTAGCGCCTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTCCAGCTATGGAATTAAAGTGTATCAATCTTC
 ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
 CAAGATTGAAATGATGCTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGTATTGATCCAGCTTCAAAACTAGTCAGTA
 CTTGTCATGTAGCAACTGAAGGTAACCTCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAGACCAAGGCTGTTAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTCTATATCTCA
 AATTATCCAGAACGACAAGCAAACAAACATGACTCTAATAACGGCTCTAG
 TGCTGTAATTATAAAATATAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAACAAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTCCTACAAGTCTGTGATAAAACAAAGATAATAAACACTTTGT
 TTGGGTATACATGATTCTAATCGTAAAATTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTATCAGGTTGAAAGCA
 GCACAAATCGGGTTACTAATCCAAGTAAAACCTTCAGGATGGGAAAA
 AATTGATAATATTGAATCAATCGATCTTAACCTCTAATAAGAAATCAGAGG
 TGA

SEQ ID NO. 8509

STRAIN 1169NT

TTTTTATGGGTACAATCTAACCTAATAAGAGTCAGTAAAAACT
 AACTACAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCT
 TTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGATG
 CTAATAAAAGGTAAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATC
 ACAGCTGGTCAGCAGTTAGTTCAATATGATAACAACACTGCACAAGCAGC
 CTACGCACTGCTAATCGTCAATTAAATAAAAGTAGCGCCTCAGATTAATA
 ATCTAAAGACAACAGGAAGTCTCCAGCTATGGAATCAAGTGTATCAATCT
 TCTTCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAA
 TCGTCTACAGCAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAAC
 AACTTCAAGATTGAAATGATGCTTATGCAGATGCACAGGCAGAAGTAAAT
 AAAGCACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGG
 GACAGTTGTTGAAGTTAATAGTGTATTGATCCAGCTTCAAAACTAGTC
 AAGTAATTGTCATGTAGCAACTGAAGGTTAACTCCAAGTACAAGGAACG
 ATGAGTGTAGTGTATTGCTAATGTTAAAAAGACCAAGGCTGTTAAAT
 AAAATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCTATATA
 TCTCAAATTATCCAGAACGACAACAAACAAATGACTCTAATAACGGC
 TCTAGTGCTGTAATTATAAAATATAAAAGTAGATATTACTAGCCCTCTCGA
 TGCATTAAAACAAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATA
 AGCACCTTATGTCCCTACAAGTTCTGTGATAAAACAAAGATAATAAACAC
 TTTGTTGGGTATACAATGATTCTAATCGTAAAATTCCAAAGTTGAAGT
 CAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTATCAGGTTGAA
 AAGCAGGACAAATCGTGGTTACTAATCCAAGTAAAACCTTCAGGATGGG
 CAAAAAATTGATAATATTGAATCAATCGATCTTAACCTCTAATAAGAAATC
 AGAGGTGAA

SEQ ID NO. 8510

STRAIN JM9130013

SEQUENCE LISTING

TTTTTATGGGTACAATCTAACCTAATAAGAGTCAGTAAAAACTAACTA
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTGATGCTAAT
 AAAGGTAAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTCATATGATAACAACACTGCACAAGCAGCCTACG
 AACTGCTAATCGTCAATTAATAAAAGTAGCGCGTCAGATTAATAATCTA
 AAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGGCTCAATCGACTAGTGGTGCACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
 CAAGATTGAATGATGCTATGCAGATGCACAGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTACAGGACAG
 TTGTTGAAGTTAATAGTGTATTGATCCAGCTTAAAAACTAGTCAGTA
 CTGTCATGAGCTAGCAACTGAGGGTAAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAGACCAGTCTGTTAAAATAAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGGTAAAATTTCATATCTCA
 AATTATCCAGAACGAGAACAAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAATTATAAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAACAAGGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGTTCTACAAGTCTGTGACAACAAAGATAATAAACACTTTGT
 TTGGGTATAACATGATTCTAATGTTAAATTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTCAGGTTTGAAAGCA
 GGACAAATCGGTTACTAATCCAAGCAAAACTTCAGGATGGGCAAAA
 AATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAAA

SEQ ID NO. 8511

STRAIN 2603 frame: 1

MSKRQNLGISKKGAIISGLSVALIVVIGGFLWVQSQPNKSAVKTNYKVFNVREGSVSSST
 LLTGAKANQEYVYFDANKGNRATVTVKVGDKITAGQQLVQYDTTTAQAAAYDTANRQLN
 KVARQINNLKTTGSLPAMESSDQSSSSQGQGTQSTSGATNRQLQNYQSQANASYNQQLQ
 DLNDAYADAQAEVNKAQKALNDTIVTSDVSGTVEVNSDIPASKTSQVLVHVATEGKLQ
 VQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKSEVK

SEQ ID NO. 8512

STRAIN 090 frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKRQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRQLQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTIVTSDV
 SGTVVEVNSDIPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKSEVK

SEQ ID NO. 8513

STRAIN A909 frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKRQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRQLQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTIVTSDV
 SGTVVEVNSDIPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKSEVK

SEQ ID NO. 8514

STRAIN H36B frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKRQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRQLQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTIVTSDV
 SGTVVEVNSDIPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 AFKDGQKIDNIESIDLNSNKSEVK

SEQUENCE LISTING

SEQ ID NO. 8515

STRAIN 18RS21

frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRRLQONYQSQANASYNQQLQDLDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVY
 PDK EWEKGKISYISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEV
 VNGDKH LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAG
 QIVVTPSK TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8516

STRAIN M732

frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRRLQONYQSQANASYNQQLQDLDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVY
 PDK EWEKGKISYISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEV
 VNGDKH LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAG
 QIVVTPSK TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8517

STRAIN COH1

frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRRLQONYQSQANASYNQQLQDLDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVY
 PDK EWEKGKISYISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEV
 VNGDKH LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAG
 QIVVTPSK TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8518

STRAIN M781

frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRRLQONYQSQANASYNQQLQDLDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVY
 PDK EWEKGKISYISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEV
 VNGDKH LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAG
 QIVVTPSK TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8519

STRAIN M781

frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRRLQONYQSQANASYNQQLQDLDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVY
 PDK EWEKGKISYISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEV
 VNGDKH LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAG
 QIVVTPSK TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8520

STRAIN CJB110

frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRRLQONYQSQANASYNQQLQDLDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVY
 PDK EWEKGKISYISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEV
 VNGDKH LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAG
 QIVVTPSK TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8521

STRAIN 1169NT

frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKANQEYVYFDANKGNRATVTVK

SEQUENCE LISTING

VGDKITAGQQQLVQYDTTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRQQNYQSQANASYNQQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEKGKISYISNYPEAEANNNDNSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
 LIVPTSSVINKDNKHFWVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8522

STRAIN JM9130013 frame: 1

FLWVQSQPNKSAVKTNYKVFNVREGVSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQQLVQYDTTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGAQSTSGATNRQQNYQSQANASYNQQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQSVKIKSKVYPDK
 EWEKGKISYISNYPEAEANNNDNSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
 LIVPTSSVTNPKDNKHFWVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8601

STRAIN 2603

atgaaaaaaaaatttggaaatttattgtcctcacactactgacccctttttggtatcttgcgg
 caacaaactaaacaagaaggactaaaacaactattctaaaatgcctaaaattgaaggc
 ttcacctattatggaaaaattccctgaaaatccgaaaaaaagtaattaattttacatattct
 tacactgggtatttattaaaacttaggtttaatgtttcaagttacagttagacttagaa
 aaagatagccccgtttttggtaaacaactgaaagaagctaaaaattaaactgctgtatgat
 acagaagctattggccgcacaaaaacccgtatcatggtttcgatcaagatccaaac
 atcaatactctgaaaaattgcaccaacttttagttattaaatatggcacaattat
 ttagatatgtgccagccctggggaaagtattcgtaaagaaaaagaagtaatcagtgg
 gttagccaatgaaaaactaaaactctcgctgtcaaaaaagattacaccatattttaaag
 cctaacactactttactattatggattttatgataaaaaatatctattatatggtaat
 aattttggacgcgggtggagaactaatctatgattactaggttatgtccccagaaaa
 gtoaaaaaaagatgtctttaaaaaagggtgtttaccgttgcagaagcaatcggtat
 tacgttggagattatgcccttggtaataaaaaacaaacgactaaaaaaggcagcttcatca
 cttaaagaaaagtgtctggaaagatattaccagctgtcaaaaaaggccatcatagaa
 agtaactacgcgttttattctcgacccttatctttagaagctcaattaaatca
 tttacaaaggctatcaaagaaaaatacaaat

SEQ ID NO. 8602

STRAIN 090

GAAGGCTTCACCTATTATGGAAAAATTCTGAAAATCCGAAAAAGTAAT
 TAATTTTACATATTCTTACACTGGGTATTTATTAAACTAGGTGTTAATG
 TTCAAGTTACAGTTAGACTAGAAAAAGATAGCCCCGTTTTGGTAAG
 CAACTGAAAAGAGCTAAAAAAATTAACTGCTGATGATAACAGAGCTATTGC
 CGCAGAAAACCTGATTTAATCATGGTTTCGATCAAGATCCAAACATCA
 ATACTCTGAAAAAAATTGCAACCTTACTGTTATTAAATATGGTGACCAA
 AATTATTTAGATATGATGCCAGCCTGGGGAAAGTATTGGTAAAGAAAA
 AGAAGCTAATCAGTGGTTAGCCAATGGAAAACCTAAACTCTCGCTGCCA
 AAAAAGATTACACCATATCTTAAAGCTAACACTACTTTACTATTATG
 GATTTTATGATAAAAATCTATTATGGTATAAATTTGGACGCGG
 tGGAGAACTAATCTATGATTCACTAGGTTATGCTGCCCCAgAAAAAGTCA
 AAAAAGATGTctttaaaaaAGGGTGGTTACCGTTTcgaAGAAGCAATC
 GGtGATTACGTGGAGATTATGCCCTGTAAATATAACAAAAGACTAA
 AAAAGCAGCTTCACTAAAGAAAGTGTCTGGAAAGAATTACCG
 CTGTCaAAAAAGGGCACATCATAGAAAGTAactACGACGTTTATTTC
 TCTGACCCCTCTATCTTACAAGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8603

STRAIN A909

GAAGGCTTCACCTATTATGGAAAAATTCTG
 AAAATCCGAAAAAAAGTAATTAAATTCTTACATATTCTTACACTGGATATT
 TTAAAAACTAGGAGTTAATGTTCAAGTTACAGTTAGACTTAGAAAAAGA
 TAGCCCCGTTTGGTAAACAACTGAAAGGAGCTAAAAAATTAACTGCTG
 ATGATACAGAAAGCTATTGCCGCACAAAACCTGATTAAatCATGGTTTT
 GATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCACCAACTTGT
 TATTAATATGGTGCACAAAATTATTTAGATGATGCCAGCTTGGGGA

SEQUENCE LISTING

AAGTATTGGTAAAGAAAAAGAAGCTAATCAGTGGTTAGCCaTGGAAA
 ACTAAAACCTCGCTGCCAAAAAGATTACACCATATCTAAAACCTAA
 CACTACTTTACCAATTGGATTTATGATAAAAATATCTATTTATATG
 GTAATAATTGGACGCGGTGGAGAACTAATCTATGATTCACTAGGTTAT
 GCTGCCCCAGAAAAGTCAAAAAGATGTCTTTAAAAAGGGTGGTTAC
 CGTTCGCAAGAACGCAATCGGTgATTACGTTGGAGATTATGCCCTGTTA
 ATATAACAAAAGCAGTCAAAAGCAGCTTCACTTAAAGAAAGTGA
 GTCTGGAAGAATTACAGCTGTCAAAAAGGGCACATCATAGAAAAGTAA
 CTACGACGTGTTTATTCCTGACCCTcTATCTTAGAAGCTCAATTAA
 AATCATTACAAA

SEQ ID NO. 8604

STRAIN H36B

GAAGGCTTCACCTATTATGGAAAA
 ATTCTGAAAATCCGAAAAAAAGTAATTAAATTACATATTCTTACACTGG
 ATATTATTAACACTAGGAGTTAATGTTCAAGTTACAGTTAGACTTAG
 AAAAGATAgCCCGTTTGGTAAGCAACTGAAAGGAGCTAAAAAAATTA
 ACTGCTGATGATACAGAAGCTATTGCGCAGACAAAACCTGATTAA
 GGTTTTGATCAAGATCCAAACATCAATACTCTGAAAAAAATGCAACCA
 CTTAGTTATTAAATATGGTGCACAAAATTATTTAGATAgATgATGCCAGCT
 TTGGGGAAAGTATTGGTAAAGAAAAAGCTAATCAGTGGTTAGCCA
 ATGGAAAACCTAAACTCTCGTGCACAAAAGATTACACCATATCTAA
 GGCTaACACTACTTTACTATTAGATTTATGATAAAAATATCTAT
 TTATATGGTAATAATTGGCGCGGtGGAgAACTAATCTATGATtCACT
 AGGTTATGCTGCCCAgAAAAAGTCAAAAAGATGTCTTAAAAAGGGT
 GGTTTACCGTTTCAAGAACGCAATCGGTgATTACGTTGGAGATTATGCC
 CTTGTTAATATAACAAAAGCAGTCAAAAAGGGCACATCATAG
 AAGTGAATGTTGGAGAATTACAGCTGTCAAAAAGGGCACATCATAG
 AAAGTAACACTACGACGTGTTTATTCCTGACCCTCTATCTTAGAAGCT
 CAATTAAAATCATTACAAA

SEQ ID NO. 8605

STRAIN 18RS21

GAAGGCTTCACCTATTATGGA
 AAAATTCTGAAAATCCGAAAAAAAGTAATTAAATTACATATTCTTACAC
 TGGTATTATTAACACTAGGTTAATGTTCAAGTTACAGTTAGACT
 TAGAAAAGATAGCCCCGTTTGGTAAACAACTGAAAGAAGCTAAAAAA
 TTAACTGCTGATGATACAGAAGCTATTGCGCAGACAAAACCTGATTAA
 CATGGTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCAC
 CAACTTACTTAAATATGGTGCACAAAATTATTTAGATAgATgATGCCA
 GCCTTGGGGAAAGTATTGGTAAAGAAAAAgAACTAATCAGTGGTTAG
 CCAATGGAAAACCTAAACTCTCGTGTCAAAAAGATTACACCATATCT
 TAAAGCTAACACTACTTTACTATTATGGATTATGATAAAAATATC
 TATTATGTTAATATAATTGGACCGGTGGAGAACTAATCTATGATT
 ACTAGGTTATGCTGCCCAgAAAAAGTCAAAAAGATGTCTTAAAAAG
 GGTTGTTACCGTTTGCAGAACGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTGTTAATATAACAAAACgACTAAAAAGCAGCTTCACTTAA
 AGAAAGTGAATGCTGGAAGAATTACAGCTGTCAAAAAGGGCACATCA
 TAGAAAAGTAACACTACGACGTGTTTATTCCTGACCCTCTATCTTAGAA
 GCTCAATTAAAATCATTACAAA

SEQ ID NO. 8606

STRAIN M732

GAAGGCTTCACCTATTATGG
 AAAATTCTGAAAATCCGAAAAAAAGTAATTAAATTACATATTCTTACA
 CTGGTATTATTAACACTAGGTTAATGTTCAAGTTACAGTTAGAC
 TTAGAAAAGATAGCCCCGTTTGGTAAAGCAACTGAAAGAAGCTAAAAAA
 ATTAACCTGCTGATGATACAGAAGCTATTGCGCAGACAAAACCTGATTAA
 TCATGGTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
 CCAACTTACTTAAATATGGTGCACAAAATTATTTAGATAgATgATGCC
 AGCCTTGGGGAAAGTATTGGTAAAGAAAAAGAAGCTAATCAGtGGGTAA
 GCCAATGGAAAACCTCTCGTGCACAAAAGATTACACCATATC
 TTAAGCCTAACACTACTTTACTATTATGGATTATGATAAAAATAT
 CTATTATGTTAATATAATTGGACGCGGtGGAgAACTAATCTATGATT

SEQUENCE LISTING

CACTAGGTTATGCTGCCAGAAAAAGTCAAAAAAGATGTCTTAAAAAA
 GGGTGGTTACCGTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTAAATATAACAAAAGCACTAAAAAAGCAGCTCATCACTTA
 AAGAAAGTGTGATGCTGGAGAAATTACAGCTGTCAAAAAAGGGCACATC
 ATAGAAAAGTAACACTACGACGTGTTTATTCTCTGACCCTCTATCTTAGA
 AGCTCAATTAAAATCATTACAAA

SEQ ID NO. 8607

STRAIN COH1

GAAGGCTTCACCTATTATG
 GAAAAATTCTGAAAATCCGAAAAAAGTAATTAATTACATATTCTTAC
 ACTGGTATTAAACTAGGTGTTAATGTTCAAGTTACAGTTAGA
 CTTAGAAAAGATAGCCCGTTTGTAAAGCAACTGAAAGAAGCTAAAAA
 AATTAACTGCTGATGATAACAGAAGCTATTGCCGACAAAAACCTGATTAA
 ATCATGGTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGC
 ACCAACTTAACTGTTAATATGGTCACAAAATTATTTAGATATGATGC
 CAGCCTTGGGAAAGTaaTTCGGTAAAGAAAAAGAAGCTAATCAGTGGGTT
 AGCCAATGGAAAACACTAAACACTCTCGCTGCCAAAAAAGATTACACCATAT
 CTTAAAGCTAACACTACTTTACTATTATGGATTTATGATAAAAATA
 TCTATTATATGGTAATAATTGGACGCGGTGGAGAACTAATCTATGAT
 TCACTAGGTTAGCTGCCAGAAAAGTCAAAAAAGATGTCTTAAAAA
 AGGGTGGTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTAAATATAACAAAACGACTAAAAAAGCAGCTTACACTT
 AAAGAAAGTGTGATGCTGGAGAAATTACAGCTGTCAAAAAAGGGCACAT
 CATAGAAAAGTAACACTACGACGTGTTTATTCTCTGACCCTCTATCTTAGA
 AGCTCAATTAAAATCATTACAAA

SEQ ID NO. 8608

STRAIN M781

GAAGGCTTCACCTATTATG
 AAAAATTCTGAAAATCCGAAAAAAGTAATTAATTACATATTCTTAC
 CTGGTATTAAACTAGGTGTTAATGTTCAAGTTACAGTTAGAC
 TTAGAAAAGATAGCCCGTTTGTAAAGCAACTGAAAGAAGCTAAAAA
 ATTAACTGCTGATGATAACAGAAGCTATTGCCGACAAAAACCTGATTAA
 TCATGGTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
 CCAACTTTAGTTATTAATATGGTCACAAAATTATTTAGATATGATGCC
 AGCCTTGGGAAAGTATTGGTAAAGAAAAAGAAGCTAATCAGTGGGTTA
 GCCAATGGAAAACACTCTCGCTGCCAAAAAAGATTACACCATATC
 TTAAAGCCTAACACTACTTTACTATTATGGATTTATGATAAAAATAT
 CTATTTATATGGTAATAATTGGACGCGGTGGAGAACTAATCTATGATT
 CACTAGGTTAGCTGCCAGAAAAGTCAAAAAAGATGTCTTAAAAAA
 GGGTGGTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 TGCCCTTGTAAATATAACAAAAGCACTAAAAAAGCAGCTTACACTTA
 AAGAAAGTGTGATGCTGGAGAAATTACAGCTGTCAAAAAAGGGCACATC
 ATAGAAAAGTAACACTACGACGTGTTTATTCTCTGACCCTCTATCTTAGA
 AGCTCAATTAAAATCATTACAAA

SEQ ID NO. 8609

STRAIN CJB110

GAAGGCTTCACCTATTATG
 AAAAATTCTGAAAATCCGAAAAAAGTAATTAATTACATATTCTTACAC
 TGGTATTAAACTAGGTGTTAATGTTCAAGTTACAGTTAGACT
 TAGAAAAAGATAGCCCGTTTGTAAAGCAACTGAAAGAAGCTAAAAA
 TTAACTGCTGATGATAACAGAAGCTATTGCCGACAAAAACCTGATTAA
 CATGGTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCAC
 CAACTTTAGTTATTAATATGGTCACAAAATTATTTAGATATGATGCCA
 GCCTTGGGAAAGTATTGGTAAAGAAAAAGAAGCTAATCAGTGGGTTAG
 CCAATGGAAAACACTAAACACTTTACTATTATGGATTTATGATAAAAATATC
 TAAAGCCTAACACTACTTTACTATTATGGATTTATGATAAAAATATC
 TATTATATGGTAATAATTGGACGCGGTGGAGAACTAATCTATGATT
 ACTAGGTTAGCTGCCAGAAAAGTCAAAAAAGATGTCTTAAAAAAAG
 GGTGGTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 GCCCTTGTAAATATAACAAAAGCACTAAAAAAGCAGCTTACACTTA
 AGAAAGTGTGATGCTGGAGAAATTACAGCTGTCAAAAAAGGGCACATCA

SEQUENCE LISTING

TAGAAAGTAAC TACGACGTGTTTATTCTCTGACCCTCTATCTTAGAA
GCTCAATTAAAATCATTACAAA

SEQ ID NO. 8610

STRAIN 1169NT

GAAGGCTTCACCTATTATGGAAAAATT
CCTGAAAATCCGAAAAAGTAATTAATTACATATTCTTACACTGGGTA
TTTATTAAAATCTGGTTAATGTTCAAGTTACAGTTAGACTTAGAAA
AAGATAGCCCCGTTTGTGTAAGCAACTGAAAGAAGCTAAAAATTAACT
GCTGATGATA CAGAAGCTATTGCCgcACAAaaACCTGATTTAATCATGGT
TTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGACCCAACCTT
TAGTTATTAAATATGGTGACAAAATTATTTAgATATGATGCCAGCCTTG
GGGAAAGTATTGGTAAAGAAAAAGaaGCTAATCAGTGGGTTAGCCAATG
GAAAACCTAAACTCTCGCTGCCAAAAAGATTTACACCATACTTAAAGC
CTAACACTACTTTACTATTATGGATTTATGATAAAAATATCTATTAA
TATGGTAATAATTGGACGCCGTTGGAGAACTAATCTATGATTCAGTAGG
TTATGCTGCCCAgAAAAAGTCAAAAAAGATGTCTTAAAAAAGGGTGGT
TTACCGTTTCgCAAGAAGCAATCGGTATTACGTGGAGATTATGCCCTT
GTAAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
TGATGTCTGGAAGAATT TACCAGCTGTCAAAAAGGGCACATCATAGAAA
GTAACTACGACGTGTTTATTCTCTGACCCTCTATCTTAGAAGCTCAA
TTAAAATCATTACAAA

SEQ ID NO. 8611

STRAIN JM9130013

GAAGGCTTCACCTATTATG
GAAAATTCCTGAAAATCCGAAAAAGTAATTAATTACATATTCTTAC
ACTGGATATTATTAAAATCTGGAGTTAATGTTCAAGTTACAGTTAGA
CTTAGAAAAGATAGCCCCGTTTGTGTAAGCAACTGAAAGGAGCTAAA
AATAACTGCTGATGATA CAGAAGCTATTGCCGACAAAACCTGATTTA
ATCATGGTTTTGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGC
ACCAACTTGTATTAAATATGGTGACAAAATTATTTAgATATGATGC
CAGCTTGGGAAAGTATTGGTAAAGAAAAAGAAGCTAATCAGTGGGTT
AGCAATGGAAAACCTAAACTCTCGCTGCCAAAAAAGATTACACCATA
CTTAAACCTAACACTACTTTACCATTATGGATTTATGATAAAAATA
TCTATTATATGGTAATAATTGGACCGGGGGAGAACTAATCTATGAT
TCACTAGTTATGCTGCCCAgAAAAAGTCAAAAAAGATGTCTTAAAAA
AGGGTGGTTACCGTTTCCgCAAGAAGCAATCGGTATTACGTGGAGATT
ATGCCCTGTTAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTT
AAAGAAAGTGTCTGGAAGAATT TACCAGCTGTCAAAAAGGGCACAT
CATAGAAAGTAAC TACGACGTGTTTATTCTCTGACCCTCTATCTTAG
AAGCTCAATTAAAATCATTACAAA

SEQ ID NO. 8612

STRAIN 2603 frame: 1

MKKIGIIVLTLTFFLVSCGQQTQESTKTTISKMPKIEGFTYYGKIPENPKVINFY
YTGYLLKLGVNVSSYSLDLEKDS PVFGKQLKEAKKLTA
INTLKKIAPTLVICKYGAQNYLDMMMPALGKVFKEKEANQWV
SQWKTQTLAACKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSL
YVGDYALVNINKTTKAASSLKE SDVWKNLPAVKGH
IESNYDVYFSDPLSLEAQLKSFT
FTKAIKENTN

SEQ ID NO. 8613

STRAIN 090 frame: 1

EGFTYYGKIPENPKVINFY SYTGYLLKLGVNVSSYSLDLEKDS PVFGKQLKEAKKLTA
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVICKYGAQNYLDMMMPALGKVFKEKEAN
QWV
SQWKTQTLAACKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSL
YVGDYALVNINKTTKAASSLKE SDVWKNLPAVKGH
IESNYDVYFSDPLSLEAQLKSFT

SEQ ID NO. 8614

STRAIN A909 frame: 1

EGFTYYGKIPENPKVINFY SYTGYLLKLGVNVSSYSLDLEKDS PVFGKQLKGAKKLTA
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVICKYGAQNYLDMMMPALGKVFKEKEAN

SEQUENCE LISTING

QWVSQWKTCTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8615

STRAIN H36B frame: 1
 EGFTYYGKIPENPKKVINFYTSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
 DDTEAIAAAQKPDLMVFDQDPNINTLKKIAPTLVIVKYGAQNYLDMMMPALGKVGKEKEAN
 QWVSQWKTCTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8616

STRAIN 18RS21 frame: 1
 EGFTYYGKIPENPKKVINFYTSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
 DDTEAIAAAQKPDLMVFDQDPNINTLKKIAPTLVIVKYGAQNYLDMMMPALGKVGKEKEAN
 QWVSQWKTCTLAVKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8617

STRAIN M732 frame: 1
 EGFTYYGKIPENPKKVINFYTSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
 DDTEAIAAAQKEDLIMVFDQDPNINTLKKIAPTLVIVKYGAQNYLDMMMPALGKVGKEKEAN
 QWVSQWKTCTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8618

STRAIN COH1 frame: 1
 EGFTYYGKIPENPKKVINFYTSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
 DDTEAIAAAQKEDLIMVFDQDPNINTLKKIAPTLVIVKYGAQNYLDMMMPALGKVGKEKEAN
 QWVSQWKTCTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619

STRAIN M781 frame: 1
 EGFTYYGKIPENPKKVINFYTSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
 DDTEAIAAAQKPDLMVFDQDPNINTLKKIAPTLVIVKYGAQNYLDMMMPALGKVGKEKEAN
 QWVSQWKTCTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620

STRAIN CJB110 frame: 1
 EGFTYYGKIPENPKKVINFYTSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
 DDTEAIAAAQKPDLMVFDQDPNINTLKKIAPTLVIVKYGAQNYLDMMMPALGKVGKEKEAN
 QWVSQWKTCTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621

STRAIN 1169NT frame: 1
 EGFTYYGKIPENPKKVINFYTSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
 DDTEAIAAAQKPDLMVFDQDPNINTLKKIAPTLVIVKYGAQNYLDMMMPALGKVGKEKEAN
 QWVSQWKTCTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622

STRAIN JM9130013 frame: 1
 EGFTYYGKIPENPKKVINFYTSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
 DDTEAIAAAQKPDLMVFDQDPNINTLKKIAPTLVIVKYGAQNYLDMMMPALGKVGKEKEAN

SEQUENCE LISTING

QWVSQWKTKTAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTKAASSLKESDVWKNLPAVKKGHIESNYDVYFSDPLSLEAQLKSFT

SEQ ID NO. 8701

STRAIN 2603

ATGAAATTATCGAAGAAGTTATTGTTTCGGCTGCTGTT
TTAACAAATGGTGGCGGGGTCACAGTGTGAACAGTAGCTCAGTTGCGACTGGAATGAGT
ATTGTAAGAGCTGCAGAAGTGTACAAGAACGCCAGCGAAAACAACAGTAAATATCTAT
AAATTACAAGCTGATAGTTATAAATCGGAAATTACTCTAATGGTGTATCGAGAATAAA
GACGGCGAAGTAATATCTAACTATGCTAACTTGGTGACAATGTAAGGTTGCAAGG
GTACAGTTAACGTTAAAGTCAGGATATTCTGTTGATGAATTGAAAAATTG
ACAACAGTTGAAGCAGCAGATGCAAGGTTGGAACGATTCTGAGAAGGTTGTCAGTCTA
CCTCAAAAACAATGCTCAAGGTTGGTGTGATGCTCTGGATTCAAAAGTAATGTG
AGATACTTGTATGAGAAGATTAAAGAATTCAACATTACCAAAGCTTATGCT
GTACCGTTGTGTTGAAATTACCAAGTGTCAACTCTACAGGTACAGGTTCTCTGAA
ATTAATATTACCCCTAAACGTTGTACTGATGAACAAAACAGATAAGATGTTAA
AAATTAGGTCAAGGACGATGCAAGGTTACGATTGGTGAAGAATTCAAATGGTCTTGAA
TCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAATTACTGATAAAATTGCA
GATGGCTTGACTTATAAATCTGTTGGAAAAATCAAGATTGGTCGAAACACTGAATAGA
GATGAGCACTACACTATTGATGAACCAACAGTTGATAACCAAAATACATTAAAAATTACG
TTAAACCAAGGAAATTAAAGGAAATTGCTGAGCTACTTAAAGGAATGACCCATTGTTAA
AATCAAGATGCTTGTATAAAGCTACTGCAAAATACAGATGATGCGGCATTGGAAATT
CCAGTTGCATCAACTATTAAATGAAAAAGCAGTTAGGAAAGCAATTGAAAATACTTT
GAACATTCAATATGACCATCTCTGATAAGCTGACAATCCTAACATCTAATCCTCCA
AGAAAACCAGAAGTTCATACTGGTGGAAAAGATTGTAAGAAAGACTCAACAGAAACA
CAAACACTAGGTGGTGCTGAGTTGATTTGTTGCTTCTGATGGGACAGCAGTAAAATGG
ACAGATGCTTTATTAAAGCGAATACTAATAAAACTATATTGCTGGAGAAGCTGTTACT
GGGCAACCAATCAAATTGAAATCACATACAGCGGTACGTTGAGATTAAAGGTTGGCT
TATGCAGTTGATGCGAATGCAAGAGGGTACAGCAGTAACCTACAAATTAAAGGAAACAAA
GCACCAAGGTTATGTAATCCCTGATAAAGAAATCGAGTTACAGTATCACAACATCT
TATAATACAAACAAACTGACATCACGGTTGATAGTGTGATGCAACACTGATACAATT
AAAAACAAACAAACGTTCTCAATCCCTAATACTGGTGGTATTGGTACGGCTATTTGTC
GCTATCGGTGTCGGTGTGGCTTTGCTGTTAAGGGGATGAAGCGTGTACAAAAGAT
AAC

SEQ ID NO. 8702

STRAIN 090

GCAGAAGTGTACAAGAACGCCAGCGAAAAC
AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATT
CTCTAATGGTGGTATCGAGAATAAAGACGCCAGTAATCTAACTAT
GCTAAACTTGGTGCACATGTAAGGTTGCAAGGTGTACAGTTAAACG
TTATAAAGTCAGACGGATATTCTGTTGATGAATTGAAAAATTGACAA
CAGTTGAAGCAGCAGATGCAAAAGTGGACGATCTTGAAGAAGGTGTC
AGTCTACCTCAAAAACATTAATGCTCAAGGTTGGTGTGATGCTCTGGA
TTCAAAAGTAATGTGAGACTTGTATGTTAGAAGATTAAAGAATTCA
CTTCAAACATTACCAAAGCTTATGCTGTACCGTTGTTGGAATTACCA
GTTGCTAACTCTACAGGTACAGGTTCTTcTGAAATTAAATTACCC
AAAAACGTTGAACTGATGAACCAAAACAGATAAGATGTTAAAAAAT
TAGGTCAAGGACGATGCAAGGTTACCGATTGGTGAAGAATTCAAATGGTTC
TTGAAATCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAAT
TACTGATAAATTGCAAGGCTTGACTTATAAATCTGTTGAAAAATCA
AGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
CCAACAGTTGATAACCAAAATACATTAAAATTACGTTAAACAGAGAA
ATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCATTGTTAAAATC
AAGATGCTCTGATAAAAGCTACTGCAAATACAGATGATGCGGCATTGG
GAAATTCCAGTTGCATCAACTATTAAATGAAAAAGCAGTTAGGAAAAGC
AATTGAAAATACTTTGAACTTCATATGACCATACTCCTGATAAGCTG
ACAATCCAAAACCATCTAATCCTCCAAGAAAACAGAAGTTCTACTGGT
GGGAAACGATTGTAAGAAAAGACTCAACAGAAACACAAACACTAGGTGG
TGCTGAGTTGATTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAG
ATGCTCTTATAAAGCGAATACTAATAAAACTATATTGCTGGAGAAGCT
GTTACTGGGCAACCAATCAAATTGAAATCACATACAGCGGTACGTTGA
GATTAAAGGTTGGCTTATGCAAGTTGATGCGAATGCGAGAGGGTACAGCAG

SEQUENCE LISTING

TAACTTACAAATTAAAAGAACAAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAACATCGAGTTACAGTATCACAAACATCTTATAATACAAAACC
 AACTGACATCACGGTGTAGTGCTGATGCAACACCTGATACAATTAAAAA
 ACAACAAACGTCCTTC

SEQ ID NO. 8703

STRAIN A909

GCAGAAGTGTACAAGAACGCCAGCGAA
 AACAAACAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTTAAAGGTTGCAAGGTGTACAGTTAA
 ACGTTATAAAGTCAAGACGGATATTCTGTTGATGAAATTGAAAAATTGA
 CAACAGTTGAAGCAGCAGTGCAGAAAGTGGAAACGATTCTGAGAAGGT
 GTCAGTCTACCTCAAAAACAAATGCTCAAGGTTGGTCGATGCTCT
 GGATTCAAAGTAATGTGAGACTATGTTGAGAAGATTAAAGAATT
 CACCTTCAAACAGTAACTTGTGAGACTATGTTGAGAAGATTAAAGAATT
 CCAGTTGCTAAGTCTACAGGTACAGGTTCTCTGAAATTAAATTTA
 CCCTAaaAACGTTGTAAGTGTGAAACCAAAACAGATAAAGATGTTAAA
 AATTAGGTCAAGGACGATGCAAGGTTATACGATTGGTAAGAATTCAAATGG
 TTCTGAAATCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGA
 AATTACTGATAAATTGCAAGATGGCTGACTTATAAATCTGTTGGAAAAA
 TCAAGATTGGTCGAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTAAACCAAAATACATTAAAAATTACGTTAAACCAGA
 GAAATTAAAGAATTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAA
 ATCAAGATGCTCTTGATAAAGCTACTGCAAAATACAGATGATGGGCATT
 TTGGAAATTCCAGTTGCACTAACTTAAATGAAAAAGCAGTTTAGGAAA
 AGCAATTGAAAATACTTTGAACTTCAATATGACCCATACTCCTGATAAAG
 CTGACAATCCAAAACCATCTAACCTCCAAGAAAACAGAAGTTCATACT
 GGTGGGAAACGATTGTTAAAGAAAGACTCAACAGAAACACAAACACTAGG
 TGGTGTGAGTTGATTGTTGGCTCTGATGGACAGCAGTAAATGGA
 CAGATGCTCTTAAAGCGAATACTAATAAAACTATATTGCTGGAGAA
 GCTGTTACTGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTT
 TGAGATTAAAGGTTGGCTTATGCAAGTTGATGCGAATGCGAGGGTACAG
 CAGTAACCTACAAATTAAAAGAACAAAAGCAGAGAAGGTTATGTAATC
 CCTGATAAAGAACATCGAGTTACAGTATCACAAACATCTTATAATACAAA
 ACCAACTGACATCACGGTGTAGTGCTGATGCAACACCTGATACAATTAA
 AAAACAACAA

SEQ ID NO. 8704

STRAIN 18RS21

GCAGAAGTGTACAAGAACGCCAGCGAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTCTAATGGTGGTATCGAGAATAAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACCTGGTACAATGTTAAAGGTTGCAAGGTGTACAGTTAAACG
 TTATAAAGTCAAGACGGATATTCTGTTGATGAAATTGAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTGGAAACGATTCTGAGAAGGTGTC
 AGTCTACCTCAAAAACAAATGCTCAAGGTTGGTCGATGCTCTGGA
 TTCAAAAAGTAATGTGAGACTTGTATGAGAAGATTAAAGAATTCA
 CTTCAACATTACCAAAGCTTATGCTGTACCGTTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTCTCTGAAATTAAATTTACCC
 TAAAAACGTTGAACTGATGAAACAAAACAGATAAAGATGTTAAATAAT
 TAGGTCAGGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAAT
 TACTGATAAATTGCAAGATGGCTTGTACTTAAATCTGTTGAAAAATCA
 AGATTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAAAATTACGTTAAACCAAGAGAA
 ATTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAATC
 AAGATGCTTTGATAAAGCTACTGCAAAATACAGATGATGCGCATTG
 GAAATTCCAGTTGCACTATTAAATGAAAAAGCAGTTTAGGAAAAGC
 ATTGAAAATACTTTGAACTTCAATATGACCATACTCCTGAAAGCTG
 ACAATCCAAAACCATCTAACCTCCAAGAAAACAGAAGTTCTACACTGGT
 GGGAAACGATTGATAAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGCTGAGTTGATTGTTGGCTTCTGATGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACATATTGCTGGAGAAGCT

SEQUENCE LISTING

GTACTGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTGA
 GATTAAAGGTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
 TAACITACAAATTAAAAGAACAAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAGAACATCGAGTTACAGTATCACAAACATCTTATAATACAAAACC
 AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8705

STRAIN M732

GCAGAAGTGTACAAGAACGCCAGCGAAAACAACAGT
 AAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTA
 ATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAA
 CTTGGTGACAATGTTGAGGTTGCAAGGTGTACAGTTAAACGTTATAA
 AGTCAAGACGGATTTCTGATGAAATTGAAAAAAATTGACAACAGTG
 AAGCAGCAGATGCAAAGGTTGGAACGATTCTGAGAAGAGGTGTCAGTCTA
 CCTCAAAAAACTAATGCTAAGGTTGGTGTGCTGATGCTGGATTCAA
 AAGTAATGTGAGATACTTGTATGAGAAGATTAAAGAATTCAACCTTCAA
 ACATTACCAAAGCTTATGCTGTACCGTTGTGTTGAAATTACCAAGTTGCT
 AACTCTACAGGTACAGGTTCCCTTCTGAAATTAAATTACCCCTAAAAA
 CGTTGAACTGATGAAACCAAAACAGATAAAGATGTTAAAAAATTAGGTC
 AGGACGATGCAAGGTTACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
 TCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAATTACTGA
 TAAATTGCACTGCTTGTACTTATAAATCTGTTGGAAAAATTCAAGATTG
 GTTCAAGAACACTGAATAGAGATGAGCACTACACTATTGATGAAACCAACA
 GTTGATAACCAAAATACATTAAACGTTAACCCAGAGAAATTAA
 AGAAAATTGCTGAGCTACTAAAGGAATGACCCCTGTTAAAATCAAGATG
 CTCTTGATAAAAGCTACTGCAAATACAGATGATGCGGCATTGGAAATT
 CCAGTTGCACTATTAAATGAAAAAGCAGTTAGGAAAGCAATTGA
 AAATACCTTGAACCTCAATATGACCATACTCCTGATAAAGCTGACAATC
 CAAACCATCTAACCTCCAAGAAAACCAGAAGTCATACTGGTGGGAA
 CGATTGAAAGAACACTCAACAGAAAACACAAACACTAGGTGGTGTG
 GTTGTGATGGCTTGTGATGGGACAGCAGTAAATGGACAGATGCTC
 TTATAAAGCGAAATCTAAATAAAACTATATTGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTGAGATTAA
 AGGTTGGCTTATGCAAGTTGATGCGAATGCAAGGGTACAGCAGTAACCT
 ACAAAATTAAAGAACAAAAGCACCAGAAGGTTATGTAATCCCTGATAAA
 GAAATCGAGTTACAGTATCACAAACATCTTATAATACAAACCAACTGA
 CATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAACAACA
 AACGTCCTTCA

SEQ ID NO. 8706

STRAIN COH1

GCAGAAGTGTACAAGAACGCCAGCGAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATT
 CTTnTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTACAATGTAAGGTTGCAAGGTGTACAGTTAAACG
 TTATAAAGCTAACAGCGATAATTCTGTTGATGAAATTGAAAAATTGACAA
 CAGTGAAAGCAGATGCAAAGGTTGGAACGATTCTGAGAAGGTTGTC
 AGTCTACCTAAAAACTAATGCTCAAGGTTGGTGTGATGCTCTGGA
 TTCAAAAGGAAATGTGAGGATACTTGTATGAGAAGATTAAAGAATTCA
 CTTCAACACATTACCAAAGCTTATGCTGTACCGTTGTGTTGAAATTCCA
 GTTGCTAACTCTACAGGTACAGGTTCCCTTCTGAAATTAAATTACCC
 TAAAAACGTTGAACTGATGAAACCAAAACAGATAAAGATGTTAAAAAAT
 TAGGTCAAGGACGATGCAAGGTTACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAAT
 TACTGATAAATTGCAAGATGGCTGACTTATAAATCTGTTGGAAAAATCA
 AGATTGGTTCGAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAAAATTACGTTAAACCAAGAGAA
 ATTAAAGAACATTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAATC
 AAGATGCTCTTGATAAAAGCTACTGCAAATACAGATGATGCGGCATTGG
 GAAATTCCAGTTGCACTATTAAATGAAAAAGCAGTTAGGAAAAGC
 AATTGAAAATACTTTGAACTTCAATATGACCATACTCCTGATAAAGCTG
 ACAATCCAAAACCATCTAACCTCCAAGAAAACCAAGAAGTTCATACTGGT
 GGGAAACGATTGAAAGAACACTCAACAGAAACACAAACACTAGGTGG

SEQUENCE LISTING

TGCTGAGTTGATTTGGCTCTGATGGACAGCAGTAAATGGACAG
 ATGCTCTTAAAGCGAATACTAATAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTGA
 GATTAAAGGTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
 TAACCTACAAATTAAAAGAACAAAAGCAGAGGTTATGTAATCCCT
 GATAAAAGAACATCGAGTTACAGTATCACAACATCTTATAATACAAAACC
 AACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAAA
 ACAACAAACGTCCTTC

SEQ ID NO. 8707

STRAIN M781

GCAGAAGTGTACAAGAACGCCAGCGAAAACAG
 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT
 TCTAATGGTGGTATCGAGAATAAGACGGCGAAGTAATATCTAACTATGC
 TAAACTGGTACAATGTAAGGTTGCAAGGTGTACAGTTAACGTT
 ATAAAGTCAGACGGATATTCTGTTGATGAAATTGAAAAATTGACAACA
 GTTGAAGCACCAGATGAAAAGTTGAAACGATTCTGAAAGAAGGTGTCA
 GTCACCTCAAAAACAACTATGCTCAAGGTTGGTCGATGCTCTGGATT
 CAAAAAGTAATGTGAGATACTTGTATGAGAAGATTAAAGAATTCAAC
 TCAACACATTACCAAAAGCTTATGCTGTACCGTTGTGTTGAAATTACAGT
 TGCTAACTCTACAGGTACAGGTTCCCTTCTGAAATTAAATTACCTA
 AAAACGTTGTAACTGATGAAACAAAAACAGATAAAAGATGTTAAAAATT
 GGTGAGCAGTGCAGTTATCGATTGGTGAAGAATTCAAATGGTTCTT
 GAAATCTACAATCCCTGCAATTAGGTGACTATGAAAATTGAAATT
 CTGATAAAATTGCAAGATGGCTTGACTTAAATCTGTTGAAAAATCAAG
 ATTGGTTGAAACACTGAATAGAGATGAGCACTACACTATTGATGAACC
 AACAGTTGATAACCAAAATACATTAAAATTACGTTAAACCAGAGAAAT
 TTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCTTGTAAAAATCAA
 GATGCTTTGATAAAAGCTACTGCAAATACAGATGATGCGGCAATTGG
 AATCCAGTTGCACTCAACTTTAATGAAAAGCAGTTTAGGAAAAGCAA
 TTGAAAATACTTTGAACTTCAATGACCATACTCCTGATAAAAGCTGAC
 AATCCAAAACCATCTAACCTCCCAAGAAAACAGAAAGTTCTACTGGTGG
 GAAACGATTGTAAGAAAGACTCAACAGAAAACCAAACACTAGGTGGTG
 CTGAGTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGAT
 GCTCTTAAAGCGAATACTAATAAAACTATATTGCTGGAGAAGCTGT
 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTGAGA
 TTAAAGGTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTA
 ACTTACAAATTAAAAGAACAAAAGCACCAGAAGGTTATGTAATCCCTGA
 TAAAGAAATCGAGTTACAGTATCACAACATCTTATAATACAAAACCAA
 CTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAAA
 ACAAAACGT

SEQ ID NO. 8708

STRAIN CJB110

GCAGAAGTGTACAAGAACGCCAGCGAA
 AACAGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATTGGAAA
 TTACTCTAATGGTGGTATCGAGAATAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTGGTACAATGTAAGGTTGCAAGGTGTACAGTTAA
 ACCTTATAAAAGTCAGACGGATATTCTGTTGATGAAATTGAAAAATTGA
 CAACAGTTGAGCAGCAGATGCAAAAGTTGGAACGATTCTGAAAGAAGGT
 GTCACTACCTCAAAAACAACTATGCTCAAGGTTGGTCGATGCTCT
 GGATTCAAAAAGTAATGTGAGATACTTGTATGAGAAGATTAAAGAATT
 CACCTCAAAACATTACCAAGCTTATGCTGTACCGTTGTGTTGAAATT
 CCAGTTGCTAACTCTACAGGTACAGGTTCTCTGAAATTAAATT
 CCCTAAAAACGTTGTAACTGATGAAACAAAACAGATAAAGATGTTAAA
 AATTAGGTCAAGGACGATGCAAGGTTACGATTGGTGAAGAATTCAAATGG
 TTCTGAAATCTACAATCCCTGCCAATTAGGTGACTATGAAAATTG
 AATTACTGATAAAATTGCAAGATGGCTGACTTATAAATCTGTTGGAAAAA
 TCAAGATTGGTCGAAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAAAATTACGTTAAACCGAGA
 GAAATTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCTTGTAAAA
 ATCAAGATGCTTTGATAAAAGCTACTGCAAATACAGATGATGCGGCAATT
 TTGGAAATTCCAGTTGCAACTATTAAATGAAAAAAGCAGTTTAGGAAA
 AGCAATTGAAAATACTTTGAACTTCAATATGACCAACTCCTGATAAAG

SEQUENCE LISTING

CTGACAATcCAAACCACATCTAATCCTCCAAGAAAACCAGAAAGTTCATACT
 GGTGGGAAACGATTGTAAGAAAGACTCAACAGAAACACAAACACTAGG
 TGGTGTGAGTTGATTGTTGGCTCTGATGGGACAGCAGTAAAATGGA
 CAGATGCTCTTAAAGCGAATACTAATAAAAACACTATATTGCTGGAGAA
 GCTGTTACTGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTT
 TGAGATTAAAGGTTGGCTTATGCAGTTGATGCCAATGCAAGAGGGTACAG
 CAGTAACCTACAAATTAAAGAAACAAAGCACCAGAAGGTTATGTAATC
 CCTGATAAAGAAATGAGTTACAGTATCACAAACATCTTATAATCCAAA
 ACCAACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTA
 AAAACAACAAACGTCCTTC

SEQ ID NO. 8709

STRAIN JM9130013

GCAGAAGTGTACAAGAACGCCAGCGAAAACAGCAGTA
 AATATCTATAAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAA
 TGGTGTGACAATGAAAAGGTTGCAAGGTGTACAGTTAACGTTATAAA
 GTCAAGACGGATATTCTGTTGATGAATTGAAAAATTGACAACAGTTGA
 AGCAGCAGATGCAAAAGTGGAACGATTCTGAAAGAAGGTGTCAGTCTAC
 CTCAAAAAACTAATGCTCAAGGTTGGTCGATGCTCTGGATTCAAAA
 AGTAATGTAAGGAACTTGATGTAGAAGATTAAAGAATTACACCTTCAAA
 CATTACCAAAGCTTATGCTGTACCGTTGTTGGAAATTACAGTTGCTA
 ACTCTACAGGTTACAGGTTCTCTGAAATTAAATTACCCCTAAAAAC
 GTTGTAACTGATGAACCAAAACAGATAAAAGATGTTAAAATTAGGTCA
 GGACGATGCAAGGTTACAGATTGGTAAGAATTCAAATGGTCTTGAAAT
 CTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAATTACTGAT
 AAATTGCGAGATGGCTTGAATTGACTTATAAATCTGTTGGAAAATCAAGATTGG
 TTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACCAACAG
 TTGATAACCAAAACATATAAAATTACGTTAACACCAGAGAAATTAAA
 GAAATTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAAGATGC
 TCTTGATAAAAGCTACTGCAAATACAGATGATGCCGCAATTGTTGGAAATTTC
 CAGTTGCACTCAACTATTAAATGAAAAGCAGTTTAGGAAAAGCAATTGAA
 AATACTTTGAACTTCAATGACCAACTCTGATAAAAGCTGACAATCC
 AAAACCATCTAATCCTCAGAAAACAGAACAGAAAGTCTACTGGTGGGAAAC
 GATTGTAAGAAAGACTCAACAGAACACAAACACTAGGGTGTGCTGAG
 TTTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTCT
 TATTAAAGCAATACTAAATTAAACTATATTGCTGGAGAAGCTGTTACTG
 GGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTGAGATTAA
 GTTGTGTTGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCTA
 CAAATTAAAAGAAACAAAGCACCAGAAGGTTATGTAATCCCTGATAAAAG
 AAATCGAGTTACAGTATCACAAACATCTTATAATACAAAACCAACTGAC
 ATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAACAACAA
 ACGTCCTTC

SEQ ID NO. 8710

STRAIN 2603 frame: 1

MKLSKKLLFSAAVLMVAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTVN1YKLQADSY
 KSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYKVKTDISVDELKKLTTVEAAD
 AKVGTILEEGVSLPQKTNQGLVVDALDSKSNSVRYLYVEDLKNSPSNITKAYAVPFVLEL
 PVANSTGTGFLSEINIPKNVVTDEPKTDKDVKKLGQDDAGYTIGEEFKWFLKSTIPANL
 GDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQNTLKITFKPEKFK
 EIAALLKGMTLVKNQDALDKATANTDDAAFLEIPVASTINEKAVLGKAIENTFELQYDHT
 PDKADNPKPNSPPRKPEVHTGGKRFVKKDSTETQTLGGAEFDLLASDGTAVKWTDALIKA
 NTMKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVI
 PDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPNTGGIGTAIFVAIGAAM
 AFAVKGMKRTKDN

SEQ ID NO. 8711

STRAIN 090 frame: 1

AEVSQERPAKTTVN1YKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNQGLVVDALDSKSNSVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIPKNVVTDEPKTDKDVKKLGQ
 DDAGYTIGEEFKWFLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS

SEQUENCE LISTING

TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8712

STRAIN 18RS21 frame: 1
 AEVSQERPAKTAVNIIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKLGQ
 DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8713

STRAIN M732 frame: 1
 AEVSQERPAKTTVNIIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKLGQ
 DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8714

STRAIN M781 frame: 1
 AEVSQERPAKTAVNIIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKLGQ
 DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 R

SEQ ID NO. 8715

STRAIN COH1 frame: 1
 AEVSQERPAKTAVNIIYKLQADSYKSEITXNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKLGQ
 DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8716

STRAIN CJB110 frame: 1
 AEVSQERPAKTAVNIIYKLQADSYKLEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKLGQ
 DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQUENCE LISTING

SEQ ID NO. 8717

STRAIN JM9130013 frame: 1

AEVSQERPAKTAVNIIYKIQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVTILEEGVSLPQKTNQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIPKVNVTDEPKTDKDVKKLGQ
 DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNN
 RPS

SEQ ID NO. 8718

STRAIN A909 frame: 1

AEVSQERPAKTTVNIYKIQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVTILEEGVSLPQKTNQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIPKVNVTDEPKTDKDVKKLGQ
 DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNN

SEQ ID NO. 8801

STRAIN 2603

ATGCCTAACGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTCTAACGGAATGGCAA
 AAGCGTAACCTTGAATTAAAAACGAAAGAAGATGAAGAAGAACACAAAACGTATT
 AACGAAAATACGTTAGATAAAAGAAGTAAATTAAATTTCTCTGAAGAACCT
 CAAAATACTAAATTAAAGAAGCTTCAAGCTTCAAGACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAGCTTAGCCTAAACTATCGCATTAGAACT
 GCACCTTATTTGTAGTAGCATTCTAGTCATTAGTTCCGTTCTACTAACCT
 TTTAGTAAGCAAAACATAACAGTTAGTGGAAATCAGCATACACCTGATGATATTG
 ATAGAGAAAACGAATTACCAAAACGATTATTCTTTCTTAAATTAAACATAAA
 GCTATTGAACAACGTTAGCTGCAGAAGATGTAGGGTAAAAACAGCTCAGATGACTTAT
 CAATTCTCAATAAGTTCAATTCAAGTTCAAGAAAATAAGATTATTGCATATGCACAT
 ACAAAAGCAAGGATATCAACCTGCTTGGAAACTGGAAAAAGGCTGATCCTGAAATAGT
 TCAGAGCTACCAAGCATTCTAACATTAACTGATAAGGAAGATAAGTATTAGCTA
 TTAATTAAAGATTAAAGGCTTATGACCCCTGATTAAAGTGGAGATTCAAGGTGATAAGT
 TTAGCTGATTCTAAACGACACCTGACCTCTGCTGTTAGATATGCACGATGGAAATAGT
 ATTAGAATACCTTATCTAAATTAAAGAAGACTTCTTTTACAAACAAATTAAAGAAG
 AACCTTAAGGAACCTCTATTGTTGATATGGAAGTGGGAGTTACACAAACAAATACC
 ATTGAATCAACCCCTGTTAAAGCAGAAGATAACAAAATAACTCAAAACTAAT
 ACACAAAATGGTCAGGTTGCGGAAATAGTCAGGACAAACAAATACTCAAATACTAAT
 CAACAAGGACAACAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8802

STRAIN H36B

CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTT
 GTCTAACGGAATGGCAAAGCGTAACCTTGAATTAAAAACGCAA
 AGAAGATGAAGAAGAACAAAACGTATTAAACGAAAATTACGCTTAGATA
 AAAAGTAATTAAATATTCTCTGAAGAACCTCAAAATACTACT
 AAAATTAAAGAAGCTTCAATTCTCAAGATTTCAAGACCTAAGATTGAAA
 GAAACAGAAAAAGAAAAATAGTCACAGCTTAGCCTAAACTATCGCA
 TTAGAACTGCACCTATATTGTAGTAGCATTCTAGTCATTAGTTCC
 GTTTCTACTAACCTCTTGTAGTAAGAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTGATAGAGAAAAGAATATTCAA
 AAAACGATTATTCTTCTTAAATTAAACATAAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTAGGGTAAAAACAGCTCAGATGACTTATCA
 ATTCTCAATAAGTTCAATTCAAGTTCAAGAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGCTTGGAAACTGGAAAAAG
 GCTGATCCTGAAATAGTCAGAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAAGATTAAAGGCTT
 TAGACCCCTGATTTAATAAGTGGAGATTCAAGGTGATAAGTTAGCTGATTCT

SEQUENCE LISTING

AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCAATTCTAAATTAAAGAAAGACTCCCTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAAACAAATACCAATTGAATCAACCCCTGTTAAAGCAGAAGATA
 AAAAAAATAAATCAACTGATAAAACACAACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCCCTCAAATGTTAAT

SEQ ID NO. 8803

STRAIN 18RS21

CCTAAGAACAAATCAGATACCCCAGAAAAAGAACAGTT
 GTCTTAACGGATGGCAAAAGCGTAACCTGAAATTAAAAACGCAA
 AGAAGATGAAGAACAAACAAACGTTAACGAAAAATTACGCTTAGATA
 AAAAGAGTAATTAATTTCTCTCTGAAAGAACCTCAAATAACTACT
 AAAATTAAGAAGCTTCATTTCAAAGATTCAAGACCTAACGATTGAAAA
 GAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACAAATCGCA
 TTAGAACCTGACCTATATTGTTAGTAGCATTCTAGTCATTAGTTCC
 GTTTCTACTAACCTCTTTAGTAAGAAAAACAAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGATAGAGAAAAGAATATTCAA
 AAAACGATTATTCCTTTCTTTAAACATAAAAGCTATTGAAACAA
 CGTTAGCTGAGAACAGATGTTAGGGTAAACAGCTCAGATGACTTATCA
 ATTCCAAATAAGTTCTATTCAGTTAACGAAAAAAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGCTCTGGAAAAG
 GCTGATCCTGAAATAGTCAGAGCTACCAAAGCACTTCTAACAAATTAA
 CCTTGATAAGAACAGATGTTAGCTAACGTTAACGATTAAAGGCTT
 TAGACCCCTGATTTAAATAAGTGGATTCAGGTGATAAGTTAGCTGATTCT
 AAAACGACACCTGACCTCTGCTGTTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTAAAGAAAGACTCCCTTTACAAACAAA
 TTAAGAACCTTAAGGAACCTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAAACAAATACCAATTGAATCAACCCCTGTTAAAGCAGAAGATA
 AAAAAAATAAATCAACTGATAAAACACAACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCCCTCAAATGTTAAT

SEQ ID NO. 8804

STRAIN M732

CCTAAGAACAAATCAGATACCCCAGAAAAAGAACAG
 TTGCTTAACGGATGGCAAAAGCGTAACCTGAAATTAAAAACGC
 AAAAGAGATGAAGAACAAACAAACGTTAACGAAAAATTACGCTTAGA
 TAAAAGAGTAATTAATTTCTCTCTGAAAGAACCTCAAATACTA
 CTAAATTAAGAAGCTTCATTTCAAAGATTCTAACCTAACGATTGAA
 AAGAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACAAATCG
 CATTAGAACCTATATTGTTAGTAGCATTCTAGTCATTAGTT
 CCGTTCTACTAACCTTTAGTAAGCAAAAACAAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTGATAGAAAAACAAATATTCA
 AAAAAACGATTATTCCTTTCTTAATTTAAACATAAAAGCTATTGAAAC
 AACGTTAGCTGAGAACAGATGTTAGGGTAAACAGCTCAGATGACTTAT
 CAAATTCCAAATAAGTTCTATTCAGTTAACGAAAAATAAGATTATTGC
 ATATGCACATACAAAGCAAGGATATCAGCCTGCTTGGAAAAG
 AGGCTGATCCTGAAATAGTCAGAGCTACCAAAGCATTCTAACAAATT
 AACCTGATAAGGAAGATGTTAGCTAACGTTAACGATTAAAGATTAAAGGC
 TTTAGACCTGATTTAAATAAGTGGATTCAGGTGATAAGTTAGCTGATT
 CTAACACGACACCTGACCTCTGCTGTTAGATATGCATGATGGAAATAGT
 ATTGAAATACCATTATCTAAATTAAAGAAAGACTCCCTTTACAAACA
 AATTAAGAACCTTAAGGAACCTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAAAGTACTATTGAATCAACCCCTGTTAGGGAAAGAT
 ACAAAAAATAATCAACTGATAAAACACAACAAAATGGTCAGGTTGC
 GGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCCCTCAAATGTTAAT

SEQ ID NO. 8805

STRAIN COH1

CCTAAGAACAAATCAGATACCCCAGAAAAAGAACAGTT
 GTCTTAACGGATGGCAAAAGCGTAACCTGAAATTAAAAACGCAA

SEQUENCE LISTING

AGAAGATGAAGAACAAAACGTTAACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAAATTTCTCTGAAGAACCTCAAAATACTACT
 AAAATTAAAGAAGCTTCATTTCCAAGATTCAACAGCTAGCCAAAACCTAAGATTGAAA
 GAAACAGAAAAAAAGAAAAAAATAGTCACAGCTAGCCAAAACCTAATCGCA
 TTGAACTGCACCTATATTGTAGTAGCATTCTAGTCATTAGTTCC
 GTTTCTACTAACTCCTTTAGTAAGCAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTGTAGAAGAAAACGAAATATTCAA
 AAAACGATTATTCTTTCTTAATTAAACATAAGCTATTGAACAA
 CGTTAGCTGCAGAAGATGTATGGGAAAAACAGCTCAGATGACTTATCA
 ATTCCCAATAAGTTCATATTCAAGTTCAAGAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAGCCTGCTGGAAACTGGAAAAAG
 GCTGATCCTGAAATAGTCAGAGCTACCAAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAAGATTAAAGGCTT
 TAGACCTGATTTAATAAGTGGAGATTCAAGGTGATAAGTTAGCTGATTCT
 AAAACGACACTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGTAT
 TAGAATACCAATTCTAAATTAAAGAAAGACTCCTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTCTATTGTTGATATGAAAGTGGGAGTT
 TACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATAC
 AAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGC
 AAAATAGTCAGGACAAACAAATACTCAAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCCACCCCTCAAAATGTTAAT

SEQ ID NO. 8806

STRAIN M781

CCTAAGAACAAATCAGATAACCCAGAAAAAGAACAG
 TTGCTTAACGGAATGGCAAAAGCGTAACCTTGAAATTAAAGAACGC
 AAAGAAGATGAAGAACAAAACGTTAACGAAAAATTACGCTTAGA
 TAAAAGAAGTAAATTAAATTTCTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAAGAAGCTTCATTTCCAAGATTCAAAACCTAAGATTGAA
 AAGAACAGAAAAAGAAAAATAGTCACAGCTAGCCAAAACCTAATCG
 CATTAGAACCTGACCTATATTGTAGTAGCATTCTAGTCATTAGTT
 CCGTTTCTACTAACTCCTGCTGTTAGATATGCATGATGGAAATAGT
 GGAAATCAGCATACACCTGATGATATTGTAGAAGAAAACGAAATATTCA
 AAAAACGATTATTCTTTCTTAATTAAACATAAGCTATTGAAC
 AACGTTAGCTGCAGAAGATGTATGGTAAAAACAGCTCAGATGACTTAT
 CAATTCCCAATAAGTTCATATTCAAGTTCAAGAAAATAAGATTATTGC
 ATATGCACATACAAAGCAAGGATATCAGCCTGCTGGAAACTGGAAAAA
 AGGCTGATCCTGAAATAGTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAAAGCTATTAAAGATTAAAGC
 TTTAGACCTGATTTAATAAGTGAGATTCAAGGTGATAAGTTAGCTGATT
 CTAAACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
 ATTGAAATACCAATTCTAAATTAAAGAAAGACTCCTTTACAAACA
 AATTAAAGAACCTTAAGGAACCTCTATTGTTGATATGAAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGC
 GGAAAATAGTCAGGACAAACAAATACTCAAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCCCTCAAAATGTTAAT

SEQ ID NO. 8807

STRAIN CJB110

CCTAAGAACAAATCAGATAACCCAGAAAAAGAACAG
 TTGCTTAACGGAATGGCAAAAGCGTAACCTTGAAATTAAAGAACGC
 AAAGAAGATGAAGAACAAAACGTTAACGAAAAATTACGCTTAGA
 TAAAAGAAGTAAATTAAATTTCTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAAGAAGCTTCATTTCCAAGATTCAAAACCTAAGATTGAA
 AAGAACAGAAAAAGAAAAATAGTCACAGCTAGCCAAAACCTAATCG
 CATTAGAACCTGACCTATATTGTAGTAGCATTCTAGTCATTAGTT
 CCGTTTCTACTAACTCCTTTAGTAAGCAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTGTAGAAGAAAACGAAATATTCA
 AAAAACGATTATTCTTTCTTAATTAAACATAAGCTATTGAAC
 AACGTTAGCTGCAGAAGATGTATGGTAAAAACAGCTCAGATGACTTAT
 CAATTCCCAATAAGTTCATATTCAAGTTCAAGAAAATAAGATTATTGC
 ATATGCACATACAAAGCAAGGATATCAGCCTGCTGGAAACTGGAAAAA
 AGGCTGATCCTGAAATAGTCAGAGCTACCAAAGCACTTCTTAACAATT

SEQUENCE LISTING

AACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTAAAGGC
 TTAGACCTGATTTAATAAGTGAGATTCAAGGTGATAAGTTAGCTGATT
 CTAACGACACCTGACCTCCTGCTTAGATATGCGATGATGGAAATAGT
 ATTAGAATACCAATTCTAAATTAAAGAAAGACTTCCTTTACAAACA
 AATTAAGAAGAACCTTAAGGAACCTCTATTGTGATATGGAAGTGGGAG
 TTACACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAAAATAATCAACTGATAAAACACAAACACAAATGGTCAGGTTGC
 GGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCCCTCAAAATGTTAAT

SEQ ID NO. 8808

STRAIN 1169NT

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGT
 TGTCTTAACGGAATGGAAAAGCGTAACCTGAAATTAAAAACGCA
 AAGAAGATGAAGAAGAACAAAACGTATTAACGAAAATTACGCTTAGAT
 AAAAGAAGTAAATTAAATATTCTCTCCTGAAGAACCTCAAATACTAC
 TAAAATTAAAGAAGCTTCATTTCAAAGATTCAAAACCTAAGATTGAA
 AGAAACAGAAAAAGAAAAATAGTCACAGCTAGCCAAACTAACGC
 ATTAGAACTGCACCTATTTATAGTAGCATTCTAGTCATTAGTTTC
 CGTTTCTACTAACTCCTTTAGTAAGCAAAAAACATAACAGTTAGTG
 GAAATCAGCATACACCTGTGATGATATTGTAGAGAAGAAACGAAATTCAA
 AAAACGATTATTTCTTTCTTAATTAAACATAAGCTATTGAACA
 ACGTTTAGCTGAGATGTATGGTAAAAACAGCTCAGATGACTTATC
 AATTCCCAACAAGTTCATATTCAAGTTCAAGAAAATAAGATTATTGCA
 TATGCACATACAAAGCAAGGATATCAGCCTGCTTGGAAACTGGAAAAA
 GGCTGATCCTGAAATAGTCAGAGCTACCAAAGCATTCTTAACAATT
 ACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTAAAGGCT
 TTAGACCCCTGATTTAATAAGTGAGATTCAAGGTGATAAGTTAGCTGATT
 TAAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTA
 TTAGAATACCATATTCTAAATTAAAGAAAGACTCCTTTACAAACAA
 ATTAAGAAGAACCTTAAGGAACCTCTATTGTGATATGGAAGTGGGAGT
 TTACACAACAACAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATA
 CAAAAAATAATCAACTGATAAAACACAAACCCAAATGGTCAGGTTGCG
 GAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACA
 ACAACAGATAGCAACGGAGCAGGCACCCACCCCTCAAAATGTTAAT

SEQ ID NO. 8809

STRAIN JM9130013

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGT
 GTCTTAACGGAATGGAAAAGCGTAACCTGAAATTAAAAACGCA
 AAGAAGATGAAGAAGAACAAAACGTATTAACGAAAATTACGCTTAGATA
 AAAGAAGTAAATTAAATATTCTCTCCTGAAGAACCTCAAATACTAC
 AAAATTAAAGAAGCTTCATTTCAAAGATTCAAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAATAGTCACAGCTAGCCAAACTAACGCA
 TTAGAACTGCACCTATATTGTAGTAGCATTCTAGTCATTAGTTCC
 GTTTCTACTAACTCCTTTAGTAAGCAAAAACATAACAGTTAGTGG
 AAATCAGCATACACCTGTGATGATATTGTAGAGAAGAAACGAAATTCAA
 AAAACGATTATTTCTTTAATTAAACATAAGCTATTGAACAA
 CGTTTAGCTGAGATGTATGGTAAAAACAGCTCAGATGACTTATCA
 ATTCCCAATAAGTTCATATTCAAGTTCAAGAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGCTTGGAAACTGGAAAAAG
 GCTGATCCTGAAATAGTCAGAGCTACCAAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTAAAGGCTT
 TAGACCCCTGATTTAATAAGTGAGATTCAAGGTGATAAGTTAGCTGATT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATATTCTAAATTAAAGAAAGACTTCCTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTCTATTGTGATATGGAAGTGGGAGTT
 TACACAACAACAAATACCAATTGAATCAACCCCTGTAAAGCAGAAGATA
 AAAAAATAATCAACTGATAAAACACAAACAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATACTCAAATACTAATCAACAAGGACA
 CAGATAGCAACAGAGCAGGCACCTAACCCCTCAAAATGTTAAT

SEQ ID NO. 8810

STRAIN A909

SEQUENCE LISTING

CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTC
 TTAACGGAATGGCAAAGCGTAACCTTGAATTAAaAAAAACGCAAAGA
 AGATGAAGAAGAaCAAAAACGTATTAACGAAAAATTACGTTAGATAAAA
 GAAGTAAATTAAATATTCTCTCCTGAAGAACCTCAAATACTACTAA
 ATTAAAGAGCTCATTTCCTCAAAGATTCAAGACCTAAAGATTGAAAAGAA
 ACAGAAAAAGAAAAATAGTCACAGCTTAGCCTAGTCATTAGTTCCGTT
 GAACTGCACCTATATTGTTAGCATTCCTAGTCATTAGTTCCGTT
 TTCCCTACTAACTCCTTTAGTAAGCAAAAACAATAACAGTTAGTGGAAA
 TCAGCATAACACCTGATGATATTGATAGAGAAAACGAATATTCAAAAAA
 ACGATTATTCTTTCTTTAAACATAAAAGCTATTGAACAACGTT
 TTAGCTGCAGAAGATGTATGGTAAAAACAGCTCAGATGACTTATCAATT
 TCCAATAAGTTICATTAACGTTCAAGAAAATAAGATTATTGCATATG
 CACATCAAAGCAAGGGATATCAACCTGCTTGGAAAAGCTGGAAAAAGGCT
 GATCCTGTAATAGTTCAGAGCTACCAAGGCATTCTTAACAATTAAACCT
 TGATAAGGAAGAGTAGTATTAAAGCTATTAAAGATTTAAAGGCTTTAG
 ACCCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTAGCTGATTCTAA
 ACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAAATAGTATTAS
 AATACCATTATCTAAATTAAAGAAAGACTTCCTTTTACAACAAATTAA
 AGAAGAACCTAAGGAACCTCTATTGTTGATATGGAAGTGGAGTTAC
 ACAACAAACAAATACCATTGAATCAACCCCTGTTAAGCAGAAGATAACAA
 AAATAAAATCAACTGATAAAACACAAmCACAAATGGTCAGGTTGCGGAAA
 ATAGTCAGGACAAACAAACTCAAATACTAATCAACAAGGACAACAG
 ATAGCAACAGAGCAGGCACCTAACCCCTAAATGTTAAT

SEQ ID NO. 8811

STRAIN 090

TAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTCCTAACGGAAT
 GGCAAAGCGTAACCTTGAATTAAAGGCAAAGAAGATGAAGAA
 GAACAAAAGCTATTAACGAAAATTACGTTAGATAAAAGAAGTaaTT
 AAATATTCTCTCCTGAAGAACCTCAAATACTACTAAATTAAAGAAGC
 TTCAATTCCAAAGATTCAACCTCAAAGGAAAAGAAACAGAAAAAA
 GAAAAAAATAGTCACAGCTTAGGCAAACACTAACGCTTACGATTAGCACC
 TATATTGTTAGTAGCATTCTAGTCATTAGTTCCGTTTCCTACTAA
 CTCCCTTTAGTAAGCAAAAACAATAACAGTTAGTGGAAAATCAGCATA
 CCTGATGATATTGATAGAAAAACGAATATTCAAAAAACGATTATT
 CTTTCTTTAAATTAAACATAAAAGCTATTGAACAACGTTAGCTGCAG
 AAGATGTTAGGGTAAACAGCTCAGATGACTTATCAATTCCAAATAAG
 TTTCATATTCAAGTTCAAGAAAATAAGATTATTGCATATGCACATA
 GCAAGGGATATCAGCCTGTTGGAAAAGCTGGAAAAAGGCTGATCCTGTA
 ATAGTTAGCAGCTACCAAAAGCACTTCTTAACAATTAAACCTTGTATAAGGAA
 GATAGTATTAAAGCTATTAAAGATTAAAGGCTTTAGACCCCTGATT
 AATAAGTGGAGATTCAAGGTGATAAGTTAGCTGATTCTAAACGACACCTG
 ACCTCCTGCTGTTAGATATGCATGATGGAAAATAGTATTAGAATA
 TCTAAATTAAAGAAAGACTTCCTTTACAACAAATTAAAGAAGAACCT
 TAAGGAACCTCTATTGTTGATATGGAAGTGGGAGTTACACAACAA
 GTACTATTGAATCAACCCCTGTAAGCAGGAAAGATAACAAAAATAATCA
 ACTGATAAAACACAAACACAAATGGTCAGGTTGCGGAAAATAGTCAGG
 ACAACAAATAACTCAAATACTAATCAACAAGGACAACAGATAGCAACAG
 AGCAGGACCCACCCCTCAAATGTTAAT

SEQ ID NO. 8812

STRAIN 2603 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKEDEEEQKRINEKLRLDKRSKLN
 NTTKIKKLHFPKISRPKIEKKQKEKIVNSLAKTNRIRTAIFVVAFLV
 ILVSFLLPF SKQKTTIVSGNQHTPDDILIEKTNQKNDYFFSLIFKH
 KAIEQRLAEDVWVKTQMTYQ FPNKFHIQVQENKIIAYAHTKQGY
 QPVLETGKKADPVNSSELPKHFLTINLDKEDSI
 KLLIKDLKALDPDLISEIQLVSLADSKTPDLLLLMDHDGNSIRIPLSK
 FKERLPFYKQIKKN LKEPSIVDMEVGVYTTNTIESTPVKAEDTK
 KNKSTDKTQTQNGQVAENSQGQTNNSNTNQ QQQIATEQAPNPQ
 QNVN

SEQ ID NO. 8813

STRAIN H36B frame: 1

PKKKSDTPEKEEVVLTEWQKRNLFLKKEDEEEQKRINEKLRLDKRSKLN
 NTTKIKKLHFPKISRPKIEKKQKEKIVNSLAKTNRIRTAIFVVAFLV
 ILVSFLLPF

SEQUENCE LISTING

SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRQLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTNTIESTPVKAEDTKNKSTDQTQNGQVAENSQGQTNNNSNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8814

STRAIN 18RS21 frame: 1
 PKKSDTPEKEEVVLTEWQKRNLIFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRQLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTNTIESTPVKAEDTKNKSTDQTQNGQVAENSQGQTNNNSNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8815

STRAIN M732 frame: 1
 PKKSDTPEKEEVVLTEWQKRNLIFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRQLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTNTIESTPVKAEDTKNKSTDQTQNGQVAENSQGQTNNNSNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8816

STRAIN COH1 frame: 1
 PKKSDTPEKEEVVLTEWQKRNLIFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRQLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTNTIESTPVKAEDTKNKSTDQTQNGQVAENSQGQTNNNSNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8817

STRAIN M781 frame: 1
 PKKSDTPEKEEVVLTEWQKRNLIFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRQLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTNTIESTPVKAEDTKNKSTDQTQNGQVAENSQGQTNNNSNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1
 PKKSDTPEKEEVVLTEWQKRNLIFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRQLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTNTIESTPVKAEDTKNKSTDQTQNGQVAENSQGQTNNNSNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1
 PKKSDTPEKEEVVLTEWQKRNLIFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRQLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTNTIESTPVKAEDTKNKSTDQTQNGQVAENSQGQTNNNSNTNQ

SEQUENCE LISTING

QGQQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNIRTAIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRЛАEDVVVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTNTIESTPVKAEDTKNKSTDKTQTNQVAENSQGQTNNNSNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNIRTAIFVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRЛАEDVVVKTAQMTYQ
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTNTIESTPVKAEDTKNKSTDKTQTNQVAENSQGQTNNNSNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEPON
 TTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNIRTAIFVVAFLVILVSVFLLTPFS
 KQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRЛАEDVVVKTAQMTYQF
 FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLLI
 KDLKALDPDLISEIQVISLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKNL
 KEPSPIVDMEVGVTNTIESTPVKAEDTKNKSTDKTQTNQVAENSQGQTNNNSNTNQO
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8901

STRAIN 2603

ATGAAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTACGTAA
 TATAAATTGGTTAGCATCGTAATTAGGTCATTCAATGGTCACAAGTCCTGTT
 TTGCGGATCAAACATACCGGTTCAAGTTAAATACAGACAGGCACTAGTGTGGATGCT
 AATAATTCTCCAATGAGACAAGTGGCTCAAGTGTGATTACTTCCAATAATGATAGTGT
 CAAGCGTCTGATAAAGTTGAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCATGGTGGAAAAACATTACCTGAAACAAGGGAAATTATGTTTAT
 AGCAAAGAAACCGAGGTGAAAAAATACACCTTCAAATCAGCCCCAGTAGCTTCTATGCA
 AAGAAAGGTGATAAAGTTCTATGACCAAGTATTAAATAAGATAATGTGAAATGGATT
 TCATATAAGTCTTTGTGGCGTACGTCGATACCGAGCTATTGAGTCACTAGATCCATCA
 GGAGGTTAGAGACTAAAGCACCTACTCCTGTAACAAATTAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTATACATTTCACATAAAAGTAGAAGTAAAAAAATGAAGCT
 AAGGTAGCGAGTCCAACCTAAATACATTGGACAAAGGAGACAGAATTTCACCGACCAA
 ATACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAAATCATTCAATGGTGTGCGT
 TTTGTTTGCTAGGAAAGCATCTTCAGTAGAAAAAAACTGAAGATAAAGAAAAAGTGTCT
 CCTCAACCACAAGCCGTATTACTAAACTGGTAGACTGACTATTCTAACGAAACAAC
 ACAGGTTTGATTTAAATTACGAATATTAAAGATGATAACGGTATCGCTGTTAAG
 GTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATTAAATGGTACAGCTGTAAC
 ACTGGGGATGCGCAACTACAAAGTAGCTGTATCATTGCTGACCATAAGAATGAGAAGGGT
 CTTTATAATATTCACTTAACTACCAAGAAGCTAGTGGGACACTGTAGGTGTAACAGGA
 ACTAAAGTGCAGTAGCTGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTAGCA
 AAGACTGGTGTATATAATTATCGGAAGTACTGAAGTAAAAAAATGAAGCTAAATATCA
 AGTCAGACCCAATTACTTAAAGGAGTACAGTGGACAAAAATAATTATGATCAAGTATTGACA
 GCAGATGGTTACCGAGTGGATTCTTACAAATCTTACTGTGGTGTGCGCTATATTCT
 GTGAAAAAGCTAACTACAAGTAGTGAAGGAGTGGAGCAGACTAAACCGACTAGT
 TATCCCAACTTACCTAAACAGGTACCTATACATTACTAAACTGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTAAATTCAAAAGGGTGAAAAAAATCATTAT
 GATCAAGTGTAGTAGATGGTCATCAGTGGATTTCATACAAGAGTTATTCCGGTATT
 CGTCGCTATATTGAAATT

SEQ ID NO. 8902

SEQUENCE LISTING

STRAIN 090

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAATATAAAATTGGTTAGCATCAGTAATTAGGGTCATT
 ATAATGGTCACAAGTCCTGTTTGCAGATCAAACATCGGTTCAAGT
 TAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTCCAATGAGA
 CAAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCT
 GATAAAAGTTGAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTAGTAGAGACAAAGCCAATGGTGAAAAAACATTACCTGAACAAGGG
 ATTATGTTATAGCAAAGAACCGAGGTGAAAATACACCTCAAAATCA
 GCCCCAGTAGCTTCTATGCAAAGAACGGTGTAAAGTTCTATGACCA
 AGTATTAAATAAGATAATGTGAAATGGATTTCATATAAGTCTTTGTG
 GCCTACGTCGATAACGCAGCTATTGAGTCAGTACAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCTGTAACAAATTCAAGGAAGCAATAATCAAGA
 GAAAATAGCAACGCAAGGAAATTATACATTTCACATAAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCAACTCAATTACATTGGACAAAGGA
 GACAGAATTTCACGACCAAAACTAATTGAAGGAAATCAGTGGTT
 ATCTTATAATCATTCAATGGTGTTCGTTGTTTGCTAGGTAAAG
 CATCTTCAGTAGAAAAACTGAAGATAAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAACTGGTAGACTGACTATTCTAACGAAACAAAC
 TACAGGTTTGATATTAAATTACGAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTGGACTGAAACAAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGAACTACTGGGATGGCAACTACAAAGTAGCTGT
 ATCATTGCTGACCATAAGAATGAGAAGGGTCTTATAATATTCAATT
 ACTACCAAGAAGCTAGTGGACACTTGTAGGTGTAAACAGGAACAAAGTG
 ACAGTAGCTGGAACTAATTCTCTCAAGAACCTATTGAAAATGGTTAGC
 AAAGACTGGTTATAATTATCGGAAGTACTGAAGTAAAAATGAAG
 CTAAAATATCAAGTCAGACCCAATTACTTTAGAAAAGGTGACAAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTACCGAGTGGATTCTTACAA
 ATCTTATAGTGGTGTTCGCTATATTCTGTGAAAAAGCTAATTACAA
 GTAGTAAAAAGCGAAATGAGGCGACTAAACCGACTAGTATCCCAAC
 TTACCTAAACAGGTACCTATACATTACTAAACTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTAAATTTCAAAAGGGTGA
 AAATACATTATGATCAAGTGTAGTAGTACTGATGGTCATCAGTGGATTCA
 TACAAGAGTTATTCCGGTATTGCTGCTATATTGAAAATT

SEQ ID NO. 8903

STRAIN A909

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTAC
 TCTCTACGTAATATAAAATTGGTTAGCATCAGTAATTAGGGTCATT
 CATAATGGTCACAAGTCCTGTTTGCAGATCAAACATCGGTTCAAG
 TTAAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTCCAATGAG
 ACAACTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTC
 TGATAAAAGTTGAAATAGTCAAAATACGGCAACAAAGGACATTACTACTC
 CTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGG
 AATTATGTTATAGCAAAGAACCGAGGTGAAAATACACCTCAAAATC
 AGCCCCAGTAGCTTCTATGCAAAGAACGGTGTAAAGTTCTATGACC
 AAGTATTAAATAAGATAATGTGAAATGGATTTCATATAAGTCTTTGT
 GGGCTACGTCGATAACGCGACTATTGAGTCAGTACAGATCCATCAGGAGGTT
 AGAGACTAAAGCACCTACTCTGTAACAAATTCAAGGAAGCAATAATCAAG
 AGAAAATAGCAACGCAAGGAAATTATACATTTCACATAAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCAACTCAATTACATTGGACAAAGG
 AGACAGAATTTCACGACCAAAACTAATTGAAGGAAATCAGTGGT
 TATCTTATAATCATTCAATGGTGTTCGTTGTTTGCTAGGTAAAG
 GCATCTTCAGTAGAAAAACTGAAGATAAAAGAAAAAGTGTCTCCTCAACC
 ACAAGCCCGTATTACTAAACTGGTAGACTGACTATTCTAACGAAACAA
 CTACAGGTTTGATATTAAATTACGAATATTAAAGATGATAACGGTATC
 GCTGCTGTTAAGGTACCGGTTGGACTGAAACAAGGAGGGCAAGATGATAT
 TAAATGGTATACAGCTGAACTACTGGGGATGGCAACTACAAAGTAGCTG
 TATCATTGCTGACCATAAGAATGAGAAGGGTCTTATAATATTCAATT
 TACTACCAAGAAGCTAGTGGACACTTGTAGGTGTAAACAGGAACAAAGT
 GACAGTAGCTGGAACTAATTCTCTCAAGAACCTATTGAAAATGGTTAG
 CAAAGACTGGTGTATAATATTATCGGAAGTACTGAAGTAAAAATGAA
 GCTAAAATATCAAGTCAGACCCAATTACTTAGAAAAAGGTGACAAAAT
 AAATTATGATCAAGTATTGACAGCAGATGGTACCGAGTGGATTCTTACA

SEQUENCE LISTING

AATCTTATAGGGTGGTCGCTATATTCTGTGAAAAAGCTAACTACA
 AGTAGTAAAAAGCGAAAGATGAGGGCAGTAAACCGACTAGTTATCCAA
 CTTACCTAAAACAGGTACCTATACATTACTAAACTGTAGATGTGAAGA
 GTCAACCTAAAGTATCAAAGTCCAGTGGATTAACTTCAAAAGGGTGA
 AAAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATT
 ATACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8904

STRAIN H36B

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCCTACGTAATATAAATTGGTTAGCATCAGTAATTAGGGTCATT
 ATAATGGTCACAAGTCCGTGTTGGGATCAAACATCGGTTCAAGT
 TAATAATCAGACAGGCAGTGTGGATGATAATAATTCTCCAATGAGA
 CAAGTGCCTCAAGTGTGATTACTTCAATAATGATAGTGTCAAGCGTCT
 GATAAAGTTGAAATAGTCAAACACGGCAACAAAGGGACATTACTACTC
 TTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGG
 ATTATGTTATAGCAAAGAACCGAGGTGAAAAACACCTCAAAATCA
 GCCCCAGTAGCTTCTATGCAAAGAACGGTGTGATAAAAGTTCTATGACCA
 AGTATTAAATAAGATAATGTGAAATGGATTTCATATAAGTCTTTGTG
 GCGTACGTCGATACGCAGCTATTGAGTCAGTACATCAGGAGGTTCA
 GAGACTAAAGCAGCTACTCTGTAACAAATTCAAGGAAGCAATAATCAAGA
 GAAAATAGCAACGCAAGGAAATTACATTTACATAAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGACTCAACTTACATTGGACAAAGGA
 GACAGAATTTCAGCACAAACTAACTATTGAAGGAAATCAGTGGTT
 ATCTTATAAATCATTCAATGGTGGTCGTTGTTTGTTTGCTAGGTAAG
 CATCTCAGTAGAAAAACTGAAGATAAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCAGTAACTAAACTGGTAGACTGACTATTCTAACGAAACAAC
 TACAGGTTTGATATTAAATTACGAAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAACGGTACCGGGTTGGACTGAACAAGGGAGGCAAGATGATAATT
 AAATGGTATACAGCTGTAACTACTGGGAGTGGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAAGAATGAGAAGGGCTTATAATATTCAATT
 ACTACCAAGAAGCTAGTGGACACTTGTAGGTGTAACAgGAACCTAAAGTG
 ACAGTAGCTGGAACTAATTCTCAAGAACCTATTGAAAATGGTTAGC
 AAAGACTGGTGGTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAG
 CTAAAATATCAAGTCAGACCCAATTACTTTAGAAAAAGGTGACAAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTACAA
 ATCTTATAAGTGGTGGTCGCTATATTCTGTGAAAAAGCTAACTACAA
 GTAGTGGAAAAGCAGAAAGATGAGGGCAGTAAACCGACTAGTTATCC
 TTACCTAAACAGGTACCTATACATTACTAAACTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAAGTCCAGTGGATTAACTTCAAAAGGGTGA
 AAATACATTATGATCAAGTGTAGTAGATGGTCATCAGTGGATT
 TACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8905

STRAIN 18RS21

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
 TCTACGTAATATAAATTGGTTAGCATCAGTAATTAGGGTCATTCA
 TAATGGTCACAAGTCCGTGTTGGGATCAAACATCGGTTCAAGT
 ATAATCAGACAGGCAGTGTGGATGCTAATAATTCTCCAATGAGAC
 AAGTGCCTCAAGTGTGATTACTTCAATAATGATAGTGTCAAGCGTCTG
 ATAAAGTTGAAATAGTCAAACACGGCAACAAAGGGACATTACTACTC
 TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGG
 TTATGTTATAGCAAAGAACCGAGGTGAAAAACACCTTCAAAATCAG
 CCCAGTAGCTTCTATGCAAAGAACGGTGTGATAAAAGTTCTATGACCAA
 GTATTAAATAAGATAATGTGAAATGGATTTCATATAAGTCTTTGTG
 CGTACGTCGATACGCAGCTATTGAGTCAGTACATCAGGAGGTTCA
 AGACTAAAGCACCTACTCTGTAACAAATTCAAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTACATTTACATAAAAGTAGAAGTAAA
 AAATGAAGCTAAGGTAGCGAGTCCAACTCAATTACATTGGACAAAGGG
 ACAGAATTTCAGCACAAACTAACTATTGAAGGAAATCAGTGGTTA
 TCTTATAAATCATTCAATGGTGGTCGTTGTTGCTAGGTAAGC
 ATCTCAGTAGAAAAACTGAAGATAAAAGAAAAAGTGTCTCCTCAAC
 AAGCCCGTATTACTAAACGGTAGACTGACTATTCTAACGAAACA
 ACAGGTTTGATATTAAATTACGAAATATTAAAGATGATAACGGTATCGC

SEQUENCE LISTING

TGCTGTTAAGGTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATTA
 AATGGTATACTACAGCTGTAACTACTGGGATGGCAACTACAAAGTAGCTGTA
 TCATTTGCTGACCATAAGAATGAGAAGGGCTTTATAATATTCATTTATA
 CTACCAAGAAGCTAGTGGACACTTGTAGGTGTAACAGGAACCTAAAGTGA
 CAGTAGCTGGAACTAATTCTCTCAAGAACCTATTGAAAATGGTTAGCA
 AAGACTGGTGTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGC
 TAAAATATCAAGTCAGACCCAATTACTTAGAAAAAGGTGACAAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTACCGAGTGGATTCTTACAAA
 TCTTATAGTGGTGTGTCGCTATTCCTGTGAAAAGCTAACTACAAG
 TAGTGAAAAGCGAAAGATGAGGCGACTAAACCCACTAGTTATCCCAACT
 TACCTAAAACAGGTACCTATACATTACTAAACTGTAGATGTGAAAAGT
 CAACCTAAAGTCAAGTCCAGTGGAAATTAAATTTCAAAAGGGTGAAAAA
 AATACATTATGATCAAGTGTAGTAGATGGTCATCAGTGGATTTCAT
 ACAAGAGTTATTCCGGTATTGCTCGCTATATTGAAATT

SEQ ID NO. 8906

STRAIN M732

CAAGTAAATGATACTAACGAAATCTTACTCTACGTAAATATAAATTGG
 TTTAGCATCAGTAATTAGGGTCATTCATAATGGTCACAAGTCTGTT
 TTGCGGATCAAActACATCGGTTCAAGTTAAATACAGACAGGCACTAGT
 GTGGATGCTAATTCTTCAATGAGACAAGTGCCTCAAGTGTGATTAC
 TTCCAATAATGATAGTGTCAAGCGCTGTGATAAAGTTGTAATAGTCAA
 ATACGGCAACAAAGGACATTACTACTCCTTGTAGTAGAGACAAAGCCAATG
 GTGGAAAAAAACATTACCTGAACAAGGGAAATTATGTTATAGCAAAGAAC
 CGAGGTGAAAAAATACACCTTCAAATCAGCCCCAGTAGCTTCTATGCAA
 AGAAAGGTGATAAAAGTTCTATGACCAAGTATTAAAGATAATGTG
 AAATGGATTTCATATAAGTCTTTGGTGGCGTAGTCGATACGCAGCTAT
 TGAGTCACTAGATCCATCAGGAGGTTAGAGACTAAAGCACCTACTCCTG
 TAACAAATTAGGAACATAATCAAGAGAAAATAGCAACGCAAGGAAAT
 TATACATTTACATAAAAGTAGAAGTAAAAAATGAAGCTAAGGTAGCGAG
 TCCAACTCAATTACATTGGACAAAGGAGACAGAATTTCAGACCAAA
 TACTAACTatTGAAGGAAATCAGTGGTTATCTTATAATCATTCAATGGT
 GTTCGTCGTTGttGCTAGTAAAGCATCTCAGTAGAAAAAAACTGA
 AGATAAAAGAAAAAGTGTCTCCTCAACCACAAGCCGTATTACTAAAATG
 GTAGACTGACTATTCTAACGAAACAACACAGGTTTGATATTTAATT
 ACGAATATTAAAGATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTG
 GACTGAACAAGGAGGGCAAGATGATATTAAATGGTACAGCTGTAACTA
 CTGGGATGGCAACTACAAAGTAGCTGTATCATTGCTGACCATAGAAT
 GAGAAGGGCTTTATAATATTCAATTACTACCAAGAACGCTAGTGGGAC
 ACTTGTAGGTGTAACAGGAACCTAAAGTGACAGTAGCTGGAACTAATTCTT
 CTCAAGAACCTATTGAAAATGGTTACCAAAGACTGGTGTATAATATT
 ATCGGAAGTACTGAAGTAAAAAATGAAGCTAAATATCAAGTCAGACCCA
 ATTACTTAGAAAAGGTGACAAAATAATTATGATCAAGTATTGACAG
 CAGATGGTTACCGAGTGGATTCTTACAAATCTTATAGTGGTTCGTCGC
 TATATTCTGAAAAAGCTAACCTACAGTAGTGAAAAGCGAAAGATGA
 GGGCACTAAACCGACTAGTTACCCAACTTACCTAAACAGGTACCTATA
 CATTACTAAACCTAGTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCCA
 GTGGAATTAAATTTCAAAAGGGTGAAAAAATACATTATGATCAAGTGT
 AGTAGTAGATGGTCATCAGTGGATTTCATACAAGAGTTATTCCGGTATT
 GTCGCTATATTGAAATT

SEQ ID NO. 8907

STRAIN COH1

AAAAAAGGACAAGTAAATGATACTAACGAAATCTTACTCTCT
 ACGTAAATATAAATTGGTTAGCATCAGTAATTAGGGTCATTACAA
 TGGTCACAAGTCTGTTTGCAGGATCAAACCTACATCGGTTCAAGTTAAT
 ATCAGACAGGCACTAGTGTGGATGCTAATAATTCTCCAATGAGACAAG
 TGCGTCAGTGTGATTACTCCAATAATGATAGTGTCAAGCGCTGATA
 AAGTTGTAATAGTCAAATACGGCAACAAAGGACATTACTACTCCTTTA
 GTAGAGACAAAGCCAATGGGGAAAAACATTACCTGAACAAGGGAAATTA
 TGTTTATAGCAAAGAAACCGAGGTGAAAAAATACACCTTCAAATCAGCCC
 CAGTAGCTTCTATGCAAAGAAAGGTGATAAAAGTTTCTATGACCAAGTA
 TTTAATAAAAGATAATGTTAATGGATTTCATATAAGTCTTTGGTGGCGT
 ACGTGATACGAGCTATTGAGTCAGTAGATCCATCAGGAGGTTAGAGA

SEQUENCE LISTING

CTAAAGCACCTACTCCTGTAACAAATTCAAGGAAGCAATAATCAAGAGAAA
 ATAGCAACGCAGGAAATTATACATTTCACATAAAAGTAGAAGTAAAGAAA
 TGAAGcTAAGGTAGCGACTCCAACCTCAATTACATTGGACAAAGGAGACA
 GAATTTTTACGACCAAAACTAACTACTATTGAAGGAAATCAGTGGTTATCT
 TATAAATCATCAATGGTGTCTCGTCTTTGTTTGCTAGGTAAAGCATC
 TTCAGTAGAAAAAACTGAAGATAAAAGAAAAAGTGTCTCCTCAACCACAAG
 CCCGTATTACTAAAAGTGTAGACTGACTATTTCTAACGAAACAACACTACA
 GGTGTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCGCTGC
 TGTGTTAAGGTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATTAAAT
 GGTATACAGCTGTAACACTGGGGATGGCAACTACAAAGTAGCTGTATCA
 TTTGCTGACCAATAAGATGAGAAGGGCTTTATAATTACATTATTAAC
 CCAAGAAGCTAGTGGACACTTGTAGGTAAACAGGAACCTAAAGTGACAG
 TAGCTGGAACTAATTCTTCAGAACCTATTGAAAATGGTTTACCAAAG
 ACTGGTGTATAATTATCGGAAGTACTGAAGTAAAAAAATGAAGCTAA
 AATATCAAGTCAGACCCAATTACTTAGAAAAAGGTGACAAAATAATT
 ATGATCAAGTATTGACAGCAGATGGTACCAAGTGGATTCTAACAAATCT
 TATAGTGGTGTTCGCTATATTCTGTGAAAAGCTAACACTACAAGTAG
 TGAAAAAGCGAAAGATGAGGGCGACTAAACCGACTAGTTATCCAACTTAC
 CTAACACAGGTACCTATACTTTACTAAACTGTAGATGTGAAAAGTCAA
 CCTAAAGTATCAAGTCCAGTGGATTAAATTCTAACAAAGGGTGAAAAAAAT
 ACATTATGATCAAGTGTAGTAGTGTGATGGTCATCAGTGGATTTCATA
 AGAGTTATTCCGGTATTCTCGCTATATTGAAATT

SEQ ID NO. 8908

STRAIN M781

AAAAAAGGACAAGTAAATGATACTAACGCAATCTT
 ACTCTCTACGTAATATAAATTGGTTAGCATCAGTAATTAGGGTCA
 TTCTATAATGGTCAACAGGCTCTGTTTGGGATCAAACATCGGTTCA
 AGTAATATCAGACAGGCAACTAGTGTGGATGCTAATAATTCTTCCAATG
 AGACAAGTGGCTCAAGTGTGATTACTTCAATAATGATAGTGTCAAGCG
 TCTGATAAAAGTGTAAATAGTCAAACATGGCAACAAAGGACATTACTAC
 TCCCTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAAG
 GGAATTATGTTTATAGCAAAGAAACCGAGGTGAAAATACACCTTCAAAA
 TCAGCCCCAGTAGCTTCTATGCAAAGAAAGGTGATAAAAGTTCTATGA
 CCAAGTATTTAATAAAGATAATGTGAAATGGATTCAATATAAGTCTTTG
 GTGGCGTACGTGATACGCACTATTGAGTCAGTAGATCCATCAGGAGGT
 TCAGAGACTAAAGCACCTACTCCTGTAACAAATTCAAGGAAGCAATAATCA
 AGAGAAAATAGCAACGCAAGGAAATTATACATTTCACATAAAGTAGAAG
 TAAAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTACATIGGACAAA
 GGAGACAGAAATTCTACGACCAAATACTAAACTATTGAAGGAAATCAGTG
 GTTATCTTATAATCATTCAATGGTGTCTCGTCTTGTGTTTGCTAGGTA
 AACCATCTCAGTAGAAAAAACTGAAGATAAAAGAAAAGTGTCTCCTCAA
 CCACAAGCCGTATTACTAAACTGGTAGACTGACTATTCTAACGAAAC
 AACTACAGGTTTGATATTTAATTACGAATATTAAAGATGATAACGGTA
 TCGCTGCTGTTAAGTACCGGTTGGACTGAACAAGGAGGGCAAGATGAT
 ATTAAATGGTATACAGCTGTAACACTGGGGATGGCAACTACAAAGTAGC
 TGTATCTTGGCTGACCAATAAGAATGAGAAGGGCTTTATAATATTCTT
 TATACTACCAAGAAGCTAGTGGGACACTTGTAGGTAAACAGGAACCTAA
 GTGACAGTAGCTGGAACTAATTCTCAAGAACCTATTGAAAATGGTTT
 ACCAAAGACTGGTGTATAATTATCGGAAGTACTGAAGTAAAAAAATG
 AAGCTAAATATCAAGTCAGACCCAATTACTTTAGAAAAAGGTGACAAA
 ATAAATTATGATCAAGTATTGACAGCAGATGGTACCAAGTGGATTCTTA
 CAAATCTTATAGTGGTGTCTCGCTATATTCTGTGAAAAAGCTAACTA
 CAAGTAGTGGAAAAGCGAAAGATGAGGGCGACTAAACCGACTAGTTATCCC
 AACCTACCTAAACAGGTACCTATACATTACTAAACTGTAGATGTGAA
 AAGTCAACCTAAAGTATCAAGTCCAGTGGATTAAATTCTAACAAAGGGT
 GAAAAAAATACATTATGATCAAGTGTAGTAGTGTGATGGTCATCAGTGGATT
 TCATACAAGAGTTATTCCGGTATTCTCGCTATATTGAAATT

SEQ ID NO. 8909

STRAIN CJB110

AAAAAAGGACAAGTAAATGATACTAACGCAATCTTACTCTC
 TACGTTAAATATAAATTGGTTAGCATCAGTAATTAGGGTCAATTCA
 ATGGTCACAAGCCTGTTTGGGATCAAACATCGGTTCAAGTTAA

SEQUENCE LISTING

TAATCAGACAGGCACACTAGTGTGGATGCTAATAATTCTCCAATGAGACAA
 GTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTGAT
 AAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTT
 ATGAGAGACAAAGCCAATGGGAAAAAACATTACCTGAACAAGGGAAATT
 ATGTTTATAGCAAAGAACCGAGGTGAAAAATACACCTTCAAATCAGCC
 CCAGTAGCTTCTATGCAAAGAAAGGTGATAAAGTTCTATGACCAAGT
 ATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTGTGGCG
 TACGTCGATACGCAGCTATTGAGTCAGTCATCAGGAGGTTAGAG
 ACTAAAGCAGCTACTCCTGTAACAAATTCAAGGAAGCAATAATCAAGAGAA
 AATAGCAACGCAAGGAAATTATACTTTACATAAAAGTAGAAGTAAAAA
 ATGAAGCTAAGGTAGCGAGTCCACTCAATTACATTGGACAAAGGAGAC
 AGAATTTCAGACCAAATACTAACTATTGAAGGAAATCAGTGGTTATC
 TTATAAATCATTCAATGGTTCGTCGTTTGTAGGTTAAAGCATT
 CTCAGTAGAAAAAACTGAAGATAAAAGAAAAGTAGTGTCTCCTCAACCACAA
 GCCCGTATTACTAAAAGGTGACTATTCTAACGAAACAACATAC
 AGGTTTGATATTAACTACGAATATTAAAGATGATAACGGTATCGCTG
 CTGTTAAGGTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATTAA
 TGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTATC
 ATTGCTGACCATAGAAGATGAGAAGGGTCTTATAATATTCAATTAACT
 ACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACAAAGTGACA
 GTAGCTGAACTAATTCTCTCAAGAACCTATTGAAAATGGTTAGCAA
 GACTGGTGTATAATATTACGGAAAGTACTGAAGTAAAAAATGAAGCTA
 AAATATCAAGTCAGACCAAATTACTTTAGAAAAGGTGACAAATAAT
 TATGATCAAGTATTGACAGCAGATGGTACCACTGGATTTCTAACAAATC
 TTATAGTGGTGTGCGCTATATTCTGTGAAAAAGCTAACACTAACGTA
 GTGAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCAACTTA
 CCTAAACAGGTACCTACATTTACTAAAAGTAGTGTGAAGAGTCA
 ACCTAAAGTATCAAGTCCAGTGGAAATTAAATTTCAAAAGGGTGAAAAAA
 TACATTATGATCAAGTGTAGTAGTGTGATGGTCATCAGTGGATTTCATAC
 AAGAGTTATTCCGTATTGCGCTATATTGAAATT

SEQ ID NO. 8910

STRAIN 1169NT

AAAAAAAGGACAAGTAAATGATACTAACGAACTTACTC
 TCTACGTAATATAAATTGGTTTAGCATCAGTAATTAGGGTCATTCA
 TAATGGTCACAAGCTCTGTTTGGGATCAAACATCGGTTCAAGTT
 AATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTCCAATGAGAC
 AAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTG
 ATAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCAATGGGAAAAACATTACCTGAACAAGGGAA
 TTATGTTATAGCAAAGAACCGAGGTGAAAATACACCTTCAAATCAG
 CCCCAGTAGCTTCTATGCAAAGAAAGGTGATAAAGTTCTATGACCAA
 GTATTAAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTGGTGG
 CGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTAG
 AGACTAAAGCACCTACTCCTGTAACAAATTCAAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTATACTTTCACATAAAAGTAGAAGTAAA
 AAATGAAGCTAAGGTAGCGAGTCCAACTCAATTACATTGGACAAAGGAG
 ACAGAATTTCAGACCAAATACTAACTATTGAAGGAAATCAGTGGTTA
 TCTTATAAATCATTCAATGGTTCGTTTGTAGGTTAAAGC
 ATCTTCAGTAGAAAAAACTGAAGATAAAAGAAAAGTAGTGTCTCCTCAACCAC
 AAGCCCGTATTACTAAAAGGTGACTGACTATTCTAACGAAACAAC
 ACAGGTTTGATATTAACTACGAATATTAAAGATGATAACGGTATCGC
 TGCTGTTAAGGTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATTAA
 ATGGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTA
 TCATTGCTGACCATAGAATGAGAAGGGTCTTATAATATTCAATTATA
 CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACAAAGTGA
 CAGTAGCTGGAACTAATTCTCTCAAGAACCTATTGAAAATGGTTAGCA
 AAGACTGGTGTATAATATTACGGAAAGTACTGAAGTAAAAAATGAAGC
 TAAAATATCAAGTCAGACCCAATTACTTTAGAAAAGGTGACAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTTCTTACAAA
 TCTTATAGTGGTGTGCGCTATATTCTGTGAAAAAGCTAACACTACAAG
 TAGTGGAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCAACT
 TACCTAAAACAGGTACCTATACATTACTAAAAGTAGTGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTAAATTTCAAAAGGGTGAAAAA

SEQUENCE LISTING

AATAACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTCAT
ACAAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8911

STRAIN JM9130013

AAAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAATATAAATTTGGTTAGCATCAGTAATTAGGGTCATT
ATAATGGTCACAAGTCTGTTTGCAGGATCAAACATACATCGGTTCAAGT
TAATAATCAGACAGGCAGTGTGGATGCTAATAATTCTCCAATGAGA
CAAGTGCCTCAAGTGTGATTACCTTCCAATAATGATAGTGTCAAGCGTCT
GATAAAAGTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
TTAGTAGAGACAACGCCATGGTGGAAAAAAACATTACCTGAACAAGGGGA
ATTATGTTATAGCAAAGAAACCGAGGTGAAAATACACCTCAAAATCA
GCCCGCAGTAGCTTCTATGCAAAGAAAGGTGATAAAGTTCTATGACCA
AGTATTTAATAAAGATAATGTGAAATGGATTATATAAGTCTTTGIG
GCGTACGTCGATACGAGCTATTGAGTCAGTACAGTCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCCTGTAACAAATTCAAGGAAGCAATAATCAAGA
GAAAATAGCAACGCAAGGAAATTATAACATTTCACATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGACTCCAACCTCAATTACATTGGACAAAGGA
GACAGAAAGTTTACGACCAAATACTAAACTATTGAAGGAAATCAGTGGTT
ATCTTATAAAATCATTCAATGGTGTTCGCTGTTTGTCTAGGTAAG
CATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAGTGTCTCCTCAACCA
CAAGCCCGTATTACTAAAACGGTAGACTGACTATTATAACGAAACAAAC
TACAGGTTTGTATTTAATTACGAATATTAAAGATGATAACGGTATCG
CTGCTGTTAAGGTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATAACAGCTGTAACTACTGGGATGGCAACTACAAAGTAGCTGT
ATCATTGCTGACCATAAGAATGAGAAGGGCTTTATAATATTCAATT
ACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACCTAAAGTG
ACAGTAGCTGGAACCTAAATTCTCTCAAGAACCTATTGAAAATGGTTAGC
AAAGACTGGTGTATAATATTATCGGAAGTACTGAAGTAAAAAAATGAAG
CTAAAATATCAAGTCAGACCCAATTACTTTAGAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACCACTGTTACCAA
ATCTTATAGTGGTGTTCGCTATATTCTGTGAAAAGCTAACTACAA
GTAGTGAACAGCGAAAGATGAGGGCAACTAAACCGACTAGTTATCCCAAC
TTACCTAAACAGGTACCTATACATTACTAAAACGTAGATGTGAAGAG
TCAACCTAAAGTATCAAGTCCAGTGGAAATTAACTTCAAAAGGGTGAAC
AAATACATTATGATCAAGTGTAGTAGATGGTCATCAGTGGATTCA
TACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8912

STRAIN 2603 frame: 1

MKKQVNDTKQSYSRKYKFLGLASVILGSFIMVTPVFADQTSVQVNNQTGTSVDANNSS
SNETSASSVITSNNDSVQASDKVVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
TEVKNTPSKSAPVAFYAKKGDKVFYDQVFNFNKKDNVKWISYKSFVRRYAAIESLDPSSGS
ETKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILT
IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQPARITKTGRLTISNETTTGF
DILITNIKDDNGIAAVKPVWTEQGGQDDIKWYTAFTTGDGNYKVAVSFADHKNEKGLYN
IHLYYQEASGTLVGVTKVTVAGTNSSQEPENGLAKTGVYNIIGSTEVKNEAKISSQT
QFTLEKGDKINYDQVLTADGYQWISYKSYSVRRYIPVKKLTSSEKAKDEATKPTSYPNL
LPKTGTYTFTKTVDVKSQPKVSSPVEFNFKGEKIHYDQVLVVDGHQWISYKSYSGIRRY
IEI

SEQ ID NO. 8913

STRAIN 090 frame: 1

KKQVNDTKQSYSRKYKFLGLASVILGSFIMVTPVFADQTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNFNKKDNVKWISYKSFVRRYAAIESLDPSSGS
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILT
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQPARITKTGRLTISNETTTGF
ILITNIKDDNGIAAVKPVWTEQGGQDDIKWYTAFTTGDGNYKVAVSFADHKNEKGLYN
HLYYQEASGTLVGVTKVTVAGTNSSQEPENGLAKTGVYNIIGSTEVKNEAKISSQT
FTLEKGDKINYDQVLTADGYQWISYKSYSVRRYIPVKKLTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFKGEKIHYDQVLVVDGHQWISYKSYSGIRRY
EI

SEQUENCE LISTING

SEQ ID NO. 8914

STRAIN A909 frame: 1

KKGVNDTKQSYSLRKYKFGLASVILGSFIMVSPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNPKDNVWISYKSFVRRYAAIESLDPGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAWSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKVTAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSEKAKDEATKPTSYPLNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8915

STRAIN H36B frame: 1

KKGVNDTKQSYSLRKYKFGLASVILGSFIMVSPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNPKDNVWISYKSFVRRYAAIESLDPGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAWSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKVTAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSEKAKDEATKPTSYPLNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8916

STRAIN 18RS21 frame: 1

KKGVNDTKQSYSLRKYKFGLASVILGSFIMVSPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNPKDNVWISYKSFVRRYAAIESLDPGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAWSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKVTAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSEKAKDEATKPTSYPLNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8917

STRAIN M732 frame: 1

QVNDTKQSYSLRKYKFGLASVILGSFIMVSPVFADQTTSVQVNNQTGTSVDANNSSNET
 SASSVITSNNDSVQASDKVVSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKETEVK
 NTPSKSAPVAFYAKKGDKVFYDQVFNPKDNVWISYKSFVRRYAAIESLDPGGSETKA
 PTPVTNSGSNNQEKIATQGNYTFSHKVEVNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAWSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKVTAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSEKAKDEATKPTSYPLNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8918

STRAIN COH1 frame: 1

KKGVNDTKQSYSLRKYKFGLASVILGSFIMVSPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNPKDNVWISYKSFVRRYAAIESLDPGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAWSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKVTAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTSSEKAKDEATKPTSYPLNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQUENCE LISTING

SEQ ID NO. 8919

STRAIN M781 frame: 1

KKGVNDTKQSYSLRKYKFGLASVILGSFIMVTPVFADQTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVSQNTATKDITPLVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDVKFYDQVFNKDNWKWISYKSFCCVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAUTTDGDNYKVAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSAKDEATKPTSPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8920

STRAIN CJB110 frame: 1

KKGVNDTKQSYSLRKYKFGLASVILGSFIMVTPVFADQTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVSQNTATKDITPLVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDVKFYDQVFNKDNWKWISYKSFCCVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAUTTDGDNYKVAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSAKDEATKPTSPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8921

STRAIN 1169NT frame: 1

KKGVNDTKQSYSLRKYKFGLASVILGSFIMVTPVFADQTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVSQNTATKDITPLVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDVKFYDQVFNKDNWKWISYKSFCCVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAUTTDGDNYKVAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSAKDEATKPTSPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8922

STRAIN JM9130013 frame: 1

KKGVNDTKQSYSLRKYKFGLASVILGSFIMVTPVFADQTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVVSQNTATKDITPLVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDVKFYDQVFNKDNWKWISYKSFCCVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAUTTDGDNYKVAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSAKDEATKPTSPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0001	453	chromosomal replication initiator protein DnaA
SAG0002	378	DNA polymerase III, beta subunit
SAG0003	293	diacylglycerol kinase catalytic domain protein, putative
SAG0004	65	conserved hypothetical protein
SAG0005	67	hypothetical protein
SAG0006	371	GTP-binding protein YchF
SAG0007	191	peptidyl-tRNA hydrolase
SAG0008	1165	transcription-repair coupling factor
SAG0009	31	hypothetical protein
SAG0010	90	S4 domain protein
SAG0011	123	cell division protein DivIC, putative
SAG0012	44	conserved hypothetical protein
SAG0013	428	protein of unknown function
SAG0014	424	MesJ/Ycf62 family protein
SAG0015	180	hypoxanthine-guanine phosphoribosyltransferase
SAG0016	658	cell division protein FtsH
SAG0017	447	pcsB protein
SAG0018	322	ribose-phosphate pyrophosphokinase
SAG0019	391	aminotransferase, class I
SAG0020	253	recombination protein O
SAG0021	283	protease, putative
SAG0022	330	fatty acid/phospholipid synthesis protein PlsX
SAG0023	79	acyl carrier protein
SAG0024	234	phosphoribosylaminoimidazole-succinocarboxamide synthase
SAG0025	1241	phosphoribosylformylglycinamide synthase, putative
SAG0026	484	amidophosphoribosyltransferase
SAG0027	340	phosphoribosylformylglycinamide cyclo-ligase
SAG0028	182	phosphoribosylglycinamide formyltransferase
SAG0029	250	acetyltransferase, GNAT family
SAG0030	515	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
SAG0031	299	peptidase, M23/M37 family
SAG0032	434	group B streptococcal surface immunogenic protein
SAG0033	232	N-acetylmannosamine-6-P epimerase, putative
SAG0034	438	sugar ABC transporter, sugar-binding protein
SAG0035	295	sugar ABC transporter, permease protein
SAG0036	276	sugar ABC transporter, permease protein
SAG0037	147	conserved hypothetical protein
SAG0038	220	conserved hypothetical protein
SAG0039	305	N-acetylneuraminate lyase, putative
SAG0040	293	ROK family protein
SAG0041	325	acetyl xylan esterase, putative
SAG0042	267	phosphosugar-binding transcriptional regulator, RpiR family, putative
SAG0043	421	phosphoribosylamine--glycine ligase
SAG0044	162	phosphoribosylaminoimidazole carboxylase, catalytic subunit
SAG0045	363	phosphoribosylaminoimidazole carboxylase, ATPase subunit
SAG0046	463	membrane protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0047	432	adenylosuccinate lyase
SAG0048	303	transcriptional regulator, Cro/CI family
SAG0049	332	Holliday junction DNA helicase RuvB
SAG0050	145	phosphotyrosine protein phosphatase, low molecular weight
SAG0051	126	MORN motif family protein
SAG0052	592	membrane protein, putative
SAG0053	880	aldehyde-alcohol dehydrogenase
SAG0054	338	alcohol dehydrogenase, propanol-preferring
SAG0055	496	threonine synthase
SAG0056	412	MATE efflux family protein
SAG0057	102	ribosomal protein S10
SAG0058	208	ribosomal protein L3
SAG0059	207	ribosomal protein L4
SAG0060	98	ribosomal protein L23
SAG0061	277	ribosomal protein L2
SAG0062	92	ribosomal protein S19
SAG0063	114	ribosomal protein L22
SAG0064	217	ribosomal protein S3
SAG0065	137	ribosomal protein L16
SAG0066	68	ribosomal protein L29
SAG0067	86	ribosomal protein S17
SAG0068	122	ribosomal protein L14
SAG0069	101	ribosomal protein L24
SAG0070	180	ribosomal protein L5
SAG0071	61	ribosomal protein S14, putative
SAG0072	132	ribosomal protein S8
SAG0073	178	ribosomal protein L6
SAG0074	118	ribosomal protein L18
SAG0075	164	ribosomal protein S5
SAG0076	59	ribosomal protein L30
SAG0077	146	ribosomal protein L15
SAG0078	434	preprotein translocase, SecY subunit
SAG0079	212	adenylate kinase
SAG0080	72	translation initiation factor IF-1
SAG0081	38	ribosomal protein L36
SAG0082	121	ribosomal protein S13
SAG0083	118	ribosomal protein S11
SAG0084	312	DNA-directed RNA polymerase, alpha subunit
SAG0085	128	ribosomal protein L17
SAG0086	85	lipoprotein, putative
SAG0087	59	hypothetical protein
SAG0088	56	hypothetical protein
SAG0089	183	conserved hypothetical protein
SAG0090	139	conserved hypothetical protein
SAG0091	144	transcriptional regulator ComX1, putative
SAG0092	230	phosphoglycerate mutase family protein
SAG0093	250	D-alanyl-D-alanine carboxypeptidase family protein
SAG0094	191	N-acetyl muramoyl-L-alanine amidase, family 4 protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0095	344	heat-inducible transcription repressor HrcA
SAG0096	190	heat shock protein GrpE
SAG0097	609	dnaK protein
SAG0098	379	dnaJ protein
SAG0099	415	transcriptional regulator, GntR family
SAG0100	258	tRNA pseudouridine synthase A
SAG0101	252	phosphomethylpyrimidine kinase, putative
SAG0102	154	conserved hypothetical protein
SAG0103	189	conserved hypothetical protein TIGR01440
SAG0104	280	conserved hypothetical protein
SAG0105	427	trigger factor
SAG0106	191	DNA-directed RNA polymerase, delta subunit, putative
SAG0107	534	CTP synthase
SAG0108	308	conserved hypothetical protein
SAG0109	148	deoxyuridine 5'-triphosphate nucleotidohydrolase
SAG0110	454	DNA repair protein RadA
SAG0111	165	carbonic anhydrase-related protein
SAG0112	439	pyridine nucleotide-disulphide oxidoreductase family protein
SAG0113	484	glutamyl-tRNA synthetase
SAG0114	322	ribose ABC transporter, periplasmic D-ribose-binding protein
SAG0115	310	ribose ABC transporter, permease protein
SAG0116	492	ribose ABC transporter, ATP-binding protein
SAG0117	132	ribose ABC transporter protein RbsD
SAG0118	303	ribokinase
SAG0119	328	ribose operon repressor RbsR
SAG0120	32	hypothetical protein
SAG0121	362	permease, putative
SAG0122	228	ABC transporter, ATP-binding protein
SAG0123	223	DNA-binding response regulator
SAG0124	356	sensor histidine kinase
SAG0125	396	argininosuccinate synthase
SAG0126	462	argininosuccinate lyase
SAG0127	293	fructose-bisphosphate aldolase
SAG0128	305	L-2-hydroxyisocaproate dehydrogenase
SAG0129	62	ribosomal protein L28
SAG0130	121	conserved hypothetical protein
SAG0131	543	DAK2 domain protein
SAG0132	294	SPFH domain/Band 7 family protein
SAG0133	38	conserved hypothetical protein
SAG0134	96	hypothetical protein
SAG0135	246	amino acid ABC transporter, ATP-binding protein
SAG0136	516	amino acid ABC transporter, amino acid-binding protein/permease protein
SAG0137	627	conserved hypothetical protein
SAG0138	279	undecaprenol kinase, putative
SAG0139	251	negative regulator of competence MecA, putative
SAG0140	386	glycosyl transferase, group 4 family protein
SAG0141	256	ABC transporter, ATP-binding protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0142	420	conserved hypothetical protein
SAG0143	410	selenocysteine lyase
SAG0144	147	NifU family protein
SAG0145	472	conserved hypothetical protein
SAG0146	395	penicillin-binding protein 4, putative
SAG0147	411	D-alanyl-D-alanine carboxypeptidase family protein
SAG0148	551	oligopeptide ABC transporter, substrate-binding protein, putative
SAG0149	304	oligopeptide ABC transporter, permease protein
SAG0150	343	oligopeptide ABC transporter, permease protein
SAG0151	348	oligopeptide ABC transporter, ATP-binding protein
SAG0152	310	oligopeptide ABC transporter, ATP-binding protein
SAG0153	283	4-diphosphocytidyl-2C-methyl-D-erythritol kinase
SAG0154	147	adc operon repressor AdcR
SAG0155	236	zinc ABC transporter, ATP-binding protein
SAG0156	270	zinc ABC transporter, permease protein
SAG0157	NA	deoxyribonuclease-related protein, degenerate
SAG0158	419	tyrosyl-tRNA synthetase
SAG0159	765	penicillin-binding protein 1B, putative
SAG0160	1191	DNA-directed RNA polymerase, beta subunit
SAG0161	1216	DNA-directed RNA polymerase beta' subunit
SAG0162	121	conserved hypothetical protein
SAG0163	323	competence protein CglA
SAG0164	282	competence protein CglB
SAG0165	151	conserved hypothetical protein
SAG0166	123	conserved domain protein
SAG0167	324	conserved hypothetical protein
SAG0168	397	acetate kinase
SAG0169	68	transcriptional regulator, Cro/CI family
SAG0170	45	hypothetical protein
SAG0171	151	hypothetical protein
SAG0172	221	protease, putative
SAG0173	256	pyrroline-5-carboxylate reductase
SAG0174	355	glutamyl-aminopeptidase
SAG0175	79	hypothetical protein
SAG0176	94	conserved hypothetical protein
SAG0177	107	thioredoxin family protein
SAG0178	208	tRNA binding domain protein
SAG0179	238	conserved hypothetical protein
SAG0180	131	single-strand binding protein
SAG0181	214	hydrolase, haloacid dehalogenase-like family
SAG0182	581	sensor histidine kinase, putative
SAG0183	246	response regulator
SAG0184	151	conserved hypothetical protein
SAG0185	242	membrane protein, putative
SAG0186	36	hypothetical protein
SAG0187	542	oligopeptide ABC transporter, oligopeptide-binding protein
SAG0188	325	oligopeptide ABC transporter, permease protein
SAG0189	273	oligopeptide ABC transporter, permease protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0190	267	peptide ABC transporter, ATP-binding protein
SAG0191	208	peptide ABC transporter, ATP-binding protein
SAG0192	676	PTS system, IIABC components
SAG0193	541	alpha amylase family protein
SAG0194	639	transcriptional antiterminator, BglG family
SAG0195	377	IS1548, transposase
SAG0196	66	conserved domain protein
SAG0197	94	PTS system, IIB component, putative
SAG0198	451	PTS system, IIC component, putative
SAG0199	285	transketolase, N-terminal subunit
SAG0200	309	transketolase, C-terminal subunit
SAG0201	419	oxidoreductase, putative
SAG0202	89	ribosomal protein S15
SAG0203	709	polyribonucleotide nucleotidyltransferase
SAG0204	250	conserved hypothetical protein
SAG0205	194	serine O-acetyltransferase
SAG0206	60	lipoprotein, putative
SAG0207	447	cysteinyl-tRNA synthetase
SAG0208	128	conserved hypothetical protein
SAG0209	251	RNA methyltransferase, TrmH family, group 3
SAG0210	172	conserved hypothetical protein
SAG0211	286	DegV family protein
SAG0212	32	hypothetical protein
SAG0213	39	hypothetical protein
SAG0214	148	ribosomal protein L13
SAG0215	130	ribosomal protein S9
SAG0216	33	hypothetical protein
SAG0217	384	site-specific recombinase, phage integrase family
SAG0218	158	transcriptional regulator, Cro/CI family
SAG0219	101	hypothetical protein
SAG0220	92	conserved hypothetical protein
SAG0221	76	hypothetical protein
SAG0222	108	conserved domain protein
SAG0223	209	conserved hypothetical protein, fusion
SAG0224	332	replication initiation protein, putative
SAG0225	144	hypothetical protein
SAG0226	418	recombination protein
SAG0227	156	hypothetical protein
SAG0228	111	conserved hypothetical protein
SAG0229	95	conserved hypothetical protein
SAG0230	96	conserved hypothetical protein
SAG0231	135	hypothetical protein
SAG0232	186	hypothetical protein
SAG0233	226	hypothetical protein
SAG0234	128	hypothetical protein
SAG0235	93	hypothetical protein
SAG0236	32	hypothetical protein
SAG0237	34	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0238	41	hypothetical protein
SAG0239	286	transcriptional regulator MutR family
SAG0240	393	transporter, putative
SAG0241	213	amino acid ABC transporter, permease protein
SAG0242	308	amino acid ABC transporter, amino acid-binding protein
SAG0243	211	amino acid ABC transporter, permease protein
SAG0244	381	amino acid ABC transporter, ATP-binding protein
SAG0245	152	protein of unknown function/lipoprotein, putative
SAG0246	268	hypothetical protein
SAG0247	116	hypothetical protein
SAG0248	90	hypothetical protein
SAG0249	116	hypothetical protein
SAG0250	193	membrane protein, putative
SAG0251	72	transcriptional regulator, Cro/CI family
SAG0252	186	acetyltransferase, GNAT family
SAG0253	192	acetyltransferase, GNAT family
SAG0254	226	acetyltransferase, GNAT family
SAG0255	315	conserved hypothetical protein
SAG0256	163	RNA polymerase sigma factor, ECF subfamily
SAG0257	53	lipoprotein, putative
SAG0258	202	transcriptional regulator, TetR family
SAG0259	365	ABC transporter efflux protein, DrrB family, putative
SAG0260	238	ABC transporter, ATP-binding protein
SAG0261	129	IS1381, transposase OrfB
SAG0262	127	IS1381, transposase OrfA
SAG0263	171	hypothetical protein
SAG0264	103	conserved hypothetical protein
SAG0265	235	conserved hypothetical protein
SAG0266	382	N-acetylglucosamine-6-phosphate deacetylase
SAG0267	180	conserved hypothetical protein
SAG0268	304	glycyl-tRNA synthetase, alpha subunit
SAG0269	213	acyl carrier protein phosphodiesterase, putative
SAG0270	679	glycyl-tRNA synthetase, beta subunit
SAG0271	85	conserved hypothetical protein
SAG0272	87	membrane protein, putative
SAG0273	502	glycerol kinase
SAG0274	609	alpha-glycerophosphate oxidase
SAG0275	232	glycerol uptake facilitator protein
SAG0276	445	NADH oxidase, putative
SAG0277	476	conserved hypothetical protein
SAG0278	661	transketolase
SAG0279	101	conserved hypothetical protein
SAG0280	244	ABC transporter, ATP-binding protein
SAG0281	534	membrane protein, putative
SAG0282	461	PTS system, IIBC components
SAG0283	267	glutamate 5-kinase
SAG0284	417	gamma-glutamyl phosphate reductase
SAG0285	298	conserved hypothetical protein TIGR00006

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0286	108	cell division protein FtsL, putative
SAG0287	752	penicillin-binding protein 2X
SAG0288	336	phospho-N-acetylmuramoyl-pentapeptide-transferase
SAG0289	447	ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0290	270	ABC transporter, substrate-binding protein
SAG0291	267	amino acid ABC transporter, permease protein
SAG0292	247	amino acid ABC transporter, ATP-binding protein
SAG0293	74	conserved hypothetical protein
SAG0294	304	thioredoxin reductase
SAG0295	486	conserved hypothetical protein
SAG0296	273	NAD synthetase
SAG0297	444	aminopeptidase C
SAG0298	750	penicillin-binding protein 1A
SAG0299	199	recombination protein U
SAG0300	172	conserved hypothetical protein
SAG0301	40	hypothetical protein
SAG0302	110	conserved hypothetical protein
SAG0303	384	conserved hypothetical protein
SAG0304	487	conserved hypothetical protein
SAG0305	160	autoinducer-2 production protein LuxS
SAG0306	535	KH domain protein
SAG0307	33	hypothetical protein
SAG0308	298	ABC transporter, ATP-binding protein
SAG0309	246	ABC transporter, permease protein, putative
SAG0310	361	conserved hypothetical protein
SAG0311	NA	DNA-binding response regulator, authentic point mutation
SAG0312	234	conserved hypothetical protein
SAG0313	209	guanylate kinase
SAG0314	104	DNA-directed RNA polymerase, omega subunit, putative
SAG0315	796	primosomal protein N'
SAG0316	311	methionyl-tRNA formyltransferase
SAG0317	440	sun protein
SAG0318	245	serine/threonine phosphatase, putative
SAG0319	651	serine/threonine protein kinase
SAG0320	231	conserved hypothetical protein
SAG0321	339	sensor histidine kinase, putative
SAG0322	213	DNA-binding response regulator
SAG0323	466	hydrolase, haloacid dehalogenase family/peptidyl-prolyl cis-trans isomerase, cyclophilin type
SAG0324	124	general stress protein, putative
SAG0325	258	pyruvate formate-lyase-activating enzyme
SAG0326	251	transcriptional regulator, DeoR family
SAG0327	327	transcriptional regulator, putative
SAG0328	107	PTS system, cellobiose-specific IIA component
SAG0329	106	PTS system, cellobiose-specific IIB component
SAG0330	433	PTS system, cellobiose-specific IIC component
SAG0331	818	formate acetyltransferase
SAG0332	222	transaldolase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0333	362	glycerol dehydrogenase
SAG0334	308	cysteine synthase A
SAG0335	214	conserved hypothetical protein TIGR00257
SAG0336	429	helicase, putative
SAG0337	221	competence protein F, putative
SAG0338	184	ribosomal subunit interface protein
SAG0339	450	aspartate kinase family protein
SAG0340	216	hydrolase, haloacid dehalogenase-like family
SAG0341	49	hypothetical protein
SAG0342	263	enoyl-CoA hydratase/isomerase family protein
SAG0343	144	transcriptional regulator, MarR family
SAG0344	323	3-oxoacyl-(acyl-carrier-protein) synthase III
SAG0345	74	acyl carrier protein
SAG0346	319	enoyl-(acyl-carrier-protein) reductase II
SAG0347	308	malonyl CoA-acyl carrier protein transacylase
SAG0348	244	3-oxoacyl-[acyl-carrier protein] reductase
SAG0349	410	3-oxoacyl-(acyl-carrier-protein) synthase II
SAG0350	166	acetyl-CoA carboxylase, biotin carboxyl carrier protein
SAG0351	140	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase
SAG0352	456	acetyl-CoA carboxylase, biotin carboxylase
SAG0353	291	acetyl-CoA carboxylase, carboxyl transferase, beta subunit
SAG0354	257	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit
SAG0355	210	conserved hypothetical protein
SAG0356	425	seryl-tRNA synthetase
SAG0357	330	membrane protein, putative
SAG0358	120	conserved hypothetical protein
SAG0359	303	PTS system, mannose-specific IID component
SAG0360	270	PTS system, mannose-specific IIC component
SAG0361	336	PTS system, mannose-specific IIAB components
SAG0362	270	hydrolase, haloacid dehalogenase-like family
SAG0363	194	hypothetical protein
SAG0364	203	membrane protein, putative
SAG0365	473	xanthine/uracil permease family protein
SAG0366	169	conserved hypothetical protein TIGR00150
SAG0367	186	acetyltransferase, GNAT family
SAG0368	435	protein of unknown function
SAG0369	98	conserved hypothetical protein
SAG0370	139	HIT family protein
SAG0371	167	hypothetical protein
SAG0372	85	hypothetical protein
SAG0373	241	ABC transporter, ATP-binding protein
SAG0374	344	ABC transporter, permease protein
SAG0375	266	conserved hypothetical protein
SAG0376	211	conserved hypothetical protein TIGR00091
SAG0377	127	conserved hypothetical protein
SAG0378	379	N utilization substance protein A
SAG0379	98	conserved hypothetical protein
SAG0380	100	ribosomal protein L7A family

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0381	927	translation initiation factor IF-2
SAG0382	122	ribosome-binding factor 'A'
SAG0383	334	protein of unknown function/lipoprotein, putative
SAG0384	138	transcriptional repressor CopY
SAG0385	744	copper-transporter ATPase CopA
SAG0386	68	copper-transporter protein CopZ
SAG0387	204	membrane protein, putative
SAG0388	270	hydrolase, haloacid dehalogenase-like family
SAG0389	880	DNA polymerase I
SAG0390	146	CoA-binding domain protein
SAG0391	159	transcriptional regulator, Fur family
SAG0392	521	cell wall surface anchor family protein
SAG0393	228	DNA-binding response regulator
SAG0394	345	sensor histidine kinase
SAG0395	246	membrane protein, putative
SAG0396	380	queuine tRNA-ribosyltransferase
SAG0397	102	conserved hypothetical protein
SAG0398	179	BioY family protein
SAG0399	258	AtsA/ElaC family protein
SAG0400	168	cytidine/deoxycytidylate deaminase family protein
SAG0401	44	hypothetical protein
SAG0402	449	glucose-6-phosphate isomerase
SAG0403	175	5-formyltetrahydrofolate cyclo-ligase family protein
SAG0404	225	rhomboid family protein
SAG0405	347	protein of unknown function/lipoprotein, putative
SAG0406	299	UTP-glucose-1-phosphate uridylyltransferase
SAG0407	338	glycerol-3-phosphate dehydrogenase (NAD(P)+)
SAG0408	109	ribonuclease P protein component
SAG0409	271	SpoIIJ family protein
SAG0410	273	R3H domain protein
SAG0411	177	conserved hypothetical protein
SAG0412	258	recX protein
SAG0413	451	RNA methyltransferase, TrmA family
SAG0414	153	conserved hypothetical protein
SAG0415	142	acetyltransferase, GNAT family
SAG0416	1233	protease, putative
SAG0417	302	glycosyl transferase, group 2 family protein
SAG0418	336	ribonucleoside-diphosphate reductase 2, beta subunit
SAG0419	137	nrdI protein
SAG0420	721	ribonucleoside-diphosphate reductase 2, alpha subunit
SAG0421	1055	cell wall surface anchor family protein
SAG0422	129	conserved hypothetical protein
SAG0423	132	conserved domain protein
SAG0424	94	hypothetical protein
SAG0425	105	carboxymuconolactone decarboxylase family protein
SAG0426	131	conserved hypothetical protein
SAG0427	129	transcriptional regulator, MerR family
SAG0428	345	alcohol dehydrogenase, zinc-containing

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0429	284	oxidoreductase, aldo/keto reductase family
SAG0430	287	cation efflux system protein
SAG0431	174	transcriptional regulator, TetR family
SAG0432	397	transcriptional regulator, AraC family
SAG0433	1389	surface protein Rib
SAG0434	61	transposase, IS256 family, truncation
SAG0435	97	DNA-damage-inducible protein J, putative
SAG0436	62	hypothetical protein
SAG0437	123	lipoprotein, putative
SAG0438	145	bacteriophage L54a, integrase, truncation
SAG0439	NA	conserved hypothetical protein, degenerate
SAG0440	84	conserved hypothetical protein
SAG0441	103	conserved domain protein
SAG0442	189	acetyltransferase, GNAT family
SAG0443	194	acetyltransferase, GNAT family
SAG0444	188	conserved hypothetical protein
SAG0445	883	valyl-tRNA synthetase
SAG0446	319	oxidoreductase, Gfo/Idh/MocA family
SAG0447	287	magnesium transporter, CorA family
SAG0448	391	transposase, IS256 family
SAG0449	354	conserved hypothetical protein
SAG0450	330	aspartate--ammonia ligase
SAG0451	149	bacteriocin transport accessory protein, putative
SAG0452	179	type II DNA modification methyltransferase, putative
SAG0453	96	hypothetical protein
SAG0454	161	phosphopantetheine adenylyltransferase
SAG0455	357	conserved hypothetical protein
SAG0456	NA	conserved hypothetical protein, degenerate
SAG0457	192	conserved hypothetical protein
SAG0458	368	conserved hypothetical protein TIGR00048
SAG0459	171	VanZF domain protein
SAG0460	581	ABC transporter, ATP-binding/permease protein
SAG0461	579	ABC transporter, ATP-binding/permease protein
SAG0462	188	anthranilate synthase component II
SAG0463	179	BioY family protein
SAG0464	330	biotin synthetase
SAG0465	164	hypothetical protein
SAG0466	371	thiolase
SAG0467	409	AMP-binding enzyme domain protein
SAG0468	210	endonuclease III
SAG0469	131	type IV prepilin peptidase-related protein
SAG0470	69	conserved hypothetical protein
SAG0471	322	glucokinase
SAG0472	126	rhodanese-like family protein
SAG0473	613	elongation factor Tu family protein
SAG0474	81	conserved hypothetical protein
SAG0475	451	UDP-N-acetylmuramoylalanine--D-glutamate ligase
SAG0476	358	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0477	378	pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
SAG0478	429	cell division protein DivIB, putative
SAG0479	426	cell division protein FtsA
SAG0480	224	cell division protein FtsZ
SAG0481	201	cell division protein, putative
SAG0482	84	YGGT family protein
SAG0483	262	YlmH protein
SAG0484	256	YlmE protein, putative
SAG0485	930	YlmF protein
SAG0486	100	YlmG protein
SAG0487	151	YlmH protein
SAG0488	753	YlmI protein
SAG0489	34	YlmJ protein
SAG0490	76	YlmK protein
SAG0491	230	YlmL protein
SAG0492	244	YlmM protein
SAG0493	564	YlmN protein
SAG0494	284	YlmO protein
SAG0495	278	YlmP protein
SAG0496	446	YlmQ protein
SAG0497	71	YlmR protein
SAG0498	290	YlmS protein
SAG0499	275	YlmT protein
SAG0500	157	YlmU protein
SAG0501	552	YlmV protein
SAG0502	278	YlmW protein
SAG0503	279	YlmX protein
SAG0504	200	YlmY protein
SAG0505	91	YlmZ protein
SAG0506	65	YlmA protein
SAG0507	310	YlmB protein
SAG0508	411	YlmC protein
SAG0509	403	YlmD protein
SAG0510	406	YlmE protein
SAG0511	270	YlmF protein
SAG0512	438	YlmG protein
SAG0513	128	YlmH protein
SAG0514	894	YlmI protein
SAG0515	286	YlmJ protein
SAG0516	643	YlmK protein
SAG0517	374	YlmL protein
SAG0518	NA	YlmM protein
SAG0519	230	YlmN protein
SAG0520	309	YlmO protein
SAG0521	236	YlmP protein
SAG0522	232	YlmQ protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0523	254	oxidoreductase, short chain dehydrogenase/reductase family
SAG0524	835	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG
SAG0525	397	aspartate aminotransferase
SAG0526	448	asparaginyl-tRNA synthetase
SAG0527	185	conserved hypothetical protein
SAG0528	327	inosine-uridine preferring nucleoside hydrolase
SAG0529	38	hypothetical protein
SAG0530	137	OsmC/Ohr family protein
SAG0531	296	conserved hypothetical protein
SAG0532	324	conserved hypothetical protein
SAG0533	303	conserved hypothetical protein
SAG0534	465	dipeptidase
SAG0535	506	zinc ABC transporter, zinc-binding adhesion liprotein
SAG0536	86	ribosomal protein L31
SAG0537	311	DHH family protein
SAG0538	340	adenosine deaminase, putative
SAG0539	147	flavodoxin
SAG0540	91	chorismate mutase, putative
SAG0541	398	voltage-gated chloride channel family protein
SAG0542	127	IS1381, transposase OrfA
SAG0543	129	IS1381, transposase OrfB
SAG0544	115	ribosomal protein L19
SAG0545	359	prophage LambdaSa1, site-specific recombinase, phage integrase family
SAG0546	67	conserved domain protein
SAG0547	185	hypothetical protein
SAG0548	265	prophage LambdaSa1, repressor protein, putative
SAG0549	47	hypothetical protein
SAG0550	74	conserved hypothetical protein
SAG0551	52	conserved hypothetical protein
SAG0552	62	hypothetical protein
SAG0553	268	hypothetical protein
SAG0554	63	prophage LambdaSa1, transcriptional regulator, Cro/CI family
SAG0555	249	prophage LambdaSa1, antirepressor, putative
SAG0556	47	hypothetical protein
SAG0557	76	hypothetical protein
SAG0558	74	hypothetical protein
SAG0559	286	conserved hypothetical protein
SAG0560	77	conserved hypothetical protein
SAG0561	46	hypothetical protein
SAG0562	84	hypothetical protein
SAG0563	53	hypothetical protein
SAG0564	160	conserved hypothetical protein
SAG0565	224	conserved domain protein
SAG0566	138	prophage LambdaSa1, single-strand binding protein
SAG0567	439	prophage LambdaSa1, reverse transcriptase/maturase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0568	67	conserved hypothetical protein
SAG0569	158	conserved hypothetical protein
SAG0570	115	hypothetical protein
SAG0571	43	hypothetical protein
SAG0572	138	conserved hypothetical protein
SAG0573	54	hypothetical protein
SAG0574	89	conserved hypothetical protein
SAG0575	110	hypothetical protein
SAG0576	43	hypothetical protein
SAG0577	177	conserved hypothetical protein
SAG0578	88	conserved hypothetical protein
SAG0579	142	conserved hypothetical protein
SAG0580	111	conserved hypothetical protein, truncation
SAG0581	118	conserved hypothetical protein
SAG0582	422	conserved hypothetical protein
SAG0583	406	conserved hypothetical protein
SAG0584	62	conserved hypothetical protein, truncation
SAG0585	471	conserved hypothetical protein
SAG0586	154	conserved hypothetical protein
SAG0587	300	prophage LambdaSa1, structural protein, putative
SAG0588	71	conserved hypothetical protein
SAG0589	143	conserved hypothetical protein
SAG0590	112	conserved hypothetical protein
SAG0591	78	conserved hypothetical protein
SAG0592	111	conserved hypothetical protein
SAG0593	185	prophage LambdaSa1, structural protein
SAG0594	81	conserved hypothetical protein
SAG0595	123	conserved hypothetical protein
SAG0596	670	prophage LambdaSa1, pblA protein, internal deletion
SAG0597	506	prophage LambdaSa1, minor structural protein, putative
SAG0598	1374	prophage LambdaSa1, N-acetylmuramoyl-L-alanine amidase, family 4
SAG0599	668	prophage LambdaSa1, minor structural protein, putative
SAG0600	109	hypothetical protein
SAG0601	70	hypothetical protein
SAG0602	100	conserved hypothetical protein
SAG0603	111	conserved hypothetical protein
SAG0604	239	prophage LambdaSa1, lysin, putative
SAG0605	323	conserved hypothetical protein
SAG0606	66	conserved hypothetical protein
SAG0607	56	conserved hypothetical protein
SAG0608	59	hypothetical protein
SAG0609	NA	prophage LambdaSa1, integrase, degenerate
SAG0610	134	conserved hypothetical protein
SAG0611	NA	transposase, degenerate
SAG0612	53	conserved hypothetical protein
SAG0613	425	transmembrane protein Vexp1
SAG0614	218	ABC transporter, ATP-binding protein Vexp2

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0615	458	transmembrane protein Vexp3
SAG0616	217	DNA-binding response regulator VncR
SAG0617	439	sensor histidine kinase VncS
SAG0618	195	transposase OrfB, IS3 family, truncation
SAG0619	66	conserved hypothetical protein
SAG0620	62	hypothetical protein
SAG0621	401	rod shape-determining protein RodA, putative
SAG0622	186	hydrolase, haloacid dehalogenase-like family
SAG0623	650	DNA gyrase, B subunit
SAG0624	574	septation ring formation regulator EzrA, putative
SAG0625	213	phosphoserine phosphatase SerB
SAG0626	161	MutT/nudix family protein
SAG0627	151	conserved hypothetical protein
SAG0628	435	enolase
SAG0629	354	conserved domain protein
SAG0630	427	3-phosphoshikimate 1-carboxyvinyltransferase
SAG0631	170	shikimate kinase
SAG0632	457	psr protein
SAG0633	451	RNA methyltransferase, TrmA family
SAG0634	70	hypothetical protein
SAG0635	245	acid phosphatase, class B
SAG0636	172	conserved hypothetical protein
SAG0637	NA	transcriptional regulator, TetR family, putative, authentic frameshift
SAG0638	109	cell wall surface anchor family protein, truncation
SAG0639	273	transposase OrfB, IS3 family
SAG0640	91	transposase OrfA, IS3 family
SAG0641	NA	Tn5252, Orf 10 protein, degenerate
SAG0642	59	hypothetical protein
SAG0643	NA	chaperonin, 33 kDa, degenerate
SAG0644	402	transcriptional regulator, AraC family
SAG0645	554	cell wall surface anchor family protein
SAG0646	307	cell wall surface anchor family protein
SAG0647	305	sortase family protein
SAG0648	260	sortase family protein
SAG0649	890	cell wall surface anchor family protein, putative
SAG0650	189	sortase family protein
SAG0651	201	protein of unknown function
SAG0652	NA	Tn5252, Orf 28 protein, degenerate
SAG0653	NA	conserved hypothetical protein, degenerate
SAG0654	34	hypothetical protein
SAG0655	57	conserved hypothetical protein
SAG0656	36	hypothetical protein
SAG0657	89	hypothetical protein
SAG0658	383	lipoprotein, putative
SAG0659	330	ABC transporter, ATP-binding protein
SAG0660	272	membrane protein
SAG0661	261	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0662	101	cylX protein
SAG0663	282	cylD protein
SAG0664	240	cylG protein
SAG0665	101	acyl carrier protein AcpC
SAG0666	158	cylZ protein
SAG0667	309	cylA protein
SAG0668	292	cylB protein
SAG0669	667	cylE protein
SAG0670	317	cylF protein
SAG0671	731	cylI protein
SAG0672	403	cylJ protein
SAG0673	191	cylK protein
SAG0674	113	hypothetical protein
SAG0675	171	putative secreted protein
SAG0676	885	proteinase, putative
SAG0677	1062	hypothetical protein
SAG0678	NA	endopeptidase O, degenerate
SAG0679	343	protein of unknown function
SAG0680	339	protein of unknown function
SAG0681	353	conserved domain protein
SAG0682	409	permease, putative
SAG0683	NA	transmembrane protein Vexp3, putative, degenerate
SAG0684	223	ABC transporter, ATP-binding protein
SAG0685	472	conserved hypothetical protein
SAG0686	261	DNA-entry nuclease, putative
SAG0687	212	DedA family protein, putative
SAG0688	218	ABC transporter, ATP-binding protein
SAG0689	257	membrane protein, putative
SAG0690	272	conserved hypothetical protein
SAG0691	294	transcriptional regulator, LysR family
SAG0692	193	regulatory protein, putative
SAG0693	377	IS1548, transposase
SAG0694	173	regulatory protein, putative, truncation
SAG0695	330	D-lactate dehydrogenase
SAG0696	516	sodium:galactoside symporter family protein, putative
SAG0697	341	2-keto-3-deoxygluconate kinase
SAG0698	599	beta-glucuronidase
SAG0699	223	transcriptional regulator, GntR family
SAG0700	205	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase
SAG0701	466	glucuronate isomerase
SAG0702	348	mannonate dehydratase
SAG0703	279	D-mannonate oxidoreductase
SAG0704	270	hydrolase, haloacid dehalogenase-like family
SAG0705	596	glycosyl hydrolase, family 3
SAG0706	361	proline dipeptidase
SAG0707	334	transcriptional regulator, RegM family
SAG0708	488	alpha amylase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0709	332	glycosyl transferase, group 1 family protein
SAG0710	444	glycosyl transferase, group 1 family protein
SAG0711	647	threonyl-tRNA synthetase
SAG0712	234	DNA-binding response regulator
SAG0713	339	conserved hypothetical protein
SAG0714	188	conserved hypothetical protein
SAG0715	216	amino acid ABC transporter, permease protein
SAG0716	231	amino acid ABC transporter, permease protein
SAG0717	266	amino acid ABC transporter, amino acid-binding protein
SAG0718	251	amino acid ABC transporter, ATP-binding protein.
SAG0719	236	DNA-binding response regulator
SAG0720	449	sensory box histidine kinase
SAG0721	269	metallo-beta-lactamase superfamily protein
SAG0722	122	conserved hypothetical protein
SAG0723	236	ribonuclease III
SAG0724	1179	chromosome segregation SMC protein
SAG0725	265	hydrolase, haloacid dehalogenase-like family
SAG0726	274	hydrolase, haloacid dehalogenase-like family
SAG0727	536	signal recognition particle-docking protein FtsY
SAG0728	270	ABC transporter, substrate-binding protein
SAG0729	300	ABC transporter, permease protein, putative
SAG0730	42	ABC transporter, ATP-binding protein
SAG0731	347	bacterial luciferase family protein
SAG0732	720	transcriptional accessory protein Tex, putative
SAG0733	142	conserved hypothetical protein
SAG0734	87	phage shock protein C, putative
SAG0735	44	hypothetical protein
SAG0736	311	HPr(Ser) kinase/phosphatase
SAG0737	257	prolipoprotein diacylglycerol transferase
SAG0738	132	conserved hypothetical protein
SAG0739	143	conserved hypothetical protein
SAG0740	91	conserved hypothetical protein
SAG0741	303	peptidase, U32 family, putative
SAG0742	428	peptidase, U32 family
SAG0743	70	conserved hypothetical protein
SAG0744	265	membrane protein, putative
SAG0745	446	Mn2+/Fe2+ transporter, NRAMP family
SAG0746	369	riboflavin biosynthesis protein RibD
SAG0747	208	riboflavin synthase, alpha subunit
SAG0748	397	riboflavin biosynthesis protein RibA
SAG0749	156	riboflavin synthase, beta subunit
SAG0750	496	lysyl-tRNA synthetase
SAG0751	300	hydrolase, haloacid dehalogenase-like family
SAG0752	213	phosphoglycerate mutase family protein
SAG0753	157	ebsC family protein, putative
SAG0754	205	conserved domain protein
SAG0755	282	peptidase, U32 family
SAG0756	174	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0757	129	protein of unknown function/lipoprotein, putative
SAG0758	599	oligoendopeptidase F, putative
SAG0759	931	phosphoenolpyruvate carboxylase
SAG0760	377	IS1548, transposase
SAG0761	422	cell division protein, FtsW/RodA/SpoVE family
SAG0762	398	translation elongation factor Tu
SAG0763	252	triosephosphate isomerase
SAG0764	230	phosphoglycerate mutase family protein
SAG0765	681	penicillin-binding protein 2b
SAG0766	198	recombination protein RecR
SAG0767	348	D-alanine--D-alanine ligase
SAG0768	455	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase
SAG0769	406	oxalate:formate antiporter
SAG0770	228	membrane protein, putative
SAG0771	512	cell wall surface anchor family protein
SAG0772	514	peptide chain release factor 3
SAG0773	126	conserved hypothetical protein
SAG0774	244	ABC transporter, ATP-binding protein
SAG0775	220	ABC transporter, permease protein
SAG0776	276	YaeC family protein, putative
SAG0777	528	ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0778	88	conserved hypothetical protein
SAG0779	254	conserved hypothetical protein
SAG0780	246	acyltransferase family protein
SAG0781	217	competence protein CelA
SAG0782	745	DNA internalization-related competence protein ComEC/Rec2
SAG0783	269	hydrolase, haloacid dehalogenase-like family
SAG0784	314	sugar-binding transcriptional regulator, LacI family
SAG0785	330	conserved hypothetical protein
SAG0786	242	conserved domain protein
SAG0787	345	DNA polymerase III, delta subunit, putative
SAG0788	202	superoxide dismutase, Fe-Mn
SAG0789	283	transcriptional antiterminator LicT
SAG0790	622	PTS system, beta-glucosides-specific IIABC components
SAG0791	475	6-phospho-beta-glucosidase
SAG0792	364	conserved hypothetical protein
SAG0793	380	glycerate kinase 2
SAG0794	418	permease, GntP family
SAG0795	354	conserved hypothetical protein
SAG0796	147	transcriptional regulator, MarR family
SAG0797	342	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
SAG0798	226	membrane protein, putative
SAG0799	233	glucosamine-6-phosphate isomerase
SAG0800	318	glutathione S-transferase family protein
SAG0801	239	ribosomal small subunit pseudouridine synthase A
SAG0802	38	hypothetical protein
SAG0803	383	major facilitator family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0804	315	competence protein CoIA
SAG0805	601	oligoendopeptidase B
SAG0806	208	hydrolase, haloacid dehalogenase-like family
SAG0807	235	O-methyltransferase family protein
SAG0808	309	protease maturation protein, putative
SAG0809	161	conserved hypothetical protein
SAG0810	872	alanyl-tRNA synthetase
SAG0811	238	membrane protein, putative
SAG0812	272	glycosyl transferase, family 8
SAG0813	81	hypothetical protein
SAG0814	95	conserved hypothetical protein
SAG0815	71	transcriptional regulator, Cro/CI family
SAG0816	253	membrane protein, putative
SAG0817	187	membrane protein, putative
SAG0818	319	ribonucleoside-diphosphate reductase 2, beta subunit
SAG0819	719	ribonucleoside-diphosphate reductase 2, alpha subunit
SAG0820	74	ribonucleoside-diphosphate reductase 2, NrdH-redoxin
SAG0821	87	phosphocarrier protein HPr
SAG0822	577	phosphoenolpyruvate-protein phosphotransferase
SAG0823	475	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent
SAG0824	417	polysaccharide deacetylase family protein
SAG0825	360	ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0826	209	uridine kinase
SAG0827	165	conserved hypothetical protein
SAG0828	554	DNA polymerase III, gamma and tau subunits
SAG0829	64	conserved hypothetical protein
SAG0830	311	biotin--acetyl-CoA-carboxylase ligase
SAG0831	398	S-adenosylmethionine synthetase
SAG0832	753	protein of unknown function
SAG0833	181	hypothetical protein
SAG0834	42	hypothetical protein
SAG0835	188	conserved hypothetical protein
SAG0836	184	conserved hypothetical protein
SAG0837	428	ABC transporter, ATP-binding protein
SAG0838	233	hypothetical protein
SAG0839	226	transcriptional regulator, TenA family
SAG0840	265	phosphomethylpyrimidine kinase
SAG0841	256	hydroxyethylthiazole kinase
SAG0842	223	thiamine-phosphate pyrophosphorylase
SAG0843	419	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
SAG0844	184	acetyltransferase, GNAT family
SAG0845	427	CBS domain protein
SAG0846	286	methionine aminopeptidase, type I
SAG0847	306	ribonuclease BN, putative
SAG0848	151	GtrA family protein
SAG0849	169	conserved hypothetical protein
SAG0850	652	DNA ligase, NAD-dependent
SAG0851	339	bmrU protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0852	766	pullulanase, putative
SAG0853	622	1,4-alpha-glucan branching enzyme
SAG0854	379	glucose-1-phosphate adenylyltransferase
SAG0855	NA	glycogen biosynthesis protein GlgD, authentic frameshift
SAG0856	476	glycogen synthase
SAG0857	66	ATP synthase F0, C subunit
SAG0858	238	ATP synthase F0, A subunit
SAG0859	165	ATP synthase F0, B subunit
SAG0860	178	ATP synthase F1, delta subunit
SAG0861	501	ATP synthase F1, alpha subunit
SAG0862	293	ATP synthase F1, gamma subunit
SAG0863	468	ATP synthase F1, beta subunit
SAG0864	137	ATP synthase F1, epsilon subunit
SAG0865	76	conserved hypothetical protein
SAG0866	423	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
SAG0867	63	conserved hypothetical protein
SAG0868	285	DNA-entry nuclease
SAG0869	346	phenylalanyl-tRNA synthetase, alpha subunit
SAG0870	173	acetyltransferase, GNAT family
SAG0871	801	phenylalanyl-tRNA synthetase, beta subunit
SAG0872	300	conserved hypothetical protein
SAG0873	1077	exonuclease RexB
SAG0874	1207	exonuclease RexA
SAG0875	305	magnesium transporter, CorA family, putative
SAG0876	458	tRNA modification GTPase TrmE
SAG0877	636	ABC transporter, ATP-binding protein
SAG0878	322	acetoin dehydrogenase, thymine PPi dependent, E1 component, alpha subunit
SAG0879	332	acetoin dehydrogenase, thymine PPi dependent, E1 component, beta subunit
SAG0880	462	acetoin dehydrogenase, thymine PPi dependent, E2 component, dihydrolipoamide acetyltransferase
SAG0881	585	acetoin dehydrogenase, thymine PPi dependent, E3 component, dihydrolipoamide dehydrogenase
SAG0882	329	lipoate-protein ligase A
SAG0883	261	cobyric acid synthase, putative
SAG0884	447	mur ligase family protein
SAG0885	283	conserved hypothetical protein TIGR00159
SAG0886	319	protein of unknown function
SAG0887	450	phosphoglucomutase/phosphomannomutase family protein
SAG0888	123	conserved hypothetical protein
SAG0889	126	conserved hypothetical protein
SAG0890	376	oxygen-independent coproporphyrinogen III oxidase, putative
SAG0891	245	conserved hypothetical protein
SAG0892	256	hydrolase, haloacid dehalogenase-like family
SAG0893	218	conserved hypothetical protein
SAG0894	1370	protein of unknown function
SAG0895	289	lipoyl-binding domain protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0896	108	oxidoreductase, putative
SAG0897	221	conserved hypothetical protein
SAG0898	83	hypothetical protein
SAG0899	57	hypothetical protein
SAG0900	56	hypothetical protein
SAG0901	127	hypothetical protein
SAG0902	45	hypothetical protein
SAG0903	44	hypothetical protein
SAG0904	56	hypothetical protein
SAG0905	138	nucleoside diphosphate kinase
SAG0906	610	GTP-binding protein LepA
SAG0907	877	protein of unknown function/lipoprotein, putative
SAG0908	203	HD domain protein
SAG0909	154	acetyltransferase, GNAT family
SAG0910	144	PilB-related protein
SAG0911	930	cation-transporting ATPase, E1-E2 family
SAG0912	367	nucleoside diphosphate kinase domain protein
SAG0913	212	chloramphenicol acetyltransferase
SAG0914	203	conserved hypothetical protein
SAG0915	405	Tn916, transposase
SAG0916	67	Tn916, excisionase
SAG0917	83	Tn916, hypothetical protein
SAG0918	76	Tn916, hypothetical protein
SAG0919	157	Tn916, hypothetical protein
SAG0920	23	Tn916, hypothetical protein
SAG0921	117	Tn916, transcriptional regulator, putative
SAG0922	61	Tn916, hypothetical protein
SAG0923	639	Tn916, tetracycline resistance protein
SAG0924	28	Tn916, tetM leader peptide
SAG0925	310	Tn916, hypothetical protein
SAG0926	333	Tn916, NLP/P60 family protein
SAG0927	725	membrane protein, putative
SAG0928	NA	Tn916, hypothetical protein, authentic frameshift
SAG0929	168	Tn916, hypothetical protein
SAG0930	165	Tn916, hypothetical protein
SAG0931	73	Tn916, hypothetical protein
SAG0932	401	Tn916, transcriptional regulator, putative
SAG0933	461	Tn916, FtsK/SpoIIIE family protein
SAG0934	128	Tn916, hypothetical protein
SAG0935	104	Tn916, hypothetical protein
SAG0936	39	Tn916, hypothetical protein
SAG0937	NA	ABC transporter, ATP-binding protein, authentic frameshift
SAG0938	122	transcriptional regulator, GntR family
SAG0939	1034	DNA polymerase III, alpha subunit
SAG0940	340	6-phosphofructokinase
SAG0941	500	pyruvate kinase
SAG0942	185	signal peptidase I, putative
SAG0943	47	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0944	604	glucosamine--fructose-6-phosphate aminotransferase, isomerizing
SAG0945	377	IS1548, transposase
SAG0946	109	phnA protein
SAG0947	213	amino acid ABC transporter, permease protein
SAG0948	209	amino acid ABC transporter, ATP-binding protein
SAG0949	276	amino acid ABC transporter, amino acid-binding protein
SAG0950	82	ribosomal protein S20
SAG0951	306	pantothenate kinase
SAG0952	196	conserved hypothetical protein
SAG0953	129	cytidine deaminase
SAG0954	349	protein of unknown function/lipoprotein, putative
SAG0955	511	sugar ABC transporter, ATP-binding protein
SAG0956	353	sugar ABC transporter, permease protein, putative
SAG0957	318	sugar ABC transporter, permease protein, putative
SAG0958	456	NADH oxidase
SAG0959	329	L-lactate dehydrogenase
SAG0960	819	DNA gyrase, A subunit
SAG0961	247	sortase SrtA
SAG0962	137	glyoxylase family protein
SAG0963	320	conserved hypothetical protein
SAG0964	375	Na+/H+ exchanger family protein
SAG0965	127	IS1381, transposase OrfA
SAG0966	129	IS1381, transposase OrfB
SAG0967	520	GMP synthase
SAG0968	232	transcriptional regulator, GntR family
SAG0969	444	gid protein
SAG0970	247	acetyltransferase, GNAT family
SAG0971	282	protein of unknown function/lipoprotein, putative
SAG0972	NA	conserved hypothetical protein, authentic frameshift
SAG0973	320	nisin-resistance protein, putative
SAG0974	250	ABC transporter, ATP-binding protein
SAG0975	651	ABC transporter, permease protein, putative
SAG0976	222	DNA-binding response regulator
SAG0977	312	sensor histidine kinase
SAG0978	356	site-specific recombinase, phage integrase family
SAG0979	553	ABC transporter, substrate-binding protein
SAG0980	257	conserved hypothetical protein
SAG0981	228	satD protein
SAG0982	521	signal recognition particle protein Ffh
SAG0983	110	conserved hypothetical protein
SAG0984	437	sensor histidine kinase CiaH
SAG0985	226	DNA-binding response regulator CiaR
SAG0986	849	aminopeptidase N
SAG0987	217	phosphate transport system regulatory protein PhoU
SAG0988	252	phosphate ABC transporter, ATP-binding protein PstB, putative
SAG0989	267	phosphate ABC transporter, ATP-binding protein PstB, putative
SAG0990	295	phosphate ABC transporter, permease protein PstA, putative
SAG0991	305	phosphate ABC transporter, permease protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG0992	286	phosphate ABC transporter, phosphate-binding protein
SAG0993	436	NOL1/NOP2/sun family protein
SAG0994	254	inositol monophosphatase family protein
SAG0995	93	conserved hypothetical protein
SAG0996	137	conserved hypothetical protein
SAG0997	310	macrolide-efflux protein mreA/riboflavin biosynthesis protein RibF
SAG0998	294	tRNA pseudouridine synthase B
SAG0999	143	acetyltransferase, GNAT family
SAG1000	423	conserved hypothetical protein
SAG1001	196	conserved hypothetical protein
SAG1002	292	protease, putative
SAG1003	876	permease, putative
SAG1004	233	ABC transporter, ATP-binding protein
SAG1005	706	DNA topoisomerase I
SAG1006	280	DprA/SMF protein, putative DNA processing factor
SAG1007	342	iron-compound ABC transporter, iron-compound-binding protein
SAG1008	253	iron compound ABC transporter, ATP-binding protein
SAG1009	324	iron compound ABC transporter, permease protein
SAG1010	320	iron compound ABC transporter, permease protein
SAG1011	182	acetyltransferase, CysE/LacA/LpxA/NodL family
SAG1012	253	ribonuclease HII
SAG1013	283	GTP-binding protein
SAG1014	190	conserved hypothetical protein
SAG1015	494	carbon starvation protein CstA, putative
SAG1016	244	response regulator
SAG1017	579	sensor histidine kinase, putative
SAG1018	40	lipoprotein, putative
SAG1019	39	hypothetical protein
SAG1020	227	lipoprotein, putative
SAG1021	107	hypothetical protein
SAG1022	177	hypothetical protein
SAG1023	48	hypothetical protein
SAG1024	183	lipoprotein, putative
SAG1025	149	hypothetical protein
SAG1026	NA	immunogenic secreted protein, degenerate
SAG1027	84	conserved hypothetical protein
SAG1028	196	hypothetical protein
SAG1029	101	hypothetical protein
SAG1030	304	protein of unknown function
SAG1031	120	conserved domain protein
SAG1032	85	conserved hypothetical protein
SAG1033	1309	FtsK/SpoIIIE family protein
SAG1034	55	hypothetical protein
SAG1035	424	conserved hypothetical protein
SAG1036	80	conserved hypothetical protein
SAG1037	157	hypothetical protein
SAG1038	1003	phage infection protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1039	96	conserved hypothetical protein
SAG1040	260	conserved domain protein
SAG1041	107	hypothetical protein
SAG1042	1060	carbamoyl-phosphate synthase, large subunit
SAG1043	358	carbamoyl-phosphate synthase, small subunit
SAG1044	307	aspartate carbamoyltransferase
SAG1045	430	dihydroorotate, multifunctional complex type
SAG1046	209	orotate phosphoribosyltransferase
SAG1047	233	orotidine 5'-phosphate decarboxylase
SAG1048	410	membrane protein, putative
SAG1049	513	ABC transporter, ATP-binding protein
SAG1050	112	ribonucleotide reductase, truncation
SAG1051	358	aspartate-semialdehyde dehydrogenase
SAG1052	47	cell wall surface anchor family protein, putative
SAG1053	30	hypothetical protein
SAG1054	531	cardiolipin synthetase
SAG1055	556	formate--tetrahydrofolate ligase
SAG1056	339	lipoate-protein ligase A
SAG1057	292	conserved hypothetical protein
SAG1058	272	conserved hypothetical protein
SAG1059	110	glycine cleavage system H protein, putative
SAG1060	328	bacterial luciferase family protein
SAG1061	399	oxidoreductase, FMN-binding
SAG1062	282	lipoate-protein ligase A family protein
SAG1063	228	flavoprotein-related protein
SAG1064	180	flavoprotein family protein
SAG1065	190	membrane protein, putative
SAG1066	572	phosphoglucomutase
SAG1067	178	IS861, transposase OrfA
SAG1068	277	IS861, transposase OrfB
SAG1069	65	hypothetical protein
SAG1070	577	ABC transporter, ATP-binding/permease protein
SAG1071	573	ABC transporter, ATP-binding/permease protein
SAG1072	200	conserved hypothetical protein
SAG1073	325	conserved hypothetical protein
SAG1074	418	serine hydroxymethyltransferase
SAG1075	183	Sua5/YciO/YrdC/YwlC family protein
SAG1076	276	modification methylase, HemK family
SAG1077	359	peptide chain release factor 1
SAG1078	189	thymidine kinases
SAG1079	60	4-oxalocrotonate tautomerase
SAG1080	47	hypothetical protein
SAG1081	312	ApbE family protein
SAG1082	200	conserved hypothetical protein
SAG1083	411	conserved hypothetical protein
SAG1084	262	formate/nitrite transporter family protein
SAG1085	424	xanthine permease
SAG1086	193	xanthine phosphoribosyltransferase

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1087	327	guanosine monophosphate reductase
SAG1088	446	drug resistance transporter, EmrB/QacA family, putative
SAG1089	230	conserved hypothetical protein
SAG1090	666	potassium uptake protein, putative
SAG1091	216	oxidoreductase, short chain dehydrogenase/reductase family
SAG1092	330	phosphate acetyltransferase
SAG1093	294	ribosomal large subunit pseudouridine synthase, RluD subfamily
SAG1094	278	conserved hypothetical protein
SAG1095	223	GTP pyrophosphokinase family protein
SAG1096	190	conserved hypothetical protein
SAG1097	324	ribose-phosphate pyrophosphokinase
SAG1098	371	cysteine desulphurase
SAG1099	115	conserved hypothetical protein
SAG1100	210	conserved hypothetical protein
SAG1101	226	DNA repair protein RadC
SAG1102	377	membrane protein, putative
SAG1103	478	6-phospho-beta-glucosidase
SAG1104	204	platelet activating factor, putative
SAG1105	273	hydrolase, haloacid dehalogenase-like family
SAG1106	309	transcriptional regulator, AraC family, putative
SAG1107	510	voltage-gated chloride channel family protein
SAG1108	357	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein
SAG1109	258	spermidine/putrescine ABC transporter, permease protein
SAG1110	264	spermidine/putrescine ABC transporter, permease protein
SAG1111	384	spermidine/putrescine ABC transporter, ATP-binding protein
SAG1112	300	UDP-N-acetylenolpyruvoylglucosamine reductase
SAG1113	162	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase
SAG1114	120	dihydronopterin aldolase
SAG1115	267	dihydropteroate synthase
SAG1116	187	GTP cyclohydrolase I
SAG1117	420	folylpolyglutamate synthase
SAG1118	295	rarD protein
SAG1119	288	homoserine kinase
SAG1120	427	homoserine dehydrogenase
SAG1121	295	polysaccharide deacetylase family protein
SAG1122	515	transporter, BCCT family protein
SAG1123	34	hypothetical protein
SAG1124	458	aldehyde dehydrogenase family protein
SAG1125	335	membrane protein, putative
SAG1126	228	protein of unknown function
SAG1127	446	conserved domain protein
SAG1128	65	transcriptional regulator, Cro/CI family
SAG1129	36	hypothetical protein
SAG1130	49	hypothetical protein
SAG1131	164	thiol peroxidase
SAG1132	219	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1133	254	conserved hypothetical protein
SAG1134	213	transcriptional regulator, GntR family/potassium uptake protein, TrkA family
SAG1135	183	gls24 protein, putative
SAG1136	65	conserved hypothetical protein
SAG1137	180	gls24 protein, putative
SAG1138	64	conserved hypothetical protein
SAG1139	193	conserved hypothetical protein
SAG1140	82	conserved hypothetical protein
SAG1141	112	conserved hypothetical protein
SAG1142	759	ATP-dependent DNA helicase PcrA
SAG1143	128	conserved hypothetical protein
SAG1144	441	uracil permease
SAG1145	448	sodium:alanine symporter family protein
SAG1146	411	cation efflux family protein
SAG1147	130	conserved hypothetical protein
SAG1148	231	membrane protein, putative
SAG1149	207	lipoprotein, putative
SAG1150	400	ribosomal protein S1
SAG1151	76	conserved hypothetical protein
SAG1152	340	branched-chain amino acid aminotransferase
SAG1153	819	DNA topoisomerase IV, A subunit
SAG1154	653	DNA topoisomerase IV, B subunit
SAG1155	212	membrane protein, putative
SAG1156	217	uracil-DNA glycosylase
SAG1157	161	conserved hypothetical protein
SAG1158	413	CMP-N-acetylneurameric acid synthetase NeuA
SAG1159	209	neuD protein
SAG1160	384	UDP-N-acetylglucosamine-2-epimerase NeuC
SAG1161	341	N-acetyl neurameric acid synthetase NeuB
SAG1162	466	polysaccharide biosynthesis protein CpsL
SAG1163	318	polysaccharide biosynthesis protein CpsK(V)
SAG1164	321	glycosyl transferase CpsJ(V)
SAG1165	327	glycosyl transferase CpsO(V)
SAG1166	295	glycosyl transferase CpsN(V)
SAG1167	241	polysaccharide biosynthesis protein CpsM(V)
SAG1168	364	polysaccharide biosynthesis protein cpsH(V)
SAG1169	163	glycosyl transferase CpsG(V)
SAG1170	149	polysaccharide biosynthesis protein CpsF
SAG1171	462	glycosyl transferase CpsE
SAG1172	229	cpsD protein
SAG1173	230	cpsC protein
SAG1174	243	capsular polysaccharide biosynthesis protein CpsB
SAG1175	485	capsular polysaccharide biosynthesis protein CpsA
SAG1176	290	transcriptional regulator, LysR family, putative
SAG1177	255	conserved hypothetical protein
SAG1178	236	purine nucleoside phosphorylase
SAG1179	418	voltage-gated chloride channel family protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1180	269	purine nucleoside phosphorylase
SAG1181	135	arsenate reductase
SAG1182	403	phosphopentomutase
SAG1183	223	ribose 5-phosphate isomerase
SAG1184	236	conserved hypothetical protein
SAG1185	262	tributyrin esterase
SAG1186	553	metallo-beta-lactamase superfamily protein
SAG1187	253	ABC transporter, ATP-binding protein
SAG1188	287	ABC transporter, permease protein
SAG1189	334	conserved hypothetical protein
SAG1190	551	adherence and virulence protein A
SAG1191	239	alpha-acetolactate decarboxylase
SAG1192	560	acetolactate synthase, catabolic
SAG1193	408	TPR domain protein
SAG1194	396	membrane protein, putative
SAG1195	153	MutT/nudix family protein
SAG1196	160	mutator MutT protein
SAG1197	1072	hyaluronidase
SAG1198	348	dTDP-glucose 4,6-dehydratase
SAG1199	197	dTDP-4-dehydrorhamnose 3,5-epimerase
SAG1200	289	glucose-1-phosphate thymidylyltransferase
SAG1201	367	iminodiacetate oxidase, putative
SAG1202	262	conserved hypothetical protein TIGR00486
SAG1203	227	conserved hypothetical protein
SAG1204	226	DNA replication protein DnaD, putative
SAG1205	172	adenine phosphoribosyltransferase
SAG1206	854	conserved domain protein
SAG1207	32	hypothetical protein
SAG1208	732	single-stranded-DNA-specific exonuclease RecJ
SAG1209	253	oxidoreductase, short chain dehydrogenase/reductase family
SAG1210	309	metallo-beta-lactamase superfamily protein
SAG1211	215	conserved hypothetical protein
SAG1212	412	GTP-binding protein HflX
SAG1213	296	tRNA delta(2)-isopentenylpyrophosphate transferase
SAG1214	58	hypothetical protein
SAG1215	305	exfoliative toxin A, putative
SAG1216	1252	pullulanase, putative
SAG1217	NA	conserved hypothetical protein, authentic frameshift
SAG1218	194	conserved hypothetical protein
SAG1219	468	peptidase, M20/M25/M40 family
SAG1220	200	nitroreductase family protein
SAG1221	NA	glycerophosphoryl diester phosphodiesterase, putative, authentic point mutation
SAG1222	593	excinuclease ABC, C subunit
SAG1223	255	conserved hypothetical protein
SAG1224	446	MATE efflux family protein
SAG1225	136	conserved hypothetical protein
SAG1226	165	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1227	198	protein of unknown function
SAG1228	96	ISSdy1, transposase OrfA
SAG1229	259	ISSdy1, transposase OrfB
SAG1230	96	conserved hypothetical protein
SAG1231	NA	transposase OrfB, IS3 family, degenerate
SAG1232	77	transposase OrfB, IS3 family, truncation
SAG1233	822	streptococcal histidine triad family protein
SAG1234	306	laminin-binding surface protein
SAG1235	425	GBSi1, group II intron, maturase
SAG1236	NA	C5a peptidase, authentic frameshift
SAG1237	444	hypothetical protein
SAG1238	202	hypothetical protein
SAG1239	76	conserved hypothetical protein
SAG1240	125	conserved hypothetical protein, truncation
SAG1241	91	transposase OrfA, IS3 family
SAG1242	67	transposase OrfB, IS3 family, truncation
SAG1243	96	ISSdy1, transposase OrfA
SAG1244	259	ISSdy1, transposase OrfB
SAG1245	38	hypothetical protein
SAG1246	389	hypothetical protein
SAG1247	399	site-specific recombinase, phage integrase family
SAG1248	75	conserved hypothetical protein
SAG1249	74	transcriptional regulator, Cro/CI family
SAG1250	621	Tn5252, relaxase
SAG1251	121	Tn5252, Orf 9 protein
SAG1252	120	Tn5252, Orf 10 protein
SAG1253	435	transposase, ISL3 family
SAG1254	546	mercuric reductase
SAG1255	130	mercuric resistance operon regulatory protein MerR
SAG1256	142	IS861, transposase OrfB, truncation
SAG1257	709	cation-transporting ATPase, E1-E2 family
SAG1258	122	cadmium efflux system accessory protein
SAG1259	99	conserved hypothetical protein
SAG1260	262	hypothetical protein
SAG1261	198	conserved hypothetical protein
SAG1262	695	cation-transporting ATPase, E1-E2 family
SAG1263	NA	conserved domain protein, authentic frameshift
SAG1264	148	transcriptional repressor CopY, putative
SAG1265	206	cadmium resistance transporter, putative
SAG1266	152	hypothetical protein
SAG1267	108	hypothetical protein
SAG1268	230	repressor protein, putative
SAG1269	44	hypothetical protein
SAG1270	471	ImpB/MucB/SamB family protein
SAG1271	116	conserved hypothetical protein
SAG1272	102	conserved hypothetical protein
SAG1273	118	conserved hypothetical protein
SAG1274	129	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1275	75	hypothetical protein
SAG1276	358	conserved hypothetical protein
SAG1277	163	hypothetical protein
SAG1278	96	hypothetical protein
SAG1279	99	conserved domain protein
SAG1280	2274	SNF2 family protein
SAG1281	183	hypothetical protein
SAG1282	63	calcium-binding protein, putative
SAG1283	1631	agglutinin receptor
SAG1284	196	abortive infection protein AbiGI
SAG1285	281	abortive infection protein AbiGII
SAG1286	933	Tn5252, Orf28
SAG1287	776	Tn5252, Orf26
SAG1288	NA	Tn5252, Orf25, degenerate
SAG1289	284	Tn5252, Orf23
SAG1290	80	hypothetical protein
SAG1291	605	Tn5252, Orf 21 protein, internal deletion
SAG1292	162	hypothetical protein
SAG1293	194	protease, putative
SAG1294	77	conserved hypothetical protein
SAG1295	127	conserved hypothetical protein
SAG1296	142	conserved hypothetical protein
SAG1297	451	C-5 cytosine-specific DNA methylase
SAG1298	31	hypothetical protein
SAG1299	272	conserved hypothetical protein
SAG1300	57	conserved hypothetical protein
SAG1301	121	ribosomal protein L7/L12
SAG1302	166	ribosomal protein L10
SAG1303	702	ATP-dependent Clp protease, ATP-binding subunit
SAG1304	32	hypothetical protein
SAG1305	314	homocysteine S-methyltransferase MmuM, putative
SAG1306	458	amino acid permease
SAG1307	216	hypothetical protein
SAG1308	167	hypothetical protein
SAG1309	30	hypothetical protein
SAG1310	182	transcriptional regulator, TetR family
SAG1311	198	GTP-binding protein
SAG1312	408	ATP-dependent Clp protease, ATP-binding subunit ClpX
SAG1313	56	conserved hypothetical protein
SAG1314	164	dihydrofolate reductase
SAG1315	279	thymidylate synthase
SAG1316	390	HMG-CoA synthase
SAG1317	427	3-hydroxy-3-methylglutaryl-CoA reductase
SAG1318	149	conserved hypothetical protein
SAG1319	214	hemolysin III, putative
SAG1320	304	conserved hypothetical protein TIGR00147
SAG1321	284	glutathione S-transferase family protein, putative
SAG1322	72	conserved domain protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1323	331	isopentenyl-diphosphate delta-isomerase
SAG1324	330	phosphomevalonate kinase
SAG1325	314	diphosphomevalonate decarboxylase
SAG1326	292	mevalonate kinase, putative
SAG1327	409	sensor histidine kinase
SAG1328	228	DNA-binding response regulator
SAG1329	208	GTP pyrophosphokinase family protein
SAG1330	68	hypothetical protein
SAG1331	979	R5 protein
SAG1332	146	transcriptional regulator, MarR family, putative
SAG1333	690	5'-nucleotidase family protein
SAG1334	136	polypeptide deformylase, putative
SAG1335	449	NADP-specific glutamate dehydrogenase
SAG1336	169	membrane protein, putative
SAG1337	589	ABC transporter, ATP-binding/permease protein
SAG1338	579	ABC transporter, ATP-binding/permease protein
SAG1339	157	acetyltransferase, GNAT family
SAG1340	622	ABC transporter, ATP-binding protein
SAG1341	402	polyA polymerase family protein
SAG1342	282	DegV family protein
SAG1343	126	protein of unknown function
SAG1344	177	hypothetical protein
SAG1345	164	conserved hypothetical protein
SAG1346	654	PTS system, fructose specific IIABC components
SAG1347	303	1-phosphofructokinase
SAG1348	247	lactose phosphotransferase system repressor
SAG1349	411	beta-lactam resistance factor
SAG1350	544	surface antigen-related protein
SAG1351	307	2-dehydropantoate 2-reductase, putative
SAG1352	356	regulatory protein, putative
SAG1353	330	pyridine nucleotide-disulphide oxidoreductase family protein
SAG1354	251	tRNA (guanine-N1)-methyltransferase
SAG1355	172	16S rRNA processing protein RimM
SAG1356	503	transcriptional regulator, RofA family
SAG1357	80	KH domain protein
SAG1358	90	ribosomal protein S16
SAG1359	415	permease, putative
SAG1360	236	ABC transporter, ATP-binding protein
SAG1361	414	conserved hypothetical protein
SAG1362	532	carbamoyl-phosphate synthase, large subunit, putative
SAG1363	356	carbamoyl-phosphate synthase, small subunit
SAG1364	173	pyrimidine operon regulatory protein
SAG1365	296	ribosomal large subunit pseudouridine synthase, RluD subfamily
SAG1366	154	lipoprotein signal peptidase
SAG1367	301	transcriptional regulator, LysR family
SAG1368	94	ribosomal protein L27
SAG1369	112	conserved hypothetical protein
SAG1370	104	ribosomal protein L21

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1371	392	conserved hypothetical protein
SAG1372	404	thiamine biosynthesis protein ThiI
SAG1373	381	cysteine desulphurase
SAG1374	150	conserved hypothetical protein
SAG1375	449	glutathione reductase
SAG1376	111	conserved hypothetical protein
SAG1377	388	chorismate synthase
SAG1378	355	3-dehydroquinate synthase
SAG1379	225	3-dehydroquinate dehydratase
SAG1380	385	conserved hypothetical protein
SAG1381	714	sulfatase
SAG1382	119	ribosomal protein L20
SAG1383	66	ribosomal protein L35
SAG1384	176	translation initiation factor IF-3
SAG1385	227	cytidylate kinase
SAG1386	174	conserved hypothetical protein
SAG1387	65	ferredoxin, 4Fe-4S
SAG1388	163	conserved hypothetical protein
SAG1389	406	peptidase T
SAG1390	544	polysaccharide biosynthesis protein, putative
SAG1391	484	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
SAG1392	264	iron compound ABC transporter, ATP-binding protein
SAG1393	310	iron compound ABC transporter, substrate-binding protein
SAG1394	341	iron compound ABC transporter, permease protein
SAG1395	333	iron compound ABC transporter, permease protein
SAG1396	217	conserved hypothetical protein
SAG1397	311	inorganic pyrophosphatase, manganese-dependent
SAG1398	262	pyruvate formate-lyase-activating enzyme
SAG1399	444	CBS domain protein
SAG1400	188	conserved hypothetical protein
SAG1401	311	conserved hypothetical protein TIGR01212
SAG1402	213	PAP2 family protein
SAG1403	194	membrane protein, putative
SAG1404	308	cell wall surface anchor family protein
SAG1405	294	sortase family protein
SAG1406	293	sortase family protein
SAG1407	705	cell wall surface anchor family protein
SAG1408	901	cell wall surface anchor family protein
SAG1409	NA	rogB protein, authentic frameshift
SAG1410	379	glycosyl transferase, group 1 family protein
SAG1411	282	glycosyl transferase, group 2 family protein
SAG1412	474	polysaccharide biosynthesis protein
SAG1413	454	membrane protein, putative
SAG1414	308	glycosyl transferase, group 2 family protein
SAG1415	311	glycosyl transferase, group 2 family protein
SAG1416	352	nucleotide sugar dehydratase, putative
SAG1417	240	nucleotidyl transferase, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1418	274	polysaccharide biosynthesis protein, putative
SAG1419	577	lipoprotein, putative
SAG1420	117	conserved hypothetical protein
SAG1421	243	glycosyl transferase, group 2 family protein
SAG1422	313	glycosyl transferase, group 2 family protein
SAG1423	384	glycosyl transferase, putative
SAG1424	284	dTDP-4-dehydrorhamnose reductase
SAG1425	113	conserved hypothetical protein
SAG1426	369	RNA polymerase sigma-70 factor
SAG1427	602	DNA primase
SAG1428	125	large conductance mechanosensitive channel protein
SAG1429	58	ribosomal protein S21
SAG1430	167	conserved hypothetical protein
SAG1431	268	amino acid ABC transporter, amino acid-binding protein
SAG1432	347	ammonium transporter family protein
SAG1433	375	conserved hypothetical protein
SAG1434	328	rhodanese family protein
SAG1435	101	conserved hypothetical protein
SAG1436	457	glycerol-3-phosphate transporter, putative
SAG1437	55	hypothetical protein
SAG1438	754	glycogen phosphorylase
SAG1439	498	4-alpha-glucanotransferase
SAG1440	342	maltose operon repressor MalR, putative
SAG1441	415	maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein
SAG1442	456	maltose ABC transporter, permease protein
SAG1443	278	maltose ABC transporter, permease protein
SAG1444	490	proton/peptide symporter family protein
SAG1445	NA	MutT/nudix family protein, authentic frameshift
SAG1446	62	hypothetical protein
SAG1447	441	conserved hypothetical protein
SAG1448	502	glycosyl transferase, group 1 family protein
SAG1449	795	preprotein translocase SecA subunit, putative
SAG1450	330	conserved domain protein
SAG1451	494	conserved hypothetical protein
SAG1452	514	conserved hypothetical protein
SAG1453	409	preprotein translocase SecY family protein
SAG1454	398	glycosyl transferase, putative
SAG1455	295	glycosyl transferase, group 2 family protein
SAG1456	NA	glycosyl transferase, family 8, degenerate
SAG1457	129	IS1381, transposase OrfB
SAG1458	127	IS1381, transposase OrfA
SAG1459	413	glycosyl transferase family 8
SAG1460	401	glycosyl transferase, family 8
SAG1461	335	conserved hypothetical protein
SAG1462	970	cell wall surface anchor family protein
SAG1463	NA	transcriptional regulator, RofA family, authentic point mutation
SAG1464	663	excinuclease ABC, B subunit

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1465	306	protease, putative
SAG1466	727	glutamine ABC transporter, glutamine-binding protein/permease protein
SAG1467	246	glutamine ABC transporter, ATP-binding protein, GlnQ putative
SAG1468	116	conserved hypothetical protein
SAG1469	52	conserved hypothetical protein
SAG1470	437	GTP-binding protein, GTP1/Obg family
SAG1471	42	conserved hypothetical protein
SAG1472	413	aminopeptidase PepS
SAG1473	192	cell wall surface anchor family protein
SAG1474	680	amidase family protein
SAG1475	240	ribosomal small subunit pseudouridine synthase A
SAG1476	280	oxidoreductase, aldo/keto reductase family
SAG1477	224	nitroreductase family protein
SAG1478	130	lactoylglutathione lyase
SAG1479	308	glycosyl transferase, group 2 family protein
SAG1480	462	amino acid permease
SAG1481	155	SsrA-binding protein
SAG1482	801	exoribonuclease, VacB/Rnb family
SAG1483	78	preprotein translocase, SecG subunit
SAG1484	48	ribosomal protein L33
SAG1485	389	multi-drug resistance protein
SAG1486	548	membrane protein, putative
SAG1487	233	ABC transporter, ATP binding protein
SAG1488	195	dephospho-CoA kinase
SAG1489	273	formamidopyrimidine-DNA glycosylase
SAG1490	282	transcriptional regulator, MutR family
SAG1491	530	hypothetical protein
SAG1492	58	hypothetical protein
SAG1493	66	hypothetical protein
SAG1494	32	hypothetical protein
SAG1495	81	CAAX amino terminal protease family protein
SAG1496	110	hypothetical protein
SAG1497	37	hypothetical protein
SAG1498	133	hypothetical protein
SAG1499	299	GTP-binding protein Era
SAG1500	132	diacylglycerol kinase
SAG1501	161	conserved hypothetical protein TIGR00043
SAG1502	268	tetracenomycin polyketide synthesis O-methyltransferase TcmP, putative
SAG1503	39	hypothetical protein
SAG1504	38	hypothetical protein
SAG1505	158	MutT/nudix family protein
SAG1506	267	hypothetical protein
SAG1507	345	PhoH family protein
SAG1508	590	67 kDa Myosin-crossreactive streptococcal antigen
SAG1509	71	conserved hypothetical protein
SAG1510	169	peptide methionine sulfoxide reductase

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1511	284	conserved hypothetical protein
SAG1512	185	ribosome recycling factor
SAG1513	242	uridylate kinase
SAG1514	226	peptide ABC transporter, ATP-binding protein
SAG1515	262	peptide ABC transporter, ATP-binding protein
SAG1516	255	peptide ABC transporter, permease protein
SAG1517	314	peptide ABC transporter, permease protein
SAG1518	538	peptide ABC transporter, peptide-binding protein
SAG1519	229	ribosomal protein L1
SAG1520	141	ribosomal protein L11
SAG1521	388	transposase, IS30 family, putative
SAG1522	460	transporter, major facilitator family
SAG1523	404	peptidase, M20/M25/M40 family
SAG1524	294	transcriptional regulator, LysR family
SAG1525	117	conserved hypothetical protein
SAG1526	178	IS861, transposase OrfA
SAG1527	277	IS861, transposase OrfB
SAG1528	571	chorismate binding enzyme
SAG1529	816	FtsK/SpoIIIE family protein
SAG1530	267	peptidyl-prolyl cis-trans isomerase, cyclophilin-type
SAG1531	277	manganese ABC transporter, permease protein
SAG1532	238	manganese ABC transporter, ATP-binding protein
SAG1533	308	manganese ABC transporter, manganese-binding adhesion lipoprotein
SAG1534	215	iron-dependent transcriptional regulator
SAG1535	229	5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase
SAG1536	89	conserved hypothetical protein
SAG1537	184	MutT/nudix family protein
SAG1538	459	UDP-N-acetylglucosamine pyrophosphorylase
SAG1539	31	hypothetical protein
SAG1540	137	conserved hypothetical protein
SAG1541	125	glyoxalase family protein
SAG1542	318	oxidoreductase, Gfo/Idh/MocA family
SAG1543	NA	conserved hypothetical protein, authentic frameshift
SAG1544	232	gluconate 5-dehydrogenase, putative
SAG1545	78	conserved hypothetical protein
SAG1546	82	conserved hypothetical protein
SAG1547	166	acetyltransferase, GNAT family
SAG1548	422	glycosyl transferase, group 2 family protein
SAG1549	127	IS1381, transposase OrfA
SAG1550	129	IS1381, transposase OrfB
SAG1551	67	hypothetical protein
SAG1552	719	conserved hypothetical protein
SAG1553	477	hypothetical protein
SAG1554	225	hypothetical protein
SAG1555	231	hypothetical protein
SAG1556	445	branched-chain amino acid transport system II carrier protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1557	665	methionyl-tRNA synthetase
SAG1558	291	tellurite resistance protein TehB
SAG1559	231	membrane protein, putative
SAG1560	40	hypothetical protein
SAG1561	405	PTS system, IIC component, putative
SAG1562	280	conserved hypothetical protein
SAG1563	275	exodeoxyribonuclease
SAG1564	118	conserved hypothetical protein
SAG1565	158	methylated-DNA-protein-cysteine S-methyltransferase
SAG1566	393	D-isomer specific 2-hydroxyacid dehydrogenase family protein
SAG1567	182	acetyltransferase, GNAT family
SAG1568	NA	phosphoserine aminotransferase, authentic frameshift
SAG1569	211	copper homeostasis protein CutC, putative
SAG1570	34	conserved hypothetical protein
SAG1571	53	hypothetical protein
SAG1572	287	tetrapyrrole methylase family protein
SAG1573	108	conserved hypothetical protein
SAG1574	287	DNA polymerase III, delta prime subunit, putative
SAG1575	211	thymidylate kinase
SAG1576	267	transposase, IS30 family, putative, truncation
SAG1577	219	AcuB family protein
SAG1578	236	branched-chain amino acid ABC transporter, ATP-binding protein
SAG1579	254	branched-chain amino acid ABC transporter, ATP-binding protein
SAG1580	317	branched-chain amino acid ABC transporter, permease protein
SAG1581	289	branched-chain amino acid ABC transporter, permease protein
SAG1582	388	branched-chain amino acid ABC transporter, amino acid-binding protein
SAG1583	81	conserved hypothetical protein
SAG1584	377	IS1548, transposase
SAG1585	196	ATP-dependent Clp protease, proteolytic subunit ClpP
SAG1586	209	uracil phosphoribosyltransferase
SAG1587	389	aminotransferase, class I
SAG1588	182	RNA methyltransferase, TrmH family, group 2
SAG1589	450	amino acid permease, putative
SAG1590	449	potassium uptake protein, Trk family
SAG1591	475	cation uptake protein, Trk family
SAG1592	83	conserved hypothetical protein TIGR00278
SAG1593	240	ribosomal large subunit pseudouridine synthase B
SAG1594	194	conserved hypothetical protein TIGR00281
SAG1595	235	conserved hypothetical protein
SAG1596	246	integrase/recombinase, phage integrase family
SAG1597	157	CBS domain protein
SAG1598	173	conserved hypothetical protein
SAG1599	324	HAM1 protein
SAG1600	264	glutamate racemase
SAG1601	79	conserved hypothetical protein
SAG1602	180	membrane protein, putative
SAG1603	173	transcriptional regulator, biotin repressor family

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1604	229	membrane protein, putative
SAG1605	167	conserved hypothetical protein
SAG1606	247	RNA methyltransferase, TrmH family
SAG1607	92	acylphosphatase
SAG1608	310	lipoprotein, putative
SAG1609	221	amino acid ABC transporter, permease protein
SAG1610	285	amino acid ABC transporter, substrate-binding protein
SAG1611	486	amidase family protein
SAG1612	160	transcription elongation factor GreA
SAG1613	600	conserved hypothetical protein
SAG1614	167	acetyltransferase, GNAT family
SAG1615	443	UDP-N-acetylmuramate--alanine ligase
SAG1616	205	conserved hypothetical protein
SAG1617	32	hypothetical protein
SAG1618	1032	Snf2 family protein
SAG1619	377	IS1548, transposase
SAG1620	436	phosphoglycerate dehydrogenase-related protein
SAG1621	300	primosomal protein DnaI
SAG1622	391	conserved hypothetical protein
SAG1623	159	conserved hypothetical protein TIGR00244
SAG1624	501	sensor histidine kinase CsrS
SAG1625	229	DNA-binding response regulator CsrR
SAG1626	177	conserved hypothetical protein
SAG1627	296	heat shock protein HtpX
SAG1628	184	lemA protein
SAG1629	237	glucose-inhibited division protein B
SAG1630	459	sodium transport family protein
SAG1631	223	potassium uptake protein, Trk family, putative
SAG1632	276	cobalt transport family protein
SAG1633	558	ABC transporter, ATP-binding protein
SAG1634	212	conserved hypothetical protein
SAG1635	402	sodium:dicarboxylate symporter family protein
SAG1636	455	branched-chain amino acid transport system II carrier protein
SAG1637	351	alcohol dehydrogenase, zinc-containing
SAG1638	230	ABC transporter, permease protein
SAG1639	356	ABC transporter, ATP-binding protein
SAG1640	458	peptidase, M20/M25/M40 family
SAG1641	274	YaeC family protein
SAG1642	277	ABC transporter, substrate-binding protein
SAG1643	229	glutamine amidotransferase, class I
SAG1644	37	hypothetical protein
SAG1645	238	conserved hypothetical protein TIGR01033
SAG1646	32	hypothetical protein
SAG1647	328	dihydroxyacetone kinase family protein
SAG1648	178	transcriptional regulator, TetR family, putative
SAG1649	37	hypothetical protein
SAG1650	329	dihydroxyacetone kinase family protein
SAG1651	192	dihydroxyacetone kinase family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1652	124	conserved hypothetical protein
SAG1653	237	glycerol uptake facilitator protein
SAG1654	134	conserved hypothetical protein
SAG1655	237	transcriptional regulator, MerR family
SAG1656	369	conserved hypothetical protein
SAG1657	83	hypothetical protein
SAG1658	244	conserved hypothetical protein
SAG1659	118	iojap-related protein
SAG1660	173	isochorismatase family protein
SAG1661	195	conserved hypothetical protein TIGR00488
SAG1662	210	conserved hypothetical protein TIGR00482
SAG1663	105	conserved hypothetical protein TIGR00253
SAG1664	372	GTP-binding protein
SAG1665	177	hydrolase, haloacid dehalogenase-like family
SAG1666	304	membrane protein, putative
SAG1667	480	glutamyl-tRNA(Gln) amidotransferase, B subunit
SAG1668	488	glutamyl-tRNA(Gln) amidotransferase, A subunit
SAG1669	100	glutamyl-tRNA(Gln) amidotransferase, C subunit
SAG1670	881	pyruvate phosphate dikinase
SAG1671	276	protein of unknown function
SAG1672	170	CBS domain protein
SAG1673	321	3-hydroxyacyl-CoA dehydrogenase family protein
SAG1674	182	isochorismatase family protein
SAG1675	261	transcriptional regulator CodY, putative
SAG1676	403	aminotransferase, class I
SAG1677	150	conserved hypothetical protein
SAG1678	460	hydrolase, haloacid dehalogenase-like family
SAG1679	320	asparaginase family protein
SAG1680	292	shikimate 5-dehydrogenase
SAG1681	304	oxidoreductase, aldo/keto reductase family
SAG1682	671	ATP-dependent DNA helicase RecG
SAG1683	512	immunogenic secreted protein, putative
SAG1684	366	alanine racemase
SAG1685	119	holo-(acyl-carrier-protein) synthase
SAG1686	335	phospho-2-dehydro-3-deoxyheptonate aldolase
SAG1687	842	preprotein translocase, SecA subunit
SAG1688	315	mannose-6-phosphate isomerase, class I
SAG1689	293	fructokinase
SAG1690	639	PTS system, IIABC components
SAG1691	479	sucrose-6-phosphate hydrolase
SAG1692	320	sucrose operon repressor ScrR
SAG1693	144	N utilization substance protein B
SAG1694	129	conserved hypothetical protein
SAG1695	186	translation elongation factor P
SAG1696	38	hypothetical protein
SAG1697	48	hypothetical protein
SAG1698	99	conserved hypothetical protein
SAG1699	30	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1700	76	hypothetical protein
SAG1701	56	hypothetical protein
SAG1702	41	hypothetical protein
SAG1703	54	hypothetical protein
SAG1704	150	cytidine/deoxycytidylate deaminase family protein
SAG1705	NA	peptidase, M24 family, authentic point mutation
SAG1706	238	conserved hypothetical protein
SAG1707	499	drug resistance transporter, EmrB/QacA family
SAG1708	38	hypothetical protein
SAG1709	942	excinuclease ABC, A subunit
SAG1710	223	conserved hypothetical protein
SAG1711	314	magnesium transporter, CorA family
SAG1712	79	ribosomal protein S18
SAG1713	163	single-strand binding protein
SAG1714	95	ribosomal protein S6
SAG1715	374	A/G-specific adenine glycosylase
SAG1716	197	transcriptional regulator, Cro/CI family
SAG1717	104	thioredoxin
SAG1718	166	PAP2 family protein
SAG1719	779	MutS2 family protein
SAG1720	180	conserved hypothetical protein
SAG1721	103	conserved hypothetical protein
SAG1722	297	ribonuclease HIII
SAG1723	197	signal peptidase I
SAG1724	806	helicase, putative
SAG1725	160	conserved hypothetical protein
SAG1726	364	DNA-damage-inducible protein P
SAG1727	770	formate acetyltransferase
SAG1728	124	FMN-binding protein
SAG1729	309	conserved hypothetical protein
SAG1730	251	conserved hypothetical protein
SAG1731	298	membrane protein, putative
SAG1732	282	glycerol uptake facilitator protein, putative
SAG1733	150	universal stress protein family
SAG1734	400	transporter, putative
SAG1735	219	transcriptional regulator, Crp/Fnr family
SAG1736	761	X-pro dipeptidyl-peptidase
SAG1737	119	hypothetical protein
SAG1738	326	polyprenyl synthetase family protein
SAG1739	582	ABC transporter, ATP-binding protein CydC
SAG1740	572	ABC transporter, ATP-binding protein CydD
SAG1741	339	cytochrome d ubiquinol oxidase, subunit II
SAG1742	475	cytochrome d oxidase, subunit I
SAG1743	402	pyridine nucleotide-disulphide oxidoreductase family protein
SAG1744	299	prenyltransferase, UbiA family
SAG1745	148	hypothetical protein
SAG1746	35	hypothetical protein
SAG1747	99	conserved hypothetical protein TIGR00103

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1748	396	cyclopropane-fatty-acyl-phospholipid synthase
SAG1749	241	transcriptional regulator, merR family
SAG1750	195	exonuclease
SAG1751	178	conserved hypothetical protein
SAG1752	390	conserved hypothetical protein TIGR00275
SAG1753	260	conserved hypothetical protein
SAG1754	89	ribosomal protein S14
SAG1755	38	hypothetical protein
SAG1756	341	conserved hypothetical protein
SAG1757	336	O-sialoglycoprotein endopeptidase family protein
SAG1758	135	ribosomal-protein-alanine acetyltransferase, putative
SAG1759	230	protein of unknown function
SAG1760	76	conserved hypothetical protein
SAG1761	559	metallo-beta-lactamase superfamily protein
SAG1762	169	conserved hypothetical protein
SAG1763	448	glutamine synthetase, type I
SAG1764	123	transcriptional regulator GlnR
SAG1765	179	conserved hypothetical protein
SAG1766	398	phosphoglycerate kinase
SAG1767	289	acid phosphatase
SAG1768	336	glyceraldehyde 3-phosphate dehydrogenase
SAG1769	692	translation elongation factor G
SAG1770	156	ribosomal protein S7
SAG1771	137	ribosomal protein S12
SAG1772	270	pur operon repressor
SAG1773	313	HD domain protein
SAG1774	424	conserved hypothetical protein
SAG1775	210	conserved hypothetical protein
SAG1776	220	ribulose-phosphate 3-epimerase
SAG1777	290	conserved hypothetical protein TIGR00157
SAG1778	283	rRNA (guanine-N1-)methyltransferase, putative
SAG1779	290	dimethyladenosine transferase
SAG1780	163	hypothetical protein
SAG1781	186	primase-related protein
SAG1782	260	deoxyribonuclease, TatD family
SAG1783	90	hypothetical protein
SAG1784	130	hypothetical protein
SAG1785	430	hypothetical protein
SAG1786	130	protein of unknown function
SAG1787	420	dltD protein
SAG1788	79	D-alanyl carrier protein
SAG1789	421	dltB protein
SAG1790	511	D-alanine-activating enzyme
SAG1791	395	sensor histidine kinase
SAG1792	224	DNA-binding response regulator
SAG1793	44	ribosomal protein L34
SAG1794	451	membrane protein, putative
SAG1795	388	transposase, IS30 family, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1796	575	amino acid ABC transporter, permease protein
SAG1797	407	amino acid ABC transporter, ATP-binding protein
SAG1798	39	hypothetical protein
SAG1799	792	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase
SAG1800	363	conserved hypothetical protein
SAG1801	559	transcriptional antiterminator, BglG family
SAG1802	253	conserved hypothetical protein
SAG1803	505	carbohydrate kinase, FGGY family
SAG1804	329	hypothetical protein
SAG1805	483	PTS system, IIC component, putative
SAG1806	318	glyoxylate reductase, NADH-dependent
SAG1807	339	hypothetical protein
SAG1808	327	sugar binding transcriptional regulator, LacI family
SAG1809	215	transaldolase family protein
SAG1810	238	carbohydrate isomerase, AraD/FucA family
SAG1811	287	hexulose-6-phosphate isomerase, putative
SAG1812	221	hexulose-6-phosphate synthase, putative
SAG1813	161	PTS system, IIA component
SAG1814	92	PTS system, IIB component
SAG1815	479	transport protein SgaT, putative
SAG1816	205	hypothetical protein
SAG1817	157	hypothetical protein
SAG1818	430	adenylosuccinate synthetase
SAG1819	340	perfringolysin O regulator protein
SAG1820	224	conserved hypothetical protein
SAG1821	750	glutamate--cysteine ligase/amino acid ligase, putative
SAG1822	272	protein of unknown function
SAG1823	418	protein of unknown function
SAG1824	291	chaperonin, 33 kDa
SAG1825	325	NifR3/Smm1 family protein
SAG1826	213	deoxynucleoside kinase family protein
SAG1827	163	phosphinothricin N-acetyltransferase
SAG1828	815	ATP-dependent Clp protease, ATP-binding subunit
SAG1829	154	transcriptional regulator CtsR
SAG1830	153	conserved hypothetical protein
SAG1831	346	translation elongation factor Ts
SAG1832	256	ribosomal protein S2
SAG1833	186	alkyl hydroperoxide reductase, subunit C
SAG1834	510	alkyl hydroperoxide reductase, subunit F
SAG1835	134	conserved hypothetical protein
SAG1836	61	conserved hypothetical protein
SAG1837	468	prophage LambdaSa2, lysin, putative
SAG1838	109	prophage LambdaSa2, holin, putative
SAG1839	136	conserved hypothetical protein
SAG1840	112	hypothetical protein
SAG1841	76	conserved domain protein
SAG1842	1224	prophage LambdaSa2, PblB, putative
SAG1843	240	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1844	911	conserved hypothetical protein
SAG1845	42	hypothetical protein
SAG1846	158	hypothetical protein
SAG1847	227	conserved hypothetical protein
SAG1848	114	conserved hypothetical protein
SAG1849	115	hypothetical protein
SAG1850	101	hypothetical protein
SAG1851	111	conserved domain protein
SAG1852	420	conserved domain protein
SAG1853	180	prophage LambdaSa2, protease, putative
SAG1854	380	conserved hypothetical protein
SAG1855	570	prophage LambdaSa2, terminase large subunit, putative
SAG1856	161	hypothetical protein
SAG1857	119	prophage LambdaSa2, HNH endonuclease family protein
SAG1858	95	hypothetical protein
SAG1859	180	prophage LambdaSa2, site-specific recombinase, phage integrase family
SAG1860	154	conserved hypothetical protein
SAG1861	119	prophage LambdaSa2, transcriptional regulator, Cro/CI family
SAG1862	86	hypothetical protein
SAG1863	138	prophage LambdaSa2, single-strand binding protein
SAG1864	68	hypothetical protein
SAG1865	74	conserved hypothetical protein
SAG1866	109	conserved hypothetical protein
SAG1867	163	conserved hypothetical protein
SAG1868	134	hypothetical protein
SAG1869	437	prophage LambdaSa2, type II DNA modification methyltransferase, putative
SAG1870	273	prophage LambdaSa2, DNA replication protein DnaC, putative
SAG1871	248	prophage LambdaSa2, bacteriophage replication protein/hypothetical protein, truncation/fusion
SAG1872	200	hypothetical protein
SAG1873	443	prophage LambdaSa2, replicative DNA helicase
SAG1874	87	hypothetical protein
SAG1875	94	conserved hypothetical protein
SAG1876	176	prophage LambdaSa2, HNH endonuclease family protein
SAG1877	236	prophage LambdaSa2, antirepressor protein, putative
SAG1878	102	conserved domain protein
SAG1879	156	hypothetical protein
SAG1880	54	hypothetical protein
SAG1881	51	hypothetical protein
SAG1882	120	prophage LambdaSa2, repressor protein, putative
SAG1883	128	conserved hypothetical protein
SAG1884	134	hypothetical protein
SAG1885	356	prophage LambdaSa2, site-specific recombinase, phage integrase family
SAG1886	32	hypothetical protein
SAG1887	689	Na ⁺ /H ⁺ exchanger family protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1888	78	hypothetical protein
SAG1889	317	microcin immunity protein MccF, putative
SAG1890	631	endopeptidase O
SAG1891	327	oxidoreductase, Gfo/Idh/MocA family
SAG1892	358	membrane protein, putative
SAG1893	59	hypothetical protein
SAG1894	214	cyclic nucleotide-binding domain protein
SAG1895	204	polypeptide deformylase
SAG1896	333	sugar binding transcriptional regulator RegR
SAG1897	634	conserved hypothetical protein
SAG1898	271	PTS system, IID component
SAG1899	288	PTS system, IIC component
SAG1900	164	PTS system, IIB component
SAG1901	398	glucuronyl hydrolase
SAG1902	144	PTS system, IIA component
SAG1903	34	hypothetical protein
SAG1904	270	oxidoreductase, short-chain dehydrogenase/reductase family
SAG1905	212	conserved hypothetical protein
SAG1906	335	carbohydrate kinase, PfkB family
SAG1907	212	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase
SAG1908	499	hypothetical protein
SAG1909	204	nitroreductase family protein
SAG1910	141	transcriptional regulator, MarR family
SAG1911	1468	DNA polymerase III, alpha subunit, Gram-positive type
SAG1912	194	N-acetylmuramoyl-L-alanine amidase, family 4 protein
SAG1913	617	prolyl-tRNA synthetase
SAG1914	419	membrane-associated zinc metalloprotease, putative
SAG1915	264	phosphatidate cytidyltransferase
SAG1916	250	undecaprenyl diphosphate synthase
SAG1917	113	preprotein translocase, YajC subunit
SAG1918	114	bacteriocin transport accessory protein, putative
SAG1919	387	malate oxidoreductase
SAG1920	445	citrate carrier protein, CCS family
SAG1921	508	sensor histidine kinase
SAG1922	229	response regulator
SAG1923	331	UDP-glucose 4-epimerase
SAG1924	535	glucan 1,6-alpha-glucosidase
SAG1925	377	sugar ABC transporter, ATP-binding protein
SAG1926	283	helix-turn-helix domain protein, fis-type
SAG1927	298	lacX protein
SAG1928	325	tagatose 1,6-diphosphate aldolase
SAG1929	310	tagatose-6-phosphate kinase
SAG1930	171	galactose-6-phosphate isomerase, LacB subunit
SAG1931	141	galactose-6-phosphate isomerase, LacA subunit
SAG1932	816	neuraminidase-related protein
SAG1933	482	PTS system, IIC component, putative
SAG1934	101	PTS system, IIB component, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1935	157	PTS system, IIA component, putative
SAG1936	258	lactose phosphotransferase system repressor
SAG1937	NA	streptococcal histidine triad family protein, degenerate
SAG1938	307	adhesion lipoprotein
SAG1939	147	protein of unknown function TIGR00256
SAG1940	738	GTP pyrophosphokinase family protein
SAG1941	800	2',3'-cyclic-nucleotide 2'-phosphodiesterase
SAG1942	151	nrdI protein
SAG1943	345	conserved hypothetical protein
SAG1944	165	conserved hypothetical protein
SAG1945	345	iron ABC transporter, iron-binding protein
SAG1946	257	DNA-binding response regulator
SAG1947	549	conserved hypothetical protein
SAG1948	275	PTS system, IID component
SAG1949	269	PTS system, IIC component
SAG1950	163	PTS system, IIB component
SAG1951	141	PTS system, IIA component, putative
SAG1952	353	membrane protein, putative
SAG1953	60	hypothetical protein
SAG1954	384	membrane protein, putative
SAG1955	282	ABC transporter, ATP-binding protein
SAG1956	96	conserved hypothetical protein, truncation
SAG1957	250	response regulator
SAG1958	276	conserved hypothetical protein
SAG1959	727	PTS system, IIABC components
SAG1960	551	sensor histidine kinase
SAG1961	225	phosphate regulon response regulator PhoB
SAG1962	218	phosphate transport system regulatory protein PhoU, putative
SAG1963	253	phosphate ABC transporter, ATP-binding protein
SAG1964	292	phosphate ABC transporter, permease protein
SAG1965	281	phosphate ABC transporter, permease protein
SAG1966	293	hemolysin precursor, putative
SAG1967	195	hypothetical protein
SAG1968	246	conserved hypothetical protein TIGR00046
SAG1969	317	ribosomal protein L11 methyltransferase
SAG1970	102	conserved hypothetical protein
SAG1971	41	hypothetical protein
SAG1972	238	transcriptional regulator, MerR family
SAG1973	156	acetyltransferase, GNAT family
SAG1974	152	MutT/nudix family protein
SAG1975	47	hypothetical protein
SAG1976	156	conserved hypothetical protein
SAG1977	163	acetyltransferase, GNAT family
SAG1978	422	ATPase, AAA family
SAG1979	253	membrane protein, putative
SAG1980	300	ABC transporter, ATP-binding protein
SAG1981	68	hypothetical protein
SAG1982	359	transcriptional regulator, Cro/CI family

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG1983	105	conserved hypothetical protein
SAG1984	188	conserved hypothetical protein TIGR00730
SAG1985	51	hypothetical protein
SAG1986	375	site-specific recombinase, phage integrase family
SAG1987	61	conserved hypothetical protein
SAG1988	342	conserved hypothetical protein
SAG1989	139	hypothetical protein
SAG1990	127	hypothetical protein
SAG1991	204	transcriptional regulator, Cro/CI family
SAG1992	518	protein of unknown function
SAG1993	373	site-specific recombinase, phage integrase family
SAG1994	108	conserved hypothetical protein
SAG1995	210	hypothetical protein
SAG1996	263	cell wall surface anchor family protein, putative
SAG1997	182	hypothetical protein
SAG1998	457	hypothetical protein
SAG1999	47	hypothetical protein
SAG2000	666	membrane protein, putative
SAG2001	756	conjugal transfer protein, interruption-C
SAG2002	129	IS1381, transposase OrfB
SAG2003	127	IS1381, transposase OrfA
SAG2004	67	conjugal transfer protein, interruption-N
SAG2005	136	conserved hypothetical protein
SAG2006	88	conserved hypothetical protein
SAG2007	317	conserved hypothetical protein
SAG2008	84	conserved hypothetical protein
SAG2009	88	conserved hypothetical protein
SAG2010	157	hypothetical protein
SAG2011	160	conserved hypothetical protein
SAG2012	90	hypothetical protein
SAG2013	189	hypothetical protein
SAG2014	449	hypothetical protein
SAG2015	99	transcriptional regulator, Cro/CI family
SAG2016	125	hypothetical protein
SAG2017	429	transcriptional regulator, Cro/CI family
SAG2018	553	FtsK/SpoIIIE family protein
SAG2019	153	hypothetical protein
SAG2020	98	hypothetical protein
SAG2021	826	cell wall surface anchor family protein
SAG2022	417	transposase, ISL3 family
SAG2023	546	mercuric reductase
SAG2024	130	mercuric resistance operon regulatory protein MerR
SAG2025	522	Mn ²⁺ /Fe ²⁺ transporter, NRAMP family
SAG2026	240	membrane protein, putative
SAG2027	205	ABC transporter, ATP-binding protein
SAG2028	36	conserved hypothetical protein
SAG2029	284	streptomycin resistance protein
SAG2030	130	hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2031	202	hypothetical protein
SAG2032	111	conserved hypothetical protein
SAG2033	162	acetyltransferase, GNAT family
SAG2034	247	membrane protein, putative
SAG2035	300	ABC transporter, ATP-binding protein
SAG2036	68	hypothetical protein
SAG2037	358	transcriptional regulator, Cro/CI family
SAG2038	204	PAP2 family protein
SAG2039	98	conserved hypothetical protein
SAG2040	186	conserved hypothetical protein TIGR00730
SAG2041	287	protease, putative
SAG2042	100	rhodanese family protein
SAG2043	255	cAMP factor
SAG2044	62	hypothetical protein
SAG2045	179	DNA topology modulation protein FlaR, putative
SAG2046	361	glycerol dehydrogenase, putative
SAG2047	235	conserved hypothetical protein
SAG2048	614	5-methyltetrahydrofolate--homocysteine methyltransferase, putative
SAG2049	745	5-methyltetrahydropteroylglutamate--homocysteine methyltransferase
SAG2050	107	conserved hypothetical protein
SAG2051	230	branched-chain amino acid transport protein AzlC, putative
SAG2052	41	hypothetical protein
SAG2053	1570	serine protease, subtilase family, putative
SAG2054	228	DNA-binding response regulator
SAG2055	462	sensor histidine kinase
SAG2056	202	chromosome assembly-related protein
SAG2057	833	leucyl-tRNA synthetase
SAG2058	415	major facilitator family protein
SAG2059	281	protein of unknown function
SAG2060	398	glycosyl transferase, family 8
SAG2061	401	glycosyl transferase, family 8
SAG2062	179	transcription antitermination protein NusG
SAG2063	630	pathogenicity protein, putative
SAG2064	57	preprotein translocase, SecE subunit, putative
SAG2065	50	ribosomal protein L33
SAG2066	773	penicillin-binding protein 2A
SAG2067	294	ribosomal large subunit pseudouridine synthase, RluD subfamily
SAG2068	546	conserved hypothetical protein
SAG2069	403	phosphopentomutase
SAG2070	223	deoxyribose-phosphate aldolase
SAG2071	400	Na ⁺ dependent nucleoside transporter
SAG2072	259	uridine phosphorylase
SAG2073	245	transcriptional regulator, GntR family
SAG2074	540	60 kDa chaperonin
SAG2075	94	chaperonin, 10 kDa
SAG2076	267	ABC transporter, ATP-binding protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2077	298	ABC transporter, permease protein
SAG2078	320	protein of unknown function/lipoprotein, putative
SAG2079	265	hydrolase, haloacid dehalogenase-like family
SAG2080	286	glyoxalase family protein
SAG2081	243	conserved hypothetical protein
SAG2082	205	anaerobic ribonucleoside-triphosphate reductase activating protein
SAG2083	163	acetyltransferase, GNAT family
SAG2084	310	virulence factor MviM, putative
SAG2085	47	conserved hypothetical protein
SAG2086	723	anaerobic ribonucleoside-triphosphate reductase
SAG2087	495	membrane protein, putative
SAG2088	40	hypothetical protein
SAG2089	105	conserved hypothetical protein
SAG2090	136	conserved hypothetical protein TIGR00250
SAG2091	88	conserved hypothetical protein
SAG2092	132	conserved hypothetical protein
SAG2093	379	recA protein
SAG2094	NA	competence/damage-inducible protein CinA, authentic frameshift
SAG2095	183	DNA-3-methyladenine glycosylase I
SAG2096	196	Holliday junction DNA helicase RuvA
SAG2097	418	transporter, putative
SAG2098	659	DNA mismatch repair protein HexB
SAG2099	33	hypothetical protein
SAG2100	67	cold shock protein, CSD family
SAG2101	858	DNA mismatch repair protein HexA
SAG2102	145	arginine repressor ArgR, putative
SAG2103	563	arginyl-tRNA synthetase
SAG2104	102	conserved hypothetical protein
SAG2105	290	conserved hypothetical protein
SAG2106	314	conserved hypothetical protein
SAG2107	583	aspartyl-tRNA synthetase
SAG2108	426	histidyl-tRNA synthetase
SAG2109	60	ribosomal protein L32
SAG2110	49	ribosomal protein L33
SAG2111	173	conserved hypothetical protein
SAG2112	494	site-specific recombinase, phage integrase family
SAG2113	82	conserved hypothetical protein
SAG2114	342	conserved hypothetical protein
SAG2115	143	hypothetical protein
SAG2116	151	conserved hypothetical protein
SAG2117	71	hypothetical protein
SAG2118	306	transcriptional regulator, Cro/CI family
SAG2119	373	conserved domain protein
SAG2120	269	hypothetical protein
SAG2121	223	hypothetical protein
SAG2122	223	DNA-binding response regulator
SAG2123	454	sensor histidine kinase
SAG2124	517	membrane protein, putative

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2125	308	carbamate kinase
SAG2126	332	ornithine carbamoyltransferase
SAG2127	431	sensor histidine kinase
SAG2128	277	response regulator
SAG2129	240	amino acid ABC transporter, ATP-binding protein
SAG2130	504	amino acid ABC transporter, amino acid-binding protein/permease protein
SAG2131	847	membrane protein, putative
SAG2132	247	conserved hypothetical protein
SAG2133	118	conserved hypothetical protein
SAG2134	772	membrane protein, putative
SAG2135	179	transcriptional regulator, TetR family, putative
SAG2136	98	conserved hypothetical protein
SAG2137	203	ribosomal protein S4
SAG2138	95	conserved hypothetical protein
SAG2139	451	replicative DNA helicase
SAG2140	150	ribosomal protein L9
SAG2141	660	DHH family protein
SAG2142	613	glucose inhibited division protein A
SAG2143	203	membrane protein, putative
SAG2144	373	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
SAG2145	222	L-serine dehydratase, iron-sulfur-dependent, beta subunit
SAG2146	290	L-serine dehydratase, iron-sulfur-dependent, alpha subunit
SAG2147	234	protein of unknown function/lipoprotein, putative
SAG2148	179	LysM domain protein
SAG2149	264	cobalt transport family protein
SAG2150	280	ABC transporter, ATP-binding protein
SAG2151	279	ABC transporter, ATP-binding protein
SAG2152	180	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
SAG2153	427	peptidase, M16 family
SAG2154	414	conserved hypothetical protein
SAG2155	117	conserved hypothetical protein
SAG2156	369	recF protein
SAG2157	278	transporter, putative
SAG2158	220	transcriptional regulator, Cro/CI family
SAG2159	493	inosine-5'-monophosphate dehydrogenase
SAG2160	161	transcriptional regulator, ArgR family
SAG2161	226	transcriptional regulator, Crp/Fnr family
SAG2162	234	conserved hypothetical protein
SAG2163	410	arginine deiminase
SAG2164	136	acetyltransferase, GNAT family
SAG2165	337	ornithine carbamoyltransferase
SAG2166	475	arginine/ornithine antiporter
SAG2167	318	carbamate kinase
SAG2168	341	tryptophanyl-tRNA synthetase
SAG2169	230	membrane protein, putative
SAG2170	290	conserved hypothetical protein

Table 1: Complete list of GBS predicted genes

ORF	Size (a.a.)	Annotation
SAG2171	539	ABC transporter, ATP-binding protein
SAG2172	859	ABC transporter, permease protein, putative
SAG2173	159	conserved hypothetical protein TIGR00246
SAG2174	409	serine protease
SAG2175	257	partitioning protein, ParB family

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0017	447	+							pcSB
SAG0031	299	+							peptidase, M23/M37 family
SAG0032	434	+				+	+		group B streptococcal surface immunogenic protein
SAG0034	438	+		+		+	+		sugar ABC transporter, sugar-binding protein
SAG0051	126	+				+	+		MORN motif family protein
SAG0079	212				+	+	+		adenylate kinase
SAG0086	85			+				+	lipoprotein, putative
SAG0093	250	+				+	+		D-alanyl-D-alanine carboxypeptidase family protein
SAG0094	191	+							N-acetylmuramoyl-L-alanine amidase, family 4 protein
SAG0108	308	+							conserved hypothetical protein
SAG0114	322	+		+					D-ribose ABC transporter, periplasmic D-ribose-binding protein
SAG0124	356	+							sensor histidine kinase
SAG0132	294	+				+	+		SPFH domain/Band 7 family protein
SAG0134	96	+						+	hypothetical protein
SAG0146	395	+							penicillin-binding protein 4, putative
SAG0147	411	+							D-alanyl-D-alanine carboxypeptidase family protein
SAG0148	551			+		+	-		oligopeptide ABC transporter, substrate-binding protein, putative
SAG0166	123	+							conserved domain protein
SAG0176	94	+							conserved hypothetical protein
SAG0187	542	+		+		+	+		oligopeptide ABC transporter, oligopeptide-binding protein
SAG0206	60			+				+	lipoprotein, putative
SAG0213	39	+						+	hypothetical protein
SAG0231	135	+							hypothetical protein
SAG0242	308			+		+	-		amino acid ABC transporter, amino acid-binding protein
SAG0245	152			+		+	-	+	protein of unknown function/lipoprotein, putative
SAG0255	315	+							conserved hypothetical protein
SAG0257	53			+				+	lipoprotein, putative
SAG0265	235	+				+	-	+	conserved hypothetical protein
SAG0290	270	+				+	+		ABC transporter, substrate-binding protein
SAG0298	750	+							penicillin-binding protein 1A

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0306	535	+							KH domain protein
SAG0321	339	+							sensor histidine kinase, putative
SAG0329	106	+							PTS system, cellobiose-specific IIB component
SAG0368	435	+				+	+		protein of unknown function
SAG0371	167	+						+	hypothetical protein
SAG0383	334	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0392	521	+	+			+	+		cell wall surface anchor family protein
SAG0394	345				+				sensor histidine kinase
SAG0405	347	+		+		+	+		protein of unknown function/lipoprotein, putative
SAG0406	299	+							UTP-glucose-1-phosphate uridylyltransferase
SAG0407	338	+							glycerol-3-phosphate dehydrogenase (NAD(P)+)
SAG0416	1233	+	+			+	+		protease, putative
SAG0421	1055		+			+	-		cell wall surface anchor family protein
SAG0433	1389		+						surface protein Rib
SAG0437	123			+					lipoprotein, putative
SAG0451	149	+		+				+	bacteriocin transport accessory protein, putative
SAG0455	357	+							conserved hypothetical protein
SAG0472	126	+				+	-		rhodanese-like family protein
SAG0482	84	+							YGGT family protein
SAG0499	275				+				hemolysin A
SAG0503	279	+				+	+		lipase/acylhydrolase
SAG0504	200	+							conserved hypothetical protein
SAG0506	65	+						+	hypothetical protein
SAG0521	236	+							carboxymethylenebutenolidase-related protein
SAG0535	506	+				+	+		zinc ABC transporter, zinc-binding adhesion lipoprotein
SAG0596	670				+				prophage LambdaSa1, pblA protein, internal deletion
SAG0603	111				+				conserved hypothetical protein
SAG0604	239				+				prophage LambdaSa1, lysis, putative
SAG0617	439				+				sensor histidine kinase VncS
SAG0624	574	+							septation ring formation regulator EzrA, putative
SAG0629	354	+							conserved domain protein
SAG0635	245	+				+	-		acid phosphatase, class B
SAG0638	109	+							cell wall surface anchor family protein, interruption-N

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0645	554		+			+	+		cell wall surface anchor family protein
SAG0646	307	+	+			+	-		cell wall surface anchor family protein
SAG0647	305	+							sortase family protein
SAG0649	890		+			+	+		cell wall surface anchor family protein, putative
SAG0658	383	+		+					lipoprotein, putative
SAG0675	171	+							putative secreted protein
SAG0676	885				+				proteinase, putative
SAG0677	1062		+						hypothetical protein
SAG0679	343	+		+		+	-		protein of unknown function
SAG0680	339	+				+	-		protein of unknown function
SAG0681	353	+							conserved domain protein
SAG0686	261	+				+	+		DNA-entry nuclease, putative
SAG0714	188	+						+	conserved hypothetical protein
SAG0717	266	+				+	+		amino acid ABC transporter, amino acid-binding protein
SAG0720	449				+				sensory box histidine kinase
SAG0738	132	+							conserved hypothetical protein
SAG0739	143	+							conserved hypothetical protein
SAG0742	428				+	+	+		peptidase, U32 family
SAG0755	282	+							peptidase, U32 family
SAG0757	129	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0764	230				+	+	+		phosphoglycerate mutase family protein
SAG0765	681	+							penicillin-binding protein 2b
SAG0771	512	+	+			+	+	+	cell wall surface anchor family protein
SAG0776	276	+		+					YaeC family protein, putative
SAG0777	528				+	+	+		ATP-dependent RNA helicase, DEAD/DEAH box family
SAG0785	330	+							conserved hypothetical protein
SAG0808	309	+		+		+	+		protease maturation protein, putative
SAG0824	417	+							polysaccharide deacetylase family protein
SAG0832	753	+				+	+		protein of unknown function
SAG0833	181	+						+	hypothetical protein
SAG0867	63	+							conserved hypothetical protein
SAG0868	285	+				+	-		DNA-entry nuclease
SAG0886	319	+				+	+		protein of unknown function

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo-protein	Other	Western blot	FACS	GBS specific	Annotation
SAG0904	56	+						+	hypothetical protein
SAG0907	877	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0926	333	+							Tn916, NLP/P60 family protein
SAG0942	185	+				+	+		signal peptidase I, putative
SAG0949	276	+		+		+	+		amino acid ABC transporter, amino acid-binding protein
SAG0954	349			+		+	-		protein of unknown function/lipoprotein, putative
SAG0961	247	+				+	-		sortase SrtA
SAG0963	320	+							conserved hypothetical protein
SAG0971	282	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG0973	320	+						+	nisin-resistance protein, putative
SAG0977	312				+				sensor histidine kinase
SAG0979	553	+		+		+	-		ABC transporter, substrate-binding protein
SAG0984	437	+							sensor histidine kinase CiaH
SAG0992	286	+		+		+	+		phosphate ABC transporter, phosphate-binding protein
									iron-compound ABC transporter, iron-compound-binding protein
SAG1007	342	+		+		+	-		protein
SAG1014	190	+				-	-		conserved hypothetical protein
SAG1018	40			+				+	lipoprotein, putative
SAG1024	183	+		+					lipoprotein, putative
SAG1029	101	+							hypothetical protein
SAG1030	304	+				+	+		protein of unknown function
SAG1037	157	+						+	hypothetical protein
SAG1052	47		+					+	cell wall surface anchor family protein, putative
SAG1072	200	+							conserved hypothetical protein
SAG1094	278				+	+	+		conserved hypothetical protein
									spermidine/putrescine ABC transporter, spermidine/putrescine-binding prot.
SAG1108	357	+				+	-		
SAG1121	295	+							polysaccharide deacetylase family protein
SAG1126	228	+				+	+		protein of unknown function
SAG1127	446	+						+	conserved domain protein
SAG1130	49	+						+	hypothetical protein
SAG1138	64	+							conserved hypothetical protein
SAG1139	193	+							conserved hypothetical protein

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG1149	207	+		+					lipoprotein, putative
SAG1184	236	+							conserved hypothetical protein
SAG1186	553			+					metallo-beta-lactamase superfamily protein
SAG1189	334	+							conserved hypothetical protein
SAG1190	551				+				adherence and virulence protein A
SAG1197	1072	+							hyaluronidase
SAG1201	367	+							imino diacetate oxidase, putative
SAG1206	854	+							conserved domain protein
SAG1214	58	+							hypothetical protein
SAG1216	1252		+			+	-		pullulanase, putative
SAG1227	198	+				+	-		protein of unknown function
SAG1233	822	+				+	-		streptococcal histidine triad family protein
SAG1234	306	+		+		+	+		laminin-binding surface protein
SAG1238	202	+							hypothetical protein
SAG1283	1631		+			+	+		agglutinin receptor
SAG1313	56	+							conserved hypothetical protein
SAG1327	409	+							sensor histidine kinase
SAG1331	979	+	+			+	+		R5 protein
SAG1333	690	+	+			+	+		5'-nucleotidase family protein
SAG1350	544	+							surface antigen-related protein
SAG1361	414	+							conserved hypothetical protein
SAG1371	392	+							conserved hypothetical protein
SAG1393	310			+					iron compound ABC transporter, substrate-binding protein
SAG1404	308	+	+			+	-		cell wall surface anchor family protein
SAG1405	294	+			+	+	+		sortase family protein
SAG1406	293	+							sortase family protein
SAG1407	705	+	+			+	+		cell wall surface anchor family protein
SAG1408	901		+						cell wall surface anchor family protein
SAG1419	577			+			+		lipoprotein, putative
SAG1431	268			+					amino acid ABC transporter, amino acid-binding protein
SAG1433	375	+							conserved hypothetical protein
SAG1441	415	+				+	+		maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG1462	970		+						cell wall surface anchor family protein
SAG1473	192	+	+					+	cell wall surface anchor family protein
SAG1474	680	+	+						amidase family protein
SAG1483	78	+							preprotein translocase, SecG subunit
SAG1488	195	+				+	+		dephospho-CoA kinase
SAG1491	530	+						+	hypothetical protein
SAG1508	590				+	+	-		67 kDa Myosin-crossreactive streptococcal antigen
SAG1518	538	+		+					peptide ABC transporter, peptide-binding protein
SAG1530	267	+		+		+	-		peptidyl-prolyl cis-trans isomerase, cyclophilin-type
SAG1533	308	+		+		+	-		manganese ABC transporter, manganese-binding adhesion liprotein
SAG1544	232	+							gluconate 5-dehydrogenase, putative
SAG1551	67	+						+	hypothetical protein
SAG1552	719	+							conserved hypothetical protein
SAG1553	477	+						+	hypothetical protein
SAG1562	280	+							conserved hypothetical protein
SAG1582	388	+		+		+	-		branched-chain amino acid ABC transporter, amino acid-binding protein
SAG1590	449				+	+	+		potassium uptake protein, Trk family
SAG1601	79	+							conserved hypothetical protein
SAG1610	285			+		+	-		amino acid ABC transporter, substrate-binding protein
SAG1618	1032				+	+	+		Snf2 family protein
SAG1624	501	+							sensor histidine kinase CsrS
SAG1628	184	+							lemA protein
SAG1631	223	+				+	-		potassium uptake protein, Trk family, putative
SAG1641	274	+				+	-		YaeC family protein
SAG1642	277	+		+		+	-		ABC transporter, substrate-binding protein
SAG1683	512	+							immunogenic secreted protein, putative
SAG1706	238	+							conserved hypothetical protein
SAG1745	148	+					+		hypothetical protein
SAG1752	390	+							conserved hypothetical protein TIGR00275
SAG1759	230				+	+	+		protein of unknown function
SAG1762	169	+							conserved hypothetical protein

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG1767	289	+		+					acid phosphatase
SAG1768	336				+	+	+		glyceraldehyde 3-phosphate dehydrogenase
SAG1774	424	+							conserved hypothetical protein
SAG1786	130	+				+	-		protein of unknown function
SAG1787	420	+							dltD protein
SAG1791	395	+							sensor histidine kinase
SAG1822	272	+				+	-		protein of unknown function
SAG1823	418				+	+	+		protein of unknown function
SAG1837	468				+				prophage LambdaSa2, lysin, putative
SAG1838	109	+							prophage LambdaSa2, holin, putative
SAG1839	136	+							conserved hypothetical protein
SAG1842	1224				+				prophage LambdaSa2, PblB, putative
SAG1912	194	+							N-acetylmuramoyl-L-alanine amidase, family 4 protein
SAG1921	508	+							sensor histidine kinase
SAG1932	816	+							neuraminidase-related protein
SAG1938	307	+		+		+	-		adhesion lipoprotein
SAG1941	800	+	+			+	-		2',3'-cyclic-nucleotide 2'-phosphodiesterase
SAG1945	345	+							iron ABC transporter, iron-binding protein
SAG1947	549				+				conserved hypothetical protein
SAG1960	551				+	+	+		sensor histidine kinase
SAG1966	293			+		+	-		hemolysin precursor, putative
SAG1996	263	+	+						cell wall surface anchor family protein, putative
SAG1997	182	+							hypothetical protein
SAG1998	457	+							hypothetical protein
SAG2021	826		+						cell wall surface anchor family protein
SAG2043	255	+							cAMP factor
SAG2053	1570	+	+						serine protease, subtilase family, putative
SAG2055	462				+				sensor histidine kinase
SAG2056	202	+					+		chromosome assembly-related protein
SAG2063	630	+	+						pathogenicity protein, putative
SAG2078	320	+		+		+	-		protein of unknown function/lipoprotein, putative
SAG2094		+				+	+		competence/damage-inducible protein CinA, authentic frameshift

Table 2

ORF	Size (aa)	Signal Peptide	Sortase motif	Lipo- protein	Other	Western blot	FACS	GBS specific	Annotation
SAG2121	223	+						+	hypothetical protein
SAG2123	454	+							sensor histidine kinase
SAG2141	660	+				+	-		DHH family protein
SAG2147	234	+		+		+	+		protein of unknown function/lipoprotein, putative
SAG2148	179	+							LysM domain protein
SAG2174	409	+							serine protease
SAG0013	428	+				+	-		protein of unknown function

Table 3

ORF	Annotation
SAG0038	conserved hypothetical protein
SAG0048	transcriptional regulator Cro/CI family
SAG0091	transcriptional regulator ComX1 putative
SAG0137	conserved hypothetical protein
SAG0686	DNA-entry nuclease putative
SAG0770	membrane protein putative
SAG0868	DNA-entry nuclease
SAG1143	conserved hypothetical protein
SAG1233	streptococcal histidine triad family protein
SAG1596	integrase/recombinase phage integrase family
SAG1616	conserved hypothetical protein
SAG1721	conserved hypothetical protein.

Table 4: Probable recently duplicated genes

Probable recently duplicated genes are indicated on the same line and are separated by a semicolon.

SAG0148 oligopeptide ABC transporter, substrate-binding protein, putative; SAG0979 ABC transporter, substrate-binding protein	SAG0151 oligopeptide ABC transporter, ATP-binding protein; SAG1515 peptide ABC transporter, ATP-binding protein
SAG0195 IS1548, transposase; SAG0693 IS1548, transposase; SAG0760 IS1548, transposase; SAG0945 IS1548, transposase; SAG1584 IS1548, transposase; SAG1619 IS1548, transposase	
SAG0230 conserved hypothetical protein; SAG1039 conserved hypothetical protein	
SAG0233 hypothetical protein; SAG1785 hypothetical protein	
SAG0261 IS1381, transposase OrfB; SAG0542 IS1381, transposase OrfA; SAG0543 IS1381, transposase OrfB; SAG0966 IS1381, transposase OrfB; SAG1457 IS1381, transposase OrfB; SAG1550 IS1381, transposase OrfB; SAG2002 IS1381, transposase OrfB	
SAG0262 IS1381, transposase OrfA; SAG0965 IS1381, transposase OrfA; SAG1549 IS1381, transposase OrfA; SAG1458 IS1381, transposase OrfA; SAG2003 IS1381, transposase OrfA	
SAG0383 protein of unknown function/lipoprotein, putative; SAG0785 conserved hypothetical protein	
SAG0405 protein of unknown function/lipoprotein, putative; SAG0954 protein of unknown function/lipoprotein, putative	
SAG0417 glycosyl transferase, group 2 family protein; SAG1422 glycosyl transferase, group 2 family protein	
SAG0429 oxidoreductase, aldo/keto reductase family; SAG1476 oxidoreductase, aldo/keto reductase family	

Table 4: Probable recently duplicated genes

SAG0432 transcriptional regulator, AraC family; SAG0644 transcriptional regulator, AraC family	SAG0434 transposase, IS256 family, truncation; SAG0448 transposase, IS256 family	SAG0438 bacteriophage L54a, integrase, truncation; SAG1986 site-specific recombinase, phage integrase family; SAG1989 hypothetical protein; SAG1993 site-specific recombinase, phage integrase family; SAG2115 hypothetical protein
SAG0442 acetyltransferase, GNAT family; SAG0443 acetyltransferase, GNAT family	SAG0447 magnesium transporter, CorA family; SAG0875 magnesium transporter, CorA family, putative	SAG0508 beta-lactam resistance factor; SAG1349 beta-lactam resistance factor
SAG0566 prophage LambdaSa1, single-strand binding protein; SAG1713 single-strand binding protein; SAG1863 prophage LambdaSa2, single-strand binding protein	SAG0603 conserved hypothetical protein; SAG1838 prophage LambdaSa2, holin, putative	SAG0604 prophage LambdaSa1, lysin, putative; SAG1837 prophage LambdaSa2, lysin, putative
SAG0618 transposase OrfB, IS3 family, truncation; SAG0639 transposase OrfB, IS3 family; SAG1232 transposase OrfB, IS3 family, truncation; SAG1242 transposase OrfB, IS3 family, truncation	SAG0640 transposase OrfA, IS3 family; SAG1241 transposase OrfA, IS3 family	SAG0646 cell wall surface anchor family protein; SAG1404 cell wall surface anchor family protein

Table 4: Probable recently duplicated genes

SAG0647 sortase family protein; SAG0648 sortase family protein; SAG0650 sortase family protein
SAG0649 cell wall surface anchor family protein, putative; SAG1408 cell wall surface anchor family protein
SAG0676 proteinase, putative; SAG2053 serine protease, subtilase family, putative
SAG0679 protein of unknown function; SAG0680 protein of unknown function; SAG0681 conserved domain protein
SAG1002 protease, putative; SAG1465 protease, putative
SAG1025 hypothetical protein; SAG1033 FtsK/SpoIIIE family protein
SAG1067 IS861, transposase OrfA; SAG1526 IS861, transposase OrfA
SAG1068 IS861, transposase OrfB; SAG1256 IS861, transposase OrfB, truncation; SAG1527 IS861, transposase OrfB
SAG1140 conserved hypothetical protein; SAG1141 conserved hypothetical protein
SAG1164 glycosyl transferase CpsJ(V); SAG1165 glycosyl transferase CpsO(V)
SAG1182 phosphopentomutase; SAG2069 phosphopentomutase
SAG1225 conserved hypothetical protein; SAG1540 conserved hypothetical protein
SAG1228 ISSdy1, transposase OrfA; SAG1243 ISSdy1, transposase OrfA
SAG1229 ISSdy1, transposase OrfB; SAG1244 ISSdy1, transposase OrfB
SAG1253 transposase, ISL3 family; SAG2022 transposase, ISL3 family

Table 4: Probable recently duplicated genes

SAG1254 mercuric reductase; SAG2023 mercuric reductase	
SAG1255 mercuric resistance operon regulatory protein MerR; SAG2024 mercuric resistance operon regulatory protein MerR	
SAG1259 conserved hypothetical protein; SAG1272 conserved hypothetical protein	
SAG1283 agglutinin receptor; SAG2021 cell wall surface anchor family protein	
SAG1297 C-5 cytosine-specific DNA methylase; SAG1869 prophage LambdaSa2, type II DNA modification methyltransferase, putative	
SAG1405 sortase family protein; SAG1406 sortase family protein	
SAG1414 glycosyl transferase, group 2 family protein; SAG1415 glycosyl transferase, group 2 family protein	
SAG1456 glycosyl transferase, family 8, degenerate; SAG2060 glycosyl transferase, family 8	
SAG1521 transposase, IS30 family, putative; SAG1576 transposase, IS30 family, putative, truncation; SAG1795 transposase, IS30 family, putative	
SAG1655 transcriptional regulator, MerR family; SAG1972 transcriptional regulator, MerR family	
SAG1979 membrane protein, putative; SAG2034 membrane protein, putative	
SAG1980 ABC transporter, ATP-binding protein; SAG2035 ABC transporter, ATP-binding protein	
SAG1982 transcriptional regulator, Cro/CI family; SAG2037 transcriptional regulator, Cro/CI family	
SAG1983 conserved hypothetical protein; SAG2039 conserved hypothetical protein	

Table 4: Probable recently duplicated genes

SAG1984 conserved hypothetical protein TIGR00730; SAG2040 conserved hypothetical protein TIGR00730

SAG1988 conserved hypothetical protein; SAG2114 conserved hypothetical protein

Table 5

Strain	Source	Capsular serotype	Reference
090	Lancefield	Ia	
515	Houston	Ia	(1)
A909	Lancefield	Ia	(2)
Davis	Channing	Ia	
DK1	Houston	Ia	
DK8	Houston	Ia	
H36b	Lancefield	Ib	(2)
(S7) 7357b	Channing	Ib	(3)
18RS21	Lancefield	II	(4)
DK21	Houston	II	
COH1	Seattle	III	(5)
COH31	Seattle	III	(6)
D136C	Lancefield	III	(4)
M781	Houston	III	(7)
M732	Houston	III	(8)
1169NT1	Atlanta	V	(9)
2603V/R	Italy	V	This study
CJB111	Houston	V	(10)
JM9130013	Japan	VIII	(11)
SMU014	Japan	VIII	(11)
CJB110	Houston	Nontypeable	(12)

Table 5

1. Wessels, M. R., Paoletti, L. C., Rodewald, A. K., Michon, F., DiFabio, J., Jennings, H. J. & Kasper, D. L. (1993) *Infect Immun* **61**, 4760-6.
2. Wilkinson, H. W. & Eagon, R. G. (1971) *Infect Immun* **4**, 596-604.
3. Madoff, L. C., Michel, J. L., Gong, E. W., Rodewald, A. K. & Kasper, D. L. (1992) *Infect Immun* **60**, 4989-94.
4. Lancefield, R. C. (1975) in *New approaches for inducing natural immunity to pyogenic organisms* ed. Robbins, J. E. A. (National Institutes of Health, Bethesda, MD), pp. 145-151.
5. Wessels, M. R., Benedi, V.-J., Kasper, D. L., Heggen, L. M. & Rubens, C. E. (1991) in *Genetics and molecular biology of streptococci, lactococci, and enterococci* eds. Dunny, G. M., Cleary, P. P. & McKay, L. L. (American society for microbiology, Washington, DC), pp. 219-223.
6. Rubens, C. E., Wessels, M. R., Heggen, L. M. & Kasper, D. L. (1987) *Proc. Natl. Acad. Sci. U S A* **84**, 7208-12.
7. Wessels, M. R., Paoletti, L. C., Kasper, D. L., DiFabio, J. L., Michon, F., Holme, K. & Jennings, H. J. (1990) *J Clin Invest* **86**, 1428-33.
8. Edwards, M. S., Wessels, M. R. & Baker, C. J. (1993) *Infect Immun* **61**, 2866-71.
9. Wilkinson, H. W. (1977) *J Clin Microbiol* **6**, 183-4.
10. Wessels, M. R., Paoletti, L. C., Pinel, J. & Kasper, D. L. (1995) *J Infect Dis* **171**, 879-84.
11. Lachenauer, C. S., Kasper, D. L., Shimada, J., Iciman, Y., Ohtsuka, H., Kaku, M., Paoletti, L. C. & Madoff, L. C. (1997) in *ICAAC*, pp. K-80.
12. Lachenauer, C. S., Creti, R., Michel, J. L. & Madoff, L. C. (2000) *Proc Natl Acad Sci U S A* **97**, 9630-5.

Table 6**Cluster 1**

SAG0230	conserved hypothetical protein
SAG0231	hypothetical protein
SAG0232	hypothetical protein
SAG0233	hypothetical protein
SAG0234	hypothetical protein
SAG0235	hypothetical protein

Cluster 2

SAG0222	conserved domain protein
SAG0223	conserved hypothetical protein, fusion
SAG0225	hypothetical protein
SAG0226	recombination protein
SAG0227	hypothetical protein
SAG0228	conserved hypothetical protein
SAG0229	conserved hypothetical protein

Cluster 3

SAG0634	hypothetical protein
SAG0635	acid phosphatase, class B
SAG0636	conserved hypothetical protein
SAG0638	cell wall surface anchor family protein, interruption-N
SAG0640	transposase OrfA, IS3 family

Table 6

SAG0642	hypothetical protein
SAG0643	chaperonin, 33 kDa, degenerate
SAG0644	transcriptional regulator, AraC family
SAG0645	cell wall surface anchor family protein
SAG0646	cell wall surface anchor family protein
SAG0647	sortase family protein
SAG0648	sortase family protein
SAG0649	cell wall surface anchor family protein, putative
SAG0650	sortase family protein
SAG0651	protein of unknown function

Cluster 4

SAG1898	PTS system, IID component
SAG1899	PTS system, IIC component
SAG1900	PTS system, IIB component
SAG1901	glucuronyl hydrolase
SAG1902	PTS system, IIA component
SAG1905	conserved hypothetical protein
SAG1906	carbohydrate kinase, PfkB family

Cluster 5

SAG0247	hypothetical protein
SAG0248	hypothetical protein

Table 6

SAG0249	hypothetical protein
SAG0674	hypothetical protein
SAG0675	putative secreted protein
SAG0676	proteinase, putative
SAG0677	hypothetical protein
SAG0680	protein of unknown function
SAG0681	conserved domain protein
SAG0684	ABC transporter, ATP-binding protein
SAG1698	conserved hypothetical protein

Cluster 6

SAG0261	IS1381, transposase OrfB
SAG0262	IS1381, transposase OrfA
SAG0965	IS1381, transposase OrfA
SAG0966	IS1381, transposase OrfB
SAG2002	IS1381, transposase OrfB

Cluster 7

SAG1027	conserved hypothetical protein
SAG1028	hypothetical protein
SAG1029	hypothetical protein
SAG1030	protein of unknown function
SAG1031	conserved domain protein

Table 6

SAG1032 conserved hypothetical protein

Cluster 8

SAG1253 transposase, ISL3 family
SAG1254 mercuric reductase
SAG1255 mercuric resistance operon regulatory protein MerR
SAG2022 transposase, ISL3 family
SAG2023 mercuric reductase
SAG2024 mercuric resistance operon regulatory protein MerR

Cluster 9

SAG1993 site-specific recombinase, phage integrase family
SAG1994 conserved hypothetical protein
SAG1995 hypothetical protein
SAG1996 cell wall surface anchor family protein, putative
SAG1997 hypothetical protein
SAG1998 hypothetical protein
SAG2000 membrane protein, putative
SAG2001 conjugal transfer protein, interruption-C
SAG2007 conserved hypothetical protein
SAG2008 conserved hypothetical protein
SAG2009 conserved hypothetical protein
SAG2010 hypothetical protein

Table 6

SAG2011	conserved hypothetical protein
SAG2012	hypothetical protein
SAG2016	hypothetical protein
SAG2017	transcriptional regulator, Cro/CI family
SAG2025	Mn ²⁺ /Fe ²⁺ transporter, NRAMP family

Cluster 10

SAG1039	conserved hypothetical protein
SAG1447	conserved hypothetical protein
SAG1448	glycosyl transferase, group 1 family protein
SAG1449	preprotein translocase SecA subunit, putative
SAG1450	conserved domain protein
SAG1452	conserved hypothetical protein
SAG1453	preprotein translocase SecY family protein
SAG1454	glycosyl transferase, putative
SAG1455	glycosyl transferase, group 2 family protein
SAG1456	glycosyl transferase, family 8, degenerate
SAG1459	glycosyl transferase family 8
SAG1460	glycosyl transferase, family 8
SAG1461	conserved hypothetical protein
SAG1462	cell wall surface anchor family protein
SAG1463	transcriptional regulator, RofA family, authentic point mutation
SAG1469	conserved hypothetical protein

Table 6

SAG1471	conserved hypothetical protein
SAG1933	PTS system, IIC component, putative

Cluster 11

SAG0009	hypothetical protein
SAG0120	hypothetical protein
SAG0157	deoxyribonuclease-related protein, degenerate
SAG0186	hypothetical protein
SAG0216	hypothetical protein
SAG0236	hypothetical protein
SAG0307	hypothetical protein
SAG0308	ABC transporter, ATP-binding protein
SAG0311	DNA-binding response regulator, authentic point mutation
SAG0518	peptide chain release factor 2, programmed frameshift
SAG0553	hypothetical protein
SAG0555	prophage LambdaSa1, antirepressor, putative
SAG0564	conserved hypothetical protein
SAG0579	conserved hypothetical protein
SAG0580	conserved hypothetical protein, truncation
SAG0611	transposase, degenerate
SAG0637	transcriptional regulator, TetR family, putative, authentic frameshift
SAG0641	Tn5252, Orf 10 protein, degenerate
SAG0652	Tn5252, Orf 28 protein, degenerate

Table 6

SAG0655	conserved hypothetical protein
SAG0678	endopeptidase O, degenerate
SAG0683	transmembrane protein Vexp3, putative, degenerate
SAG0855	glycogen biosynthesis protein GlgD, authentic frameshift
SAG0898	hypothetical protein
SAG0899	hypothetical protein
SAG0901	hypothetical protein
SAG0902	hypothetical protein
SAG0903	hypothetical protein
SAG0917	Tn916, hypothetical protein
SAG0920	Tn916, hypothetical protein
SAG0922	Tn916, hypothetical protein
SAG0924	Tn916, tetM leader peptide
SAG0928	Tn916, hypothetical protein, authentic frameshift
SAG0936	Tn916, hypothetical protein
SAG0943	hypothetical protein
SAG0972	conserved hypothetical protein, authentic frameshift
SAG1023	hypothetical protein
SAG1080	hypothetical protein
SAG1123	hypothetical protein
SAG1129	hypothetical protein
SAG1136	conserved hypothetical protein
SAG1217	conserved hypothetical protein, authentic frameshift

Table 6

SAG1231	transposase OrfB, IS3 family, degenerate
SAG1242	transposase OrfB, IS3 family, truncation
SAG1309	hypothetical protein
SAG1331	R5 protein
SAG1437	hypothetical protein
SAG1445	MutT/nudix family protein, authentic frameshift
SAG1484	ribosomal protein L33
SAG1493	hypothetical protein
SAG1539	hypothetical protein
SAG1543	conserved hypothetical protein, authentic frameshift
SAG1560	hypothetical protein
SAG1568	phosphoserine aminotransferase, authentic frameshift
SAG1570	conserved hypothetical protein
SAG1601	conserved hypothetical protein
SAG1644	hypothetical protein
SAG1646	hypothetical protein
SAG1699	hypothetical protein
SAG1705	peptidase, M24 family, authentic point mutation
SAG1708	hypothetical protein
SAG1857	prophage LambdaSa2, HNH endonuclease family protein
SAG1864	hypothetical protein
SAG1868	hypothetical protein

Table 6

SAG1869	prophage LambdaSa2, type II DNA modification methyltransferase, putative
SAG1872	hypothetical protein
SAG1874	hypothetical protein
SAG1876	prophage LambdaSa2, HNH endonuclease family protein
SAG1878	conserved domain protein
SAG1881	hypothetical protein
SAG1883	conserved hypothetical protein
SAG1886	hypothetical protein
SAG1903	hypothetical protein
SAG1937	streptococcal histidine triad family protein, degenerate
SAG1971	hypothetical protein
SAG1979	membrane protein, putative
SAG1980	ABC transporter, ATP-binding protein
SAG1981	hypothetical protein
SAG1982	transcriptional regulator, Cro/CI family
SAG1983	conserved hypothetical protein
SAG1984	conserved hypothetical protein TIGR00730
SAG1985	hypothetical protein
SAG1991	transcriptional regulator, Cro/CI family
SAG1992	protein of unknown function
SAG1999	hypothetical protein
SAG2004	conjugal transfer protein, interruption-N

Table 6

SAG2039	conserved hypothetical protein
SAG2044	hypothetical protein
SAG2052	hypothetical protein
SAG2065	ribosomal protein L33
SAG2094	competence/damage-inducible protein CinA, authentic frameshift
SAG2099	hypothetical protein

Cluster 12

SAG1164	glycosyl transferase CpsJ(V)
SAG1165	glycosyl transferase CpsO(V)
SAG1166	glycosyl transferase CpsN(V)
SAG1167	polysaccharide biosynthesis protein CpsM(V)
SAG1168	polysaccharide biosynthesis protein cpsH(V)

Cluster 13

SAG0581	conserved hypothetical protein
SAG0582	conserved hypothetical protein
SAG0583	conserved hypothetical protein
SAG0585	conserved hypothetical protein
SAG0586	conserved hypothetical protein
SAG0587	prophage LambdaSa1, structural protein, putative
SAG0588	conserved hypothetical protein
SAG0589	conserved hypothetical protein

Table 6

SAG0590	conserved hypothetical protein
SAG0591	conserved hypothetical protein
SAG0593	prophage LambdaSa1, structural protein
SAG0594	conserved hypothetical protein
SAG0595	conserved hypothetical protein
SAG0596	prophage LambdaSa1, pblA protein, internal deletion

Cluster 14

SAG0915	Tn916, transposase
SAG0918	Tn916, hypothetical protein
SAG0919	Tn916, hypothetical protein
SAG0921	Tn916, transcriptional regulator, putative
SAG0925	Tn916, hypothetical protein
SAG0926	Tn916, NLP/P60 family protein
SAG0927	membrane protein, putative
SAG0929	Tn916, hypothetical protein
SAG0930	Tn916, hypothetical protein
SAG0931	Tn916, hypothetical protein
SAG0932	Tn916, transcriptional regulator, putative
SAG0933	Tn916, FtsK/SpoIIIE family protein
SAG0934	Tn916, hypothetical protein
SAG0935	Tn916, hypothetical protein
SAG0937	ABC transporter, ATP-binding protein, authentic frameshift

Table 6**Cluster 15**

SAG1835	conserved hypothetical protein
SAG1837	prophage LambdaSa2, lysin, putative
SAG1839	conserved hypothetical protein
SAG1840	hypothetical protein
SAG1842	prophage LambdaSa2, PblB, putative
SAG1843	conserved hypothetical protein
SAG1844	conserved hypothetical protein
SAG1849	hypothetical protein
SAG1851	conserved domain protein
SAG1852	conserved domain protein
SAG1853	prophage LambdaSa2, protease, putative
SAG1854	conserved hypothetical protein
SAG1855	prophage LambdaSa2, terminase large subunit, putative
SAG1856	hypothetical protein
SAG1858	hypothetical protein
SAG1859	prophage LambdaSa2, site-specific recombinase, phage integrase family
SAG1860	conserved hypothetical protein
SAG1861	prophage LambdaSa2, transcriptional regulator, Cro/CI family
SAG1862	hypothetical protein
SAG1863	prophage LambdaSa2, single-strand binding protein
SAG1865	conserved hypothetical protein

Table 6

SAG1866	conserved hypothetical protein
SAG1867	conserved hypothetical protein
SAG1870	prophage LambdaSa2, DNA replication protein DnaC, putative
SAG1871	prophage LambdaSa2, bacteriophage replication protein/hypothetical protein, truncation/fusion
SAG1873	prophage LambdaSa2, replicative DNA helicase
SAG1877	prophage LambdaSa2, antirepressor protein, putative
SAG1879	hypothetical protein
SAG1882	prophage LambdaSa2, repressor protein, putative
SAG1884	hypothetical protein
SAG1885	prophage LambdaSa2, site-specific recombinase, phage integrase family

Cluster 16

SAG1247	site-specific recombinase, phage integrase family
SAG1250	Tn5252, relaxase
SAG1251	Tn5252, Orf 9 protein
SAG1252	Tn5252, Orf 10 protein
SAG1256	IS861, transposase OrfB, truncation
SAG1257	cation-transporting ATPase, E1-E2 family
SAG1258	cadmium efflux system accessory protein
SAG1259	conserved hypothetical protein
SAG1260	hypothetical protein
SAG1261	conserved hypothetical protein

Table 6

SAG1262	cation-transporting ATPase, E1-E2 family
SAG1263	conserved domain protein, authentic frameshift
SAG1264	transcriptional repressor CopY, putative
SAG1265	cadmium resistance transporter, putative
SAG1266	hypothetical protein
SAG1267	hypothetical protein
SAG1268	repressor protein, putative
SAG1270	ImpB/MucB/SamB family protein
SAG1271	conserved hypothetical protein
SAG1272	conserved hypothetical protein
SAG1273	conserved hypothetical protein
SAG1274	conserved hypothetical protein
SAG1276	conserved hypothetical protein
SAG1277	hypothetical protein
SAG1278	hypothetical protein
SAG1279	conserved domain protein
SAG1280	SNF2 family protein
SAG1281	hypothetical protein
SAG1283	agglutinin receptor
SAG1284	abortive infection protein AbiGI
SAG1285	abortive infection protein AbiGII
SAG1286	Tn5252, Orf28
SAG1287	Tn5252, Orf26

Table 6

SAG1288	Tn5252, Orf25, degenerate
SAG1289	Tn5252, Orf23
SAG1290	hypothetical protein
SAG1291	Tn5252, Orf 21 protein, internal deletion
SAG1292	hypothetical protein
SAG1293	protease, putative
SAG1294	conserved hypothetical protein
SAG1295	conserved hypothetical protein
SAG1296	conserved hypothetical protein
SAG1297	C-5 cytosine-specific DNA methylase
SAG1299	conserved hypothetical protein
SAG1304	hypothetical protein

Table 7

Locus	Annotation
Housekeeping	
SAG0466	thiolase
SAG0471	glucokinase
SAG0492	amino acid ABC transporter, ATP-binding protein
SAG0767	D-alanine--D-alanine ligase
SAG1086	xanthine phosphoribosyltransferase
SAG1600	glutamate racemase
SAG1680	shikimate 5-dehydrogenase
SAG1723	signal peptidase I
Surface-exposed	
SAG0079	adenylate kinase
SAG0093	D-alanyl-D-alanine carboxypeptidase family protein
SAG0163	competence protein CglA
SAG0290	ABC transporter, substrate-binding protein
SAG0368	protein of unknown function
SAG0503	lipase/acylhydrolase
SAG1473	cell wall surface anchor family protein
SAG1552	conserved hypothetical protein
SAG1641	YaeC family protein
SAG2147	protein of unknown function/lipoprotein, putative
SAG2148	LysM domain protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF00003 PcsB protein (pscB)
ORF00004 ribose-phosphate pyrophosphokinase (prsA)
ORF00005 aminotransferase, class I
ORF00006 recombination protein O
ORF00009 fatty acid/phospholipid synthesis protein PlsX (plsX)
ORF00011 phosphoribosylaminoimidazole-succinocarboxamide synthase (purC)
ORF00012 phosphoribosylformylglycinamide synthase, putative
ORF00013 amidophosphoribosyltransferase (purF)
ORF00014 phosphoribosylformylglycinamide cyclo-ligase (purM)
ORF00015 phosphoribosylglycinamide formyltransferase (purN)
ORF00020 group B streptococcal surface immunogenic protein
ORF00021 N-acetylmannosamine-6-P epimerase, putative
ORF00022 sugar ABC transporter, sugar-binding protein
ORF00023 sugar ABC transporter, permease protein
ORF00024 sugar ABC transporter, permease protein
ORF00026 conserved hypothetical protein
ORF00027 N-acetylneuraminate lyase, putative
ORF00028 expressed ROK family protein
ORF00030 phosphosugar-binding transcriptional regulator, RpiR family, putative
ORF00031 phosphoribosylamine--glycine ligase (purD)
ORF00032 phosphoribosylaminoimidazole carboxylase, catalytic subunit (purE)
ORF00033 phosphoribosylaminoimidazole carboxylase, ATPase subunit (purK)
ORF00036 adenylosuccinate lyase (purB)
ORF00037 transcriptional regulator, Cro/Cl family
ORF00038 Holliday junction DNA helicase RuvB (rvbB)
ORF00039 phosphotyrosine protein phosphatase, low molecular weight
ORF00040 MORN motif family protein
ORF00041 membrane protein, putative
ORF00043 alcohol dehydrogenase, propanol-preferring (adhP)
ORF00045 MATE efflux family protein
ORF00046 ribosomal protein S10 (rpsJ)
ORF00047 ribosomal protein L3 (rplC)
ORF00048 ribosomal protein L4 (rplD)
ORF00049 ribosomal protein L23 (rplW)
ORF00050 ribosomal protein L2 (rplB)
ORF00052 ribosomal protein S19 (rpsS)
ORF00054 ribosomal protein L22 (rplV)
ORF00055 ribosomal protein S3 (rpsC)
ORF00056 ribosomal protein L16 (rplP)
ORF00058 ribosomal protein L29 (rpmC)
ORF00059 ribosomal protein S17 (rpsQ)
ORF00060 ribosomal protein L14 (rplN)
ORF00061 ribosomal protein L24 (rplX)
ORF00063 ribosomal protein L5 (rplE)
ORF00065 ribosomal protein S8 (rpsH)
ORF00066 ribosomal protein L6 (rplF)
ORF00068 ribosomal protein L18 (rplR)
ORF00069 ribosomal protein S5 (rpsE)
ORF00070 ribosomal protein L30 (rpmD)
ORF00071 ribosomal protein L15 (rplO)
ORF00072 preprotein translocase, SecY subunit
ORF00073 adenylate kinase (adk)
ORF00074 translation initiation factor IF-1 (infA)
ORF00075 ribosomal protein L36 (rpmJ)
ORF00077 ribosomal protein S13 (rpsM)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF00078 ribosomal protein S11 (rpsK)
ORF00080 DNA-directed RNA polymerase, alpha subunit (rpoA)
ORF00093 transcriptional regulator ComX1, putative
ORF00094 phosphoglycerate mutase family protein
ORF00097 heat-inducible transcription repressor HrcA (hrcA)
ORF00098 heat shock protein GrpE (grpE)
ORF00099 dnaK protein (dnaK)
ORF00100 dnaJ protein (dnaJ)
ORF00101 transcriptional regulator, GntR family
ORF00102 tRNA pseudouridine synthase A (truA)
ORF00103 phosphomethylpyrimidine kinase, putative
ORF00104 conserved hypothetical protein
ORF00105 conserved hypothetical protein
ORF00106 conserved hypothetical protein
ORF00107 trigger factor (tig)
ORF00108 DNA-directed RNA polymerase, delta subunit, putative
ORF00109 CTP synthase (pyrG)
ORF00111 deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)
ORF00113 carbonic anhydrase-related protein
ORF00115 pyridine nucleotide-disulphide oxidoreductase family protein
ORF00116 glutamyl-tRNA synthetase (gltX)
ORF00119 ribose ABC transporter, ATP-binding protein (rbsA)
ORF00122 ribose operon repressor RbsR (rbsR)
ORF00125 ABC transporter, ATP-binding protein
ORF00126 DNA-binding response regulator
ORF00128 sensor histidine kinase
ORF00131 fructose-bisphosphate aldolase (fba)
ORF00132 L-2-hydroxyisocaproate dehydrogenase
ORF00133 ribosomal protein L28 (rpmB)
ORF00134 conserved hypothetical protein
ORF00135 DAK2 domain protein
ORF00136 expressed SPFH domain/Band 7 family protein
ORF00141 amino acid ABC transporter, ATP-binding protein
ORF00142 amino acid ABC transporter, amino acid-binding protein/permease protein
ORF00143 conserved hypothetical protein
ORF00145 undecaprenol kinase, putative
ORF00146 negative regulator of competence MecA, putative
ORF00149 ABC transporter, ATP-binding protein
ORF00150 conserved hypothetical protein
ORF00151 selenocysteine lyase (csdB)
ORF00152 NifU family protein
ORF00153 conserved hypothetical protein
ORF00155 D-alanyl-D-alanine carboxypeptidase
ORF00158 oligopeptide ABC transporter, permease protein
ORF00160 oligopeptide ABC transporter, ATP-binding protein
ORF00161 oligopeptide ABC transporter, ATP-binding protein
ORF00167 adc operon repressor AdcR (adcR)
ORF00168 zinc ABC transporter, ATP-binding protein
ORF00169 zinc ABC transporter, permease protein
ORF00172 tyrosyl-tRNA synthetase (tyrS)
ORF00173 penicillin-binding protein 1B, putative
ORF00174 DNA-directed RNA polymerase, beta subunit (rpoB)
ORF00176 DNA-directed RNA polymerase beta' subunit (rpoC)
ORF00178 conserved hypothetical protein
ORF00179 competence protein CglA (cglA)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF00180 competence protein CglB (cglB)
ORF00181 conserved hypothetical protein
ORF00183 conserved hypothetical protein
ORF00184 acetate kinase (ackA)
ORF00190 pyrroline-5-carboxylate reductase (proC)
ORF00191 glutamyl-aminopeptidase (pepA)
ORF00198 single-strand binding protein (ssb)
ORF00211 PTS system, IIABC components
ORF00212 alpha amylase family protein
ORF00214 transcriptional antiterminator, BglG family
ORF00219 PTS system, IIC component, putative
ORF00224 ribosomal protein S15 (rpsO)
ORF00225 polyribonucleotide nucleotidyltransferase (pnp)
ORF00227 serine O-acetyltransferase (cysE)
ORF00229 cysteinyl-tRNA synthetase (cysS)
ORF00230 conserved hypothetical protein
ORF00231 RNA methyltransferase, TrmH family, group 3
ORF00233 DegV family protein
ORF00236 ribosomal protein L13 (rplM)
ORF00237 ribosomal protein S9 (rpsL)
ORF00261 transcriptional regulator MutR family
ORF00262 transporter, putative
ORF00263 amino acid ABC transporter, permease protein
ORF00264 amino acid ABC transporter, amino acid-binding protein
ORF00265 amino acid ABC transporter, permease protein
ORF00266 amino acid ABC transporter, ATP-binding protein
ORF00295 N-acetylglucosamine-6-phosphate deacetylase (nagA)
ORF00296 conserved hypothetical protein
ORF00297 glycyl-tRNA synthetase, alpha subunit (glyQ)
ORF00299 glycyl-tRNA synthetase, beta subunit (glyS)
ORF00300 conserved hypothetical protein
ORF00302 glycerol kinase (glpk)
ORF00303 alpha-glycerophosphate oxidase
ORF00304 glycerol uptake facilitator protein (glpF)
ORF00306 conserved hypothetical protein
ORF00307 transketolase (tkt)
ORF00309 ABC transporter, ATP-binding protein
ORF00310 membrane protein, putative
ORF00313 PTS system, IIIBC components
ORF00314 glutamate 5-kinase (proB)
ORF00315 gamma-glutamyl phosphate reductase (proA)
ORF00316 conserved hypothetical protein TIGR00006
ORF00318 penicillin-binding protein 2X (pbpX)
ORF00319 phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY)
ORF00320 ATP-dependent RNA helicase, DEAD/DEAH box family
ORF00321 ABC transporter, substrate-binding protein
ORF00322 amino acid ABC transporter, permease protein
ORF00323 amino acid ABC transporter, ATP-binding protein
ORF00325 thioredoxin reductase (trxB)
ORF00326 conserved hypothetical protein
ORF00327 NAD synthetase (nadE)
ORF00328 aminopeptidase C (pepC)
ORF00329 penicillin-binding protein 1A (pbp1A)
ORF00330 recombination protein U (recU)
ORF00331 conserved hypothetical protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF00335 conserved hypothetical protein
ORF00336 conserved hypothetical protein
ORF00337 autoinducer-2 production protein LuxS (luxS)
ORF00338 KH domain protein
ORF00348 guanylate kinase (gmk)
ORF00349 DNA-directed RNA polymerase, omega subunit, putative
ORF00350 primosomal protein N' (priA)
ORF00351 methionyl-tRNA formyltransferase (fmt)
ORF00352 Sun protein (sun)
ORF00353 serine/threonine phosphatase, putative
ORF00354 serine/threonine protein kinase
ORF00355 conserved hypothetical protein
ORF00356 sensor histidine kinase, putative
ORF00358 DNA-binding response regulator
ORF00359 hydrolase, haloacid dehalogenase family/peptidyl-prolyl cis-trans isomerase, cyclophilin type
ORF00360 general stress protein, putative
ORF00361 pyruvate formate-lyase-activating enzyme (pflA)
ORF00362 transcriptional regulator, DeoR family
ORF00363 transcriptional regulator, putative
ORF00364 PTS system, cellobiose-specific IIA component (celC)
ORF00366 PTS system, cellobiose-specific IIB component (celA)
ORF00367 PTS system, cellobiose-specific IIC component (celB)
ORF00368 formate acetyltransferase (pflD)
ORF00369 transaldolase family protein
ORF00371 glycerol dehydrogenase (gldA)
ORF00372 cysteine synthase A (cysK)
ORF00373 conserved hypothetical protein TIGR00257
ORF00374 helicase, putative
ORF00375 competence protein F, putative
ORF00376 ribosomal subunit interface protein (yfiA)
ORF00385 enoyl-CoA hydratase/isomerase family protein
ORF00386 transcriptional regulator, MarR family
ORF00387 3-oxoacyl-(acyl-carrier-protein) synthase III (fabH)
ORF00388 acyl carrier protein (acpP)
ORF00390 enoyl-(acyl-carrier-protein) reductase II (fabK)
ORF00391 malonyl CoA-acyl carrier protein transacylase (fabD)
ORF00392 3-oxoacyl-[acyl-carrier protein] reductase (fabG)
ORF00393 3-oxoacyl-(acyl-carrier-protein) synthase II (fabF)
ORF00394 acetyl-CoA carboxylase, biotin carboxyl carrier protein (accB)
ORF00395 (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase (fabZ)
ORF00396 acetyl-CoA carboxylase, biotin carboxylase (accC)
ORF00397 acetyl-CoA carboxylase, carboxyl transferase, beta subunit (accD)
ORF00398 acetyl-CoA carboxylase, carboxyl transferase, alpha subunit (accA)
ORF00400 seryl-tRNA synthetase (serS)
ORF00403 conserved hypothetical protein
ORF00404 PTS system, mannose-specific IID component
ORF00405 PTS system, mannose-specific IIC component (manM)
ORF00406 PTS system, mannose-specific IIAB components (manL)
ORF00407 hydrolase, haloacid dehalogenase-like family
ORF00410 xanthine/uracil permease family protein
ORF00411 conserved hypothetical protein TIGR00150, putative
ORF00412 acetyltransferase, GNAT family
ORF00413 expressed protein of unknown function
ORF00415 HIT family protein (hit)
ORF00419 ABC transporter, ATP-binding protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF00421 ABC transporter, permease protein
ORF00422 conserved hypothetical protein
ORF00423 conserved hypothetical protein TIGR00091
ORF00424 conserved hypothetical protein, POINT MUTATION
ORF00425 N utilization substance protein A (nusA)
ORF00426 conserved hypothetical protein
ORF00427 ribosomal protein L7A family
ORF00428 translation initiation factor IF-2
ORF00429 ribosome-binding factor A (rbfA)
ORF00432 copper-transporter ATPase CopA
ORF00435 hydrolase, haloacid dehalogenase-like family
ORF00436 DNA polymerase I (polA)
ORF00437 CoA binding domain protein
ORF00440 DNA-binding response regulator
ORF00441 sensor histidine kinase
ORF00443 queuine tRNA-ribosyltransferase (tgt)
ORF00444 conserved hypothetical protein
ORF00449 glucose-6-phosphate isomerase (pgi)
ORF00451 rhomboid family protein
ORF00452 expressed putative lipoprotein
ORF00453 UTP-glucose-1-phosphate uridylyltransferase (galU)
ORF00454 glycerol-3-phosphate dehydrogenase (NAD(P)+) (gpsA)
ORF00455 ribonuclease P protein component (rnpA)
ORF00456 SpolIIJ family protein
ORF00458 R3H domain protein
ORF00463 conserved hypothetical protein
ORF00464 RecX protein
ORF00465 RNA methyltransferase, TrmA family
ORF00470 ribonucleoside-diphosphate reductase 2, beta subunit (nrdF)
ORF00472 ribonucleoside-diphosphate reductase 2, alpha subunit (nrdE)
ORF00482 alcohol dehydrogenase, zinc-containing
ORF00483 oxidoreductase, aldo/keto reductase family
ORF00484 cation efflux system protein
ORF00485 transcriptional regulator, TetR family
ORF00496 conserved hypothetical protein
ORF00500 acetyltransferase, GNAT family
ORF00501 conserved hypothetical protein
ORF00502 valyl-tRNA synthetase (valS)
ORF00508 aspartate--ammonia ligase (asnA)
ORF00511 type II DNA modification methyltransferase, putative
ORF00513 phosphopantetheine adenylyltransferase (coAD)
ORF00515 conserved hypothetical protein
ORF00519 conserved hypothetical protein
ORF00520 conserved hypothetical protein TIGR00048
ORF00522 ABC transporter, ATP-binding/permease protein
ORF00523 ABC transporter, ATP-binding/permease protein
ORF00524 anthranilate synthase component II (trpG)
ORF00532 endonuclease III (nth)
ORF00534 conserved hypothetical protein
ORF00535 glucokinase (glk)
ORF00536 expressed protein with rhodanese domain
ORF00537 elongation factor Tu family protein
ORF00540 UDP-N-acetylmuramoylalanine--D-glutamate ligase (murD)
ORF00541 UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (murG)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF00542 cell division protein DivIB, putative
ORF00544 cell division protein FtsA (ftsA)
ORF00545 cell division protein FtsZ (ftsZ)
ORF00546 ylmE protein, putative
ORF00547 ylmF protein (ylmF)
ORF00549 ylmH protein (ylmH)
ORF00550 cell division protein DivIVA, putative
ORF00552 isoleucyl-tRNA synthetase (ileS)
ORF00553 conserved hypothetical protein
ORF00554 MutT/nudix family protein
ORF00555 ATP-dependent Cip protease, ATP-binding subunit
ORF00557 conserved hypothetical protein
ORF00558 amino acid ABC transporter, permease protein
ORF00559 amino acid ABC transporter, ATP-binding protein
ORF00560 phosphoglucomutase/phosphomannomutase family protein
ORF00562 methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase (folD)
ORF00564 exodeoxyribonuclease VII, large subunit (xseA)
ORF00566 geranyltranstransferase, putative
ORF00567 hemolysin A
ORF00570 DNA repair protein RecN (recN)
ORF00571 expressed DegV family protein
ORF00574 DNA-binding protein HU (hup)
ORF00576 dihydroorotate dehydrogenase A (pyrDA)
ORF00577 beta-lactam resistance factor (fibB)
ORF00578 beta-lactam resistance factor (fibA)
ORF00579 murM protein, putative
ORF00580 hydrolase, haloacid dehalogenase-like family
ORF00581 HD domain protein
ORF00582 conserved hypothetical protein
ORF00583 cation-transporting ATPase, E1-E2 family
ORF00588 cell division ABC transporter, ATP-binding protein FtsE (ftsE)
ORF00589 cell division ABC transporter, permease protein FtsX (ftsX)
ORF00591 metallo-beta-lactamase superfamily protein
ORF00593 DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG
ORF00595 aspartate aminotransferase (aspC)
ORF00596 asparaginyl-tRNA synthetase (asnS)
ORF00601 conserved hypothetical protein
ORF00602 conserved hypothetical protein
ORF00603 conserved hypothetical protein
ORF00605 zinc ABC transporter, zinc-binding adhesion liprotein
ORF00606 ribosomal protein L31 (rpmE)
ORF00607 DHH family protein
ORF00609 flavodoxin
ORF00614 ribosomal protein L19 (rplS)
ORF00640 prophage LambdaSa1, single-strand binding protein (ssb)
ORF00693 DNA-binding response regulator VncR (vncR)
ORF00694 sensor histidine kinase VncS (vncS)
ORF00699 rod shape-determining protein RodA, putative (rodA)
ORF00700 hydrolase, haloacid dehalogenase-like family
ORF00701 DNA gyrase, B subunit (gyrB)
ORF00702 septation ring formation regulator EzrA, putative
ORF00705 conserved hypothetical protein
ORF00706 enolase (eno)
ORF00708 3-phosphoshikimate 1-carboxyvinyltransferase (aroA)
ORF00709 shikimate kinase (aroK)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF00710	psr protein
ORF00711	RNA methyltransferase, TrmA family
ORF00729	sortase family protein
ORF00731	sortase family protein
ORF00734	sortase family protein, FRAMESHIFT
ORF00743	ABC transporter, ATP-binding protein
ORF00744	membrane protein
ORF00745	conserved hypothetical protein
ORF00748	cylG protein (cylG)
ORF00776	DNA-entry nuclease, putative
ORF00789	2-keto-3-deoxygluconate kinase
ORF00792	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase (eda)
ORF00798	proline dipeptidase (pepQ)
ORF00799	transcriptional regulator, RegM family
ORF00802	glycosyl transferase, group 1 family protein
ORF00803	threonyl-tRNA synthetase (thrS)
ORF00804	DNA-binding response regulator
ORF00808	amino acid ABC transporter, permease protein
ORF00810	amino acid ABC transporter, ATP-binding protein
ORF00811	DNA-binding response regulator
ORF00812	sensory box histidine kinase
ORF00813	metallo-beta-lactamase family protein
ORF00815	ribonuclease III (rnc)
ORF00816	expressed putative chromosome segregation SMC protein
ORF00817	hydrolase, haloacid dehalogenase-like family
ORF00818	hydrolase, haloacid dehalogenase-like family
ORF00819	signal recognition particle-docking protein FtsY (ftsY)
ORF00820	ABC transporter, substrate-binding protein
ORF00821	ABC transporter, permease protein, putative
ORF00824	transcriptional accessory protein Tex, putative
ORF00825	conserved hypothetical protein
ORF00828	HPr(Ser) kinase/phosphatase (hprK)
ORF00830	prolipoprotein diacylglyceryl transferase (lgt)
ORF00832	conserved hypothetical protein
ORF00835	peptidase, U32 family, putative
ORF00836	peptidase, U32 family
ORF00837	conserved hypothetical protein
ORF00844	lysyl-tRNA synthetase (lysS)
ORF00846	phosphoglycerate mutase family protein
ORF00847	ebsC family protein, putative
ORF00850	peptidase, U32 family
ORF00855	oligoendopeptidase F, putative
ORF00856	phosphoenolpyruvate carboxylase (ppc)
ORF00859	cell division protein, FtsW/RodA/SpoVE family (ftsW)
ORF00861	translation elongation factor Tu (tuf)
ORF00863	triosephosphate isomerase (ipiA)
ORF00865	phosphoglycerate mutase (gpmA)
ORF00867	recombination protein RecR (recR)
ORF00868	D-alanine--D-alanine ligase
ORF00869	UDP-N-acetyl muramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase (murF)
ORF00870	oxalate:formate antiporter
ORF00871	membrane protein, putative
ORF00873	peptide chain release factor 3 (prfC)
ORF00876	ABC transporter, ATP-binding protein
ORF00880	ATP-dependent RNA helicase, DEAD/DEAH box family

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxx Annotation

ORF00882 conserved hypothetical protein
ORF00883 conserved hypothetical protein
ORF00884 acyltransferase family protein
ORF00885 competence protein CelA (celA)
ORF00887 DNA internalization-related competence protein ComEC/Rec2
ORF00889 sugar-binding transcriptional regulator, LacI family
ORF00892 DNA polymerase III, delta subunit, putative
ORF00893 superoxide dismutase, Fe-Mn (sodA)
ORF00894 transcriptional antiterminator LicT
ORF00895 PTS system, beta-glucosides-specific IIABC components
ORF00896 6-phospho-beta-glucosidase (bglA)
ORF00899 glycerate kinase 2 (garK)
ORF00904 S-adenosylmethionine:tRNA ribosyltransferase-isomerase (queA)
ORF00906 glucosamine-6-phosphate isomerase (nagB)
ORF00908 ribosomal small subunit pseudouridine synthase
ORF00911 competence protein CoiA (coiA)
ORF00912 oligoendopeptidase B (pepB)
ORF00914 O-methyltransferase family protein
ORF00916 protease maturation protein, putative
ORF00919 alanyl-tRNA synthetase (alaS)
ORF00925 transcriptional regulator, Cro/CI family
ORF00928 ribonucleoside-diphosphate reductase 2, beta subunit (nrdF)
ORF00929 ribonucleoside-diphosphate reductase 2, alpha subunit (nrdE)
ORF00930 ribonucleoside-diphosphate reductase 2, NrdH-redoxin (nrdH)
ORF00931 phosphocarrier protein HPr (ptsH)
ORF00932 phosphoenolpyruvate-protein phosphotransferase (ptsI)
ORF00933 glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent (gapN)
ORF00934 polysaccharide deacetylase family protein
ORF00935 ATP-dependent RNA helicase, DEAD/DEAH box family
ORF00936 uridine kinase (udk)
ORF00937 conserved hypothetical protein
ORF00938 DNA polymerase III, gamma and tau subunits (dnaX)
ORF00940 biotin--acetyl-CoA-carboxylase ligase
ORF00941 S-adenosylmethionine synthetase (metK)
ORF00955 UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
ORF00956 acetyltransferase, GNAT family
ORF00957 CBS domain protein
ORF00958 methionine aminopeptidase, type I (map)
ORF00959 ribonuclease BN, putative
ORF00962 conserved hypothetical protein
ORF00963 DNA ligase, NAD-dependent (ligA)
ORF00964 BmrU protein, putative
ORF00966 pullulanase, putative
ORF00973 ATP synthase F0, A subunit (atpB)
ORF00974 ATP synthase F0, B subunit (atpF)
ORF00975 ATP synthase F1, delta subunit (atpH)
ORF00976 ATP synthase F1, alpha subunit (atpA)
ORF00977 ATP synthase F1, gamma subunit (atpG)
ORF00978 ATP synthase F1, beta subunit (atpD)
ORF00979 ATP synthase F1, epsilon subunit (atpC)
ORF00981 UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
ORF00983 DNA-entry nuclease (endA)
ORF00984 phenylalanyl-tRNA synthetase, alpha subunit (pheS)
ORF00986 phenylalanyl-tRNA synthetase, beta subunit (pheT)
ORF00988 exonuclease RexB (rexB)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF00989 exonuclease RexA (rexA)
ORF00991 tRNA modification GTPase TrmE (trmE)
ORF00992 ABC transporter, ATP-binding protein
ORF00993 acetoine dehydrogenase, thymine PPi dependent, E1 component, alpha subunit
ORF00994 acetoine dehydrogenase, thymine PPi dependent, E1 component, beta subunit
ORF00995 acetoine dehydrogenase, thymine PPi dependent, E2 component, dihydrolipoamide
ORF00996 acetoine dehydrogenase, thymine PPi dependent, E3 component, dihydrolipoamide dehydrogenase
ORF00997 lipoate-protein ligase A (lplA)
ORF00998 cobyrinic acid synthase, putative
ORF00999 mur ligase family protein
ORF01000 conserved hypothetical protein TIGR00159
ORF01001 expressed protein of unknown function
ORF01002 phosphoglucomutase/phosphomannomutase family protein
ORF01005 oxygen-independent coproporphyrinogen III oxidase, putative
ORF01006 conserved hypothetical protein
ORF01007 hydrolase, haloacid dehalogenase-like family
ORF01008 conserved hypothetical protein
ORF01023 GTP-binding protein LepA (lepa)
ORF01027 PilB-related protein
ORF01030 cation-transporting ATPase, E1-E2 family
ORF01033 conserved hypothetical protein
ORF01040 Tn916, tetracycline resistance protein (tetM)
ORF01057 transcriptional regulator, GntR family
ORF01058 DNA polymerase III, alpha subunit (dnaE)
ORF01059 6-phosphofructokinase (pfk)
ORF01060 pyruvate kinase (pyk)
ORF01063 glucosamine--fructose-6-phosphate aminotransferase (isomerizing) (glmS)
ORF01066 phnA protein (phnA)
ORF01068 amino acid ABC transporter, permease protein
ORF01069 amino acid ABC transporter, ATP-binding protein
ORF01070 amino acid ABC transporter, amino acid-binding protein
ORF01072 ribosomal protein S20 (rpsT)
ORF01073 pantothenate kinase (coA)
ORF01074 conserved hypothetical protein
ORF01075 cytidine deaminase (cdd)
ORF01076 expressed putative lipoprotein
ORF01077 sugar ABC transporter, ATP-binding protein
ORF01078 sugar ABC transporter, permease protein, putative
ORF01079 sugar ABC transporter, permease protein, putative
ORF01080 NADH oxidase (nox-2)
ORF01081 L-lactate dehydrogenase (ldh)
ORF01082 DNA gyrase, A subunit (gyrA)
ORF01083 sortase SrtA (srtA)
ORF01089 GMP synthase (guaA)
ORF01090 transcriptional regulator, GntR family
ORF01091 gid protein (gid)
ORF01093 expressed putative lipoprotein
ORF01097 ABC transporter, ATP-binding protein
ORF01099 DNA-binding response regulator
ORF01101 site-specific recombinase, phage integrase family
ORF01106 signal recognition particle protein Ffh (ffh)
ORF01108 conserved hypothetical protein
ORF01109 sensor histidine kinase CiaH
ORF01110 DNA-binding response regulator CiaR (ciaR)
ORF01111 aminopeptidase N (pepN)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF01112 phosphate transport system regulatory protein PhoU (phoU)
ORF01113 phosphate ABC transporter, ATP-binding protein PstB, putative
ORF01114 phosphate ABC transporter, ATP-binding protein PstB, putative
ORF01115 phosphate ABC transporter, permease protein PstA, putative
ORF01116 phosphate ABC transporter, permease protein
ORF01117 phosphate ABC transporter, phosphate-binding protein
ORF01118 NOL1/NOP2/sun family protein
ORF01119 inositol monophosphatase family protein
ORF01120 conserved hypothetical protein
ORF01121 conserved hypothetical protein
ORF01122 macrolide-efflux protein mreA/riboflavin biosynthesis protein RibF
ORF01123 tRNA pseudouridine synthase B (truB)
ORF01125 conserved hypothetical protein
ORF01128 permease, putative
ORF01129 ABC transporter, ATP-binding protein
ORF01131 DNA topoisomerase I (topA)
ORF01132 DprA/SMF protein, putative DNA processing factor (dprA)
ORF01134 iron compound ABC transporter, ATP-binding protein
ORF01137 acetyltransferase, CysE/LacA/LpxA/NodL family
ORF01138 ribonuclease HII (rnhB)
ORF01139 GTP-binding protein
ORF01176 carbamoyl-phosphate synthase, large subunit (carB)
ORF01177 carbamoyl-phosphate synthase, small subunit (carA)
ORF01178 aspartate carbamoyltransferase (pyrB)
ORF01179 dihydroorotate, multifunctional complex type (pyrC)
ORF01180 orotate phosphoribosyltransferase (pyrE)
ORF01181 orotidine 5'-phosphate decarboxylase (pyrF)
ORF01183 ABC transporter, ATP-binding protein
ORF01184 ribonucleotide reductase, truncation
ORF01188 cardiolipin synthetase (cis)
ORF01189 formate--tetrahydrofolate ligase (fhs)
ORF01190 lipoate-protein ligase A (lplA)
ORF01198 flavoprotein-related protein
ORF01199 flavoprotein family protein
ORF01200 membrane protein, putative
ORF01201 phosphoglucomutase (pgm)
ORF01203 IS861, transposase OrfB
ORF01205 ABC transporter, ATP-binding/permease protein
ORF01206 ABC transporter, ATP-binding/permease protein
ORF01207 conserved hypothetical protein
ORF01208 conserved hypothetical protein
ORF01209 Serine hydroxymethyltransferase
ORF01210 Sua5/YciO/YrdC/YwlC family protein
ORF01211 modification methylase, HemK family
ORF01212 peptide chain release factor 1 (prfA)
ORF01213 thymidine kinases (tdk)
ORF01214 4-oxalocrotonate tautomerase (xylM)
ORF01216 ApbE family protein
ORF01220 xanthine permease (pbuX)
ORF01221 xanthine phosphoribosyltransferase (xpt)
ORF01222 guanosine monophosphate reductase (guaC)
ORF01227 phosphate acetyltransferase
ORF01228 ribosomal large subunit pseudouridine synthase, RiuD subfamily
ORF01229 expressed protein of unknown function
ORF01230 GTP pyrophosphokinase family protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF01231 conserved hypothetical protein
ORF01232 ribose-phosphate pyrophosphokinase (prsA)
ORF01233 cysteine desulphurase (iscS)
ORF01234 conserved hypothetical protein
ORF01235 conserved hypothetical protein
ORF01236 DNA repair protein RadC (radC)
ORF01238 6-phospho-beta-glucosidase (ascB)
ORF01239 platelet activating factor, putative
ORF01240 hydrolase, haloacid dehalogenase-like family
ORF01242 voltage-gated chloride channel family protein
ORF01243 spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein (potD)
ORF01244 spermidine/putrescine ABC transporter, permease protein (potC)
ORF01245 spermidine/putrescine ABC transporter, permease protein (potB)
ORF01246 spermidine/putrescine ABC transporter, ATP-binding protein (potA)
ORF01247 UDP-N-acetylenolpyruvoylglucosamine reductase (murB)
ORF01248 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase (folK)
ORF01250 dihydropteroate synthase (folP)
ORF01251 GTP cyclohydrolase I (folE)
ORF01252 folylpolyglutamate synthase (folC)
ORF01259 aldehyde dehydrogenase family protein
ORF01260 membrane protein
ORF01274 gls24 protein, putative
ORF01276 gls24 protein, putative
ORF01279 conserved hypothetical protein
ORF01282 ATP-dependent DNA helicase PcrA (pcrA)
ORF01283 conserved hypothetical protein, FRAMESHIFT
ORF01284 uracil permease (uraA)
ORF01285 sodium:alanine symporter family protein
ORF01286 cation efflux family protein
ORF01290 ribosomal protein S1 (rpsA)
ORF01292 branched-chain amino acid aminotransferase (ilvE)
ORF01294 DNA topoisomerase IV, A subunit (parC)
ORF01295 DNA topoisomerase IV, B subunit (parE)
ORF01296 membrane protein, putative
ORF01297 uracil-DNA glycosylase (ung)
ORF01317 transcriptional regulator, LysR family, putative
ORF01319 purine nucleoside phosphorylase (deoD)
ORF01321 purine nucleoside phosphorylase (deoD)
ORF01323 phosphopentomutase (deoB)
ORF01324 ribose 5-phosphate isomerase (rpiA)
ORF01327 tributyrin esterase (estA)
ORF01328 metallo-beta-lactamase superfamily protein
ORF01329 ABC transporter, ATP-binding protein
ORF01330 ABC transporter, permease protein
ORF01331 conserved hypothetical protein
ORF01332 adherence and virulence protein A (pavA)
ORF01335 TPR domain protein
ORF01336 membrane protein
ORF01338 mutator MutT protein (mutX)
ORF01339 hyaluronidase
ORF01343 iminodiacetate oxidase, putative
ORF01344 conserved hypothetical protein TIGR00486
ORF01345 conserved hypothetical protein
ORF01346 DNA replication protein Dnad, putative
ORF01347 adenine phosphoribosyltransferase (apt)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF01350 single-stranded-DNA-specific exonuclease RecJ (recJ)
ORF01351 oxidoreductase, short chain dehydrogenase/reductase family
ORF01352 metallo-beta-lactamase superfamily protein
ORF01353 conserved hypothetical protein
ORF01354 GTP-binding protein HflX (hflX)
ORF01355 tRNA delta(2)-isopentenylpyrophosphate transferase (miaA)
ORF01357 exfoliative toxin A, putative
ORF01358 pullulanase, putative
ORF01362 conserved hypothetical protein
ORF01363 peptidase, M20/M25/M40 family
ORF01364 nitroreductase family protein
ORF01367 excinuclease ABC, C subunit (uvrC)
ORF01380 streptococcal histidine triad family protein
ORF01381 laminin-binding surface protein (lmb)
ORF01397 Tn5252, relaxase
ORF01403 mercuric reductase (merA)
ORF01406 IS861, transposase OrfB, truncation
ORF01407 cation-transporting ATPase, E1-E2 family
ORF01411 conserved hypothetical protein
ORF01412 cation-transporting ATPase, E1-E2 family
ORF01415 transcriptional repressor CopY, putative
ORF01416 cadmium resistance transporter, putative
ORF01451 C-5 cytosine-specific DNA methylase
ORF01453 conserved hypothetical protein
ORF01455 ribosomal protein L7/L12 (rplL)
ORF01456 ribosomal protein L10 (rplJ)
ORF01458 ATP-dependent Clp protease, ATP-binding subunit
ORF01467 GTP-binding protein (cgpA)
ORF01468 ATP-dependent Clp protease, ATP-binding subunit ClpX (clpX)
ORF01470 dihydrofolate reductase (folA)
ORF01471 thymidylate synthase (thyA)
ORF01472 HMG-CoA synthase
ORF01473 3-hydroxy-3-methylglutaryl-CoA reductase
ORF01474 conserved hypothetical protein
ORF01475 hemolysin III, putative
ORF01476 conserved hypothetical protein TIGR00147
ORF01479 isopentenyl-diphosphate delta-isomerase
ORF01480 phosphomevalonate kinase
ORF01481 diphosphomevalonate decarboxylase (mvaD)
ORF01482 mevalonate kinase, putative
ORF01484 DNA-binding response regulator
ORF01491 polypeptide deformylase, putative
ORF01495 ABC transporter, ATP-binding/permease protein
ORF01496 ABC transporter, ATP-binding/permease protein
ORF01498 ABC transporter, ATP-binding protein
ORF01499 polyA polymerase family protein
ORF01500 DegV family protein
ORF01501 expressed protein of unknown function
ORF01504 PTS system, fructose specific IIABC components
ORF01505 1-phosphofructokinase (fruk)
ORF01506 lactose phosphotransferase system repressor (lacR)
ORF01507 beta-lactam resistance factor
ORF01511 pyridine nucleotide-disulphide oxidoreductase family protein
ORF01512 tRNA (guanine-N1)-methyltransferase (trmD)
ORF01513 16S rRNA processing protein RimM (rimM)

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF01515 transcriptional regulator, RofA family
ORF01516 KH domain protein
ORF01517 ribosomal protein S16 (rpsP)
ORF01518 permease, putative
ORF01519 ABC transporter, ATP-binding protein
ORF01520 conserved hypothetical protein
ORF01523 carbamoyl-phosphate synthase, small subunit (carA)
ORF01524 pyrimidine operon regulatory protein (pyrR)
ORF01525 ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF01526 lipoprotein signal peptidase (IspA)
ORF01527 transcriptional regulator, LysR family
ORF01528 ribosomal protein L27 (rpmA)
ORF01529 conserved hypothetical protein
ORF01530 ribosomal protein L21 (rplU)
ORF01531 conserved hypothetical protein, FRAMESHIFT
ORF01532 thiamine biosynthesis protein Thil (thil)
ORF01533 cysteine desulphurase (iscS)
ORF01536 glutathione reductase (gor)
ORF01537 conserved hypothetical protein
ORF01538 chorismate synthase (aroC)
ORF01539 3-dehydroquinate synthase (aroB)
ORF01540 3-dehydroquinate dehydratase (aroD)
ORF01541 conserved hypothetical protein
ORF01543 ribosomal protein L20 (rplT)
ORF01544 ribosomal protein L35 (rplM)
ORF01545 translation initiation factor IF-3 (infC)
ORF01546 cytidylate kinase (cmk)
ORF01548 ferredoxin, 4Fe-4S
ORF01550 peptidase t (pepT)
ORF01551 polysaccharide biosynthesis protein, putative
ORF01552 UDP-N-acetylglucosamyltransferase, putative
ORF01553 iron compound ABC transporter, ATP-binding protein (fepC)
ORF01555 iron compound ABC transporter, permease protein
ORF01556 iron compound ABC transporter, permease protein
ORF01558 inorganic pyrophosphatase, manganese-dependent (ppa)
ORF01559 pyruvate formate-lyase-activating enzyme (pflA)
ORF01560 CBS domain protein
ORF01561 conserved hypothetical protein
ORF01564 PAP2 family protein
ORF01565 membrane protein, putative
ORF01567 expressed sortase family protein
ORF01568 sortase family protein
ORF01571 robB protein FRAMESHIFT (robB)
ORF01587 conserved hypothetical protein
ORF01589 RNA polymerase sigma-70 factor (rpoD)
ORF01590 DNA primase (dnaG)
ORF01591 large conductance mechanosensitive channel protein (mscl)
ORF01592 ribosomal protein S21 (rpsU)
ORF01594 amino acid ABC transporter, amino acid-binding protein
ORF01598 rhodanese family protein
ORF01602 glycogen phosphorylase (glgP)
ORF01603 4-alpha-glucanotransferase (malQ)
ORF01604 maltose operon repressor MalR, putative
ORF01605 maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein
ORF01606 maltose ABC transporter, permease protein

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxx Annotation

ORF01607 maltose ABC transporter, permease protein
ORF01614 preprotein translocase SecA subunit, putative
ORF01619 preprotein translocase SecY family protein
ORF01634 excinuclease ABC, B subunit (uvrB)
ORF01636 glutamine ABC transporter, glutamine-binding protein/permease protein (glnP)
ORF01637 glutamine ABC transporter, ATP-binding protein, GlnQ putative
ORF01640 GTP-binding protein, GTP1/Obg family (obg)
ORF01646 amidase family protein
ORF01647 ribosomal small subunit pseudouridine synthase A (rsuA)
ORF01648 oxidoreductase, aldo/keto reductase family
ORF01651 lactoylglutathione lyase (gloA)
ORF01652 glycosyl transferase, group 2 family protein
ORF01654 SsrA-binding protein (smpB)
ORF01655 exoribonuclease, VacB/Rnb family (vacB)
ORF01657 preprotein translocase, SecG subunit
ORF01658 multi-drug resistance protein
ORF01662 dephospho-CoA kinase
ORF01663 formamidopyrimidine-DNA glycosylase (mutM)
ORF01677 GTP-binding protein Era (era)
ORF01678 diacylglycerol kinase (dgkA)
ORF01679 conserved hypothetical protein TIGR00043
ORF01685 PhoH family protein
ORF01687 conserved hypothetical protein
ORF01689 conserved hypothetical protein
ORF01690 ribosome recycling factor (frr)
ORF01691 uridylate kinase (pyrH)
ORF01693 peptide ABC transporter, ATP-binding protein FRAMESHIFT
ORF01697 ribosomal protein L1 (rplA)
ORF01698 ribosomal protein L11 (rplK)
ORF01706 IS861, transposase OrfB
ORF01707 chorismate binding enzyme
ORF01708 FtsK/SpoIIIE family protein
ORF01709 peptidyl-prolyl cis-trans isomerase, cyclophilin-type
ORF01710 manganese ABC transporter, permease protein
ORF01711 manganese ABC transporter, ATP-binding protein
ORF01712 manganese ABC transporter, manganese-binding adhesion liprotein
ORF01713 iron-dependent transcriptional regulator
ORF01714 5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase (pfs)
ORF01716 MutT/nudix family protein
ORF01718 UDP-N-acetylglucosamine pyrophosphorylase (glmU)
ORF01722 oxidoreductase, Gfo/ldh/MoCA family
ORF01725 gluconate 5-dehydrogenase, putative
ORF01726 conserved hypothetical protein
ORF01738 branched-chain amino acid transport system II carrier protein (brnQ)
ORF01739 methionyl-tRNA synthetase (metG)
ORF01745 exodeoxyribonuclease (exoA)
ORF01746 conserved hypothetical protein
ORF01752 copper homeostasis protein CutC, putative
ORF01755 tetrapyrrole methylase family protein
ORF01756 conserved hypothetical protein
ORF01758 DNA polymerase III, delta prime subunit, putative
ORF01759 thymidylate kinase (tmk)
ORF01773 ATP-dependent Clp protease, proteolytic subunit ClpP (clpP)
ORF01774 uracil phosphoribosyltransferase (upp)
ORF01777 RNA methyltransferase, TrmH family, group 2

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxxx Annotation**

ORF01781 conserved hypothetical protein TIGR00278
ORF01782 ribosomal large subunit pseudouridine synthase B (rluB)
ORF01783 conserved hypothetical protein TIGR00281
ORF01784 conserved hypothetical protein
ORF01785 integrase/recombinase, phage integrase family
ORF01786 CBS domain protein
ORF01787 conserved hypothetical protein
ORF01788 HAM1 protein
ORF01789 glutamate racemase (murl)
ORF01791 membrane protein, putative
ORF01792 transcriptional regulator, biotin repressor family
ORF01793 membrane protein, putative
ORF01795 RNA methyltransferase, TrmH family
ORF01796 acylphosphatase
ORF01797 lipoprotein, putative
ORF01799 amino acid ABC transporter, permease protein
ORF01801 amidase family protein
ORF01802 transcription elongation factor GreA (greA)
ORF01803 conserved hypothetical protein
ORF01804 acetyltransferase, GNAT family
ORF01805 UDP-N-acetylmuramate--alanine ligase (murC)
ORF01806 conserved hypothetical protein
ORF01808 expressed putative helicase
ORF01811 phosphoglycerate dehydrogenase-related protein
ORF01812 primosomal protein Dnal (dnal)
ORF01813 conserved hypothetical protein
ORF01814 conserved hypothetical protein TIGR00244
ORF01815 sensor histidine kinase CsrS (csrS)
ORF01816 DNA-binding response regulator CsrR (csrR)
ORF01817 conserved hypothetical protein
ORF01818 heat shock protein HtpX (htpX)
ORF01820 lemA protein (lemA)
ORF01821 glucose-inhibited division protein B (gidB)
ORF01822 sodium transport family protein
ORF01823 potassium uptake protein, Trk family, putative
ORF01825 ABC transporter, ATP-binding protein
ORF01828 branched-chain amino acid transport system II carrier protein (brnQ)
ORF01829 alcohol dehydrogenase, zinc-containing (adh)
ORF01830 ABC transporter, permease protein
ORF01831 ABC transporter, ATP-binding protein
ORF01833 expressed YaeC family protein
ORF01834 ABC transporter, substrate-binding protein
ORF01835 glutamine amidotransferase, class I
ORF01837 conserved hypothetical protein TIGR01033
ORF01846 glycerol uptake facilitator protein (glpF)
ORF01849 conserved hypothetical protein
ORF01851 conserved hypothetical protein
ORF01852 iojap-related protein
ORF01854 conserved hypothetical protein TIGR00488
ORF01855 conserved hypothetical protein TIGR00482
ORF01856 conserved hypothetical protein TIGR00253
ORF01857 GTP-binding protein
ORF01858 hydrolase, halocid dehalogenase-like family
ORF01860 glutamyl-tRNA(Gln) amidotransferase, B subunit (gatB)
ORF01861 glutamyl-tRNA(Gln) amidotransferase, A subunit (gatA)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxx Annotation

ORF01862 glutamyl-tRNA(Gln) amidotransferase, C subunit (gatC)
ORF01867 isochorismatase family protein
ORF01869 transcriptional regulator CodY, putative
ORF01870 aminotransferase, class I
ORF01871 universal stress protein family FRAMESHIFT
ORF01872 hydrolase, haloacid dehalogenase-like family
ORF01873 asparaginase family protein
ORF01874 shikimate 5-dehydrogenase (aroE)
ORF01876 ATP-dependent DNA helicase RecG (recG)
ORF01878 alanine racemase (alr)
ORF01879 holo-(acyl-carrier-protein) synthase (acpS)
ORF01881 preprotein translocase, SecA subunit (secA)
ORF01882 mannose-6-phosphate isomerase, class I (manA)
ORF01883 fructokinase (scrK)
ORF01885 PTS system IIABC components
ORF01886 sucrose-6-phosphate hydrolase (scrB)
ORF01887 sucrose operon repressor ScrR (scrR)
ORF01888 N utilization substance protein B (nusB)
ORF01889 conserved hypothetical protein
ORF01890 translation elongation factor P (efp)
ORF01900 cytidine/deoxycytidylate deaminase family protein
ORF01906 excinuclease ABC, A subunit (uvrA)
ORF01907 conserved hypothetical protein
ORF01908 magnesium transporter, CorA family (corA)
ORF01909 ribosomal protein S18 (rpsR)
ORF01910 single-strand binding protein (ssb)
ORF01911 ribosomal protein S6 (rpsF)
ORF01912 A/G-specific adenine glycosylase (mutY)
ORF01914 thioredoxin (trx)
ORF01915 PAP2 family protein
ORF01916 MutS2 family protein
ORF01917 conserved hypothetical protein
ORF01918 conserved hypothetical protein
ORF01919 ribonuclease HIII (rnhC)
ORF01920 signal peptidase I
ORF01921 helicase, putative
ORF01923 DNA-damage inducible protein P (dinP)
ORF01924 formate acetyltransferase (pfld)
ORF01926 conserved hypothetical protein
ORF01927 proteinase, putative, degenerate, FRAMESHIFT
ORF01929 glycerol uptake facilitator protein, putative
ORF01930 universal stress protein family
ORF01933 X-pro dipeptidyl-peptidase (pepX)
ORF01937 ABC transporter, ATP-binding protein CydC (cydC)
ORF01938 ABC transporter, ATP-binding protein CydD
ORF01945 conserved hypothetical protein TIGR00103
ORF01948 exonuclease
ORF01949 conserved hypothetical protein
ORF01950 conserved hypothetical protein TIGR00275
ORF01952 ribosomal protein S14 (rpsN)
ORF01957 O-sialoglycoprotein endopeptidase family protein
ORF01958 ribosomal-protein-alanine acetyltransferase, putative
ORF01960 expressed protein of unknown function
ORF01961 conserved hypothetical protein
ORF01962 metallo-beta-lactamase superfamily protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF01963 conserved hypothetical protein
ORF01964 glutamine synthetase, type I (glnA)
ORF01965 transcriptional regulator GlnR (glnR)
ORF01967 conserved hypothetical protein
ORF01969 phosphoglycerate kinase (pgk)
ORF01971 glyceraldehyde 3-phosphate dehydrogenase (gap)
ORF01972 translation elongation factor G (fusA)
ORF01973 ribosomal protein S7 (rpsG)
ORF01974 ribosomal protein S12 (rpsL)
ORF01975 pur operon repressor (purR)
ORF01976 HD domain protein
ORF01977 conserved hypothetical protein
ORF01978 conserved hypothetical protein
ORF01979 ribulose-phosphate 3-epimerase (rpe)
ORF01980 conserved hypothetical protein TIGR00157
ORF01983 dimethyladenosine transferase (ksgA)
ORF01985 primase-related protein
ORF01987 deoxyribonuclease, TatD family
ORF01992 dltD protein (dltD)
ORF01993 D-alanyl carrier protein (dltC)
ORF01994 dltB protein (dltB)
ORF01996 D-alanine-activating enzyme (dltA)
ORF01997 sensor histidine kinase
ORF01998 DNA-binding response regulator
ORF01999 ribosomal protein L34 (rpmH)
ORF02004 amino acid ABC transporter, ATP-binding protein
ORF02007 conserved hypothetical protein
ORF02008 transcriptional antiterminator, BglG family
ORF02017 sugar binding transcriptional regulator, LacI family
ORF02018 transaldolase family protein
ORF02019 carbohydrate isomerase, AraD/FucA family
ORF02020 hexulose-6-phosphate isomerase, putative
ORF02021 hexulose-6-phosphate synthase, putative
ORF02022 PTS system, IIA component
ORF02023 PTS system, IIB component
ORF02024 transport protein SgaT, putative
ORF02027 adenylosuccinate synthetase (purA)
ORF02033 chaperonin, 33 kDa (hslO)
ORF02034 NifR3/Smm1 family protein
ORF02037 ATP-dependent Clp protease, ATP-binding subunit
ORF02038 transcriptional regulator CtsR (ctsR)
ORF02040 translation elongation factor Ts (tsf)
ORF02041 ribosomal protein S2 (rpsB)
ORF02043 alkyl hydroperoxide reductase, subunit F (ahpF)
ORF02076 prophage LambdaSa2, single-strand binding protein (ssb)
ORF02082 prophage LambdaSa2, type II DNA modification methyltransferase, putative
ORF02086 prophage LambdaSa2, replicative DNA helicase (dnaC)
ORF02104 endopeptidase O (pepO)
ORF02110 polypeptide deformylase (def)
ORF02111 sugar binding transcriptional regulator RegR (regR)
ORF02112 conserved hypothetical protein
ORF02113 PTS system, IID component
ORF02114 PTS system, IIC component
ORF02115 PTS system, IIB component
ORF02116 glucuronyl hydrolase

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF02118 PTS system, IIA component
ORF02120 oxidoreductase, short-chain dehydrogenase/reductase family
ORF02121 conserved hypothetical protein
ORF02122 carbohydrate kinase, PfkB family
ORF02123 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase (eda)
ORF02127 DNA polymerase III, alpha subunit, Gram-positive type
ORF02129 prolyl-tRNA synthetase (proS)
ORF02130 membrane-associated zinc metalloprotease, putative
ORF02131 phosphatidate cytidylyltransferase (cdsA)
ORF02132 undecaprenyl diphosphate synthase (upps)
ORF02133 preprotein translocase, YajC subunit (yajC)
ORF02140 glucan 1,6-alpha-glucosidase (dexB)
ORF02141 sugar ABC transporter, ATP-binding protein (msmK)
ORF02142 helix-turn-helix domain protein, fis-type
ORF02144 tagatose 1,6-diphosphate aldolase (lacD)
ORF02145 tagatose-6-phosphate kinase (lacC)
ORF02146 galactose-6-phosphate isomerase, LacB subunit (lacB)
ORF02147 galactose-6-phosphate isomerase, LacA subunit (lacA)
ORF02149 PTS system, IIC component, putative
ORF02150 PTS system, IIB component, putative
ORF02152 PTS system, IIA component, putative
ORF02153 lactose phosphotransferase system repressor (lacR)
ORF02157 adhesion lipoprotein
ORF02158 expressed protein of unknown function TIGR00256
ORF02159 GTP pyrophosphokinase (relA)
ORF02161 nrdI protein (nrdI)
ORF02164 iron ABC transporter, iron-binding protein
ORF02165 DNA-binding response regulator
ORF02167 PTS system, IID component
ORF02168 PTS system, IIC component
ORF02174 ABC transporter, ATP-binding protein
ORF02176 response regulator
ORF02177 conserved hypothetical protein
ORF02178 PTS system, IIABC components
ORF02179 sensor histidine kinase
ORF02180 phosphate regulon response regulator PhoB (phoB)
ORF02182 phosphate ABC transporter, ATP-binding protein (pstB)
ORF02183 phosphate ABC transporter, permease protein
ORF02184 phosphate ABC transporter, permease protein
ORF02188 conserved hypothetical protein TIGR00046
ORF02189 ribosomal protein L11 methyltransferase (prmA)
ORF02197 conserved hypothetical protein
ORF02199 ATPase, AAA family
ORF02249 mercuric reductase (merA)
ORF02272 DNA topology modulation protein FlaR, putative
ORF02273 glycerol dehydrogenase, putative
ORF02281 DNA-binding response regulator
ORF02285 leucyl-tRNA synthetase (leuS)
ORF02290 transcription antitermination protein NusG (nusG)
ORF02293 penicillin-binding protein 2A (pbp2A)
ORF02294 ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF02296 phosphopentomutase (deoB)
ORF02297 deoxyribose-phosphate aldolase (deoC)
ORF02300 uridine phosphorylase (udp)
ORF02302 60 kda chaperonin (groEL)

Table 8: GBS genes shared with GAS and pneumococcus

ORFxxxxx Annotation

ORF02303 chaperonin, 10 kDa (groES)
ORF02305 ABC transporter, ATP-binding protein
ORF02306 ABC transporter, permease protein
ORF02307 expressed putative lipoprotein
ORF02309 glyoxalase family protein
ORF02310 conserved hypothetical protein
ORF02311 anaerobic ribonucleoside-triphosphate reductase activating protein (nrdG)
ORF02312 acetyltransferase, GNAT family
ORF02315 anaerobic ribonucleoside-triphosphate reductase (nrdD)
ORF02318 conserved hypothetical protein
ORF02320 conserved hypothetical protein
ORF02321 conserved hypothetical protein
ORF02322 recA protein (recA)
ORF02325 DNA-3-methyladenine glycosylase I (tag)
ORF02327 Holliday junction DNA helicase RuvA (ruvA)
ORF02329 DNA mismatch repair protein HexB (hexB)
ORF02333 arginine repressor ArgR, putative
ORF02334 arginyl-tRNA synthetase (argS)
ORF02337 conserved hypothetical protein
ORF02338 conserved hypothetical protein
ORF02339 aspartyl-tRNA synthetase (aspS)
ORF02340 histidyl-tRNA synthetase (hisS)
ORF02342 ribosomal protein L33 (rpmG)
ORF02357 DNA-binding response regulator
ORF02359 membrane protein, putative
ORF02360 carbamate kinase (arcC)
ORF02361 ornithine carbamoyltransferase (argF)
ORF02364 amino acid ABC transporter, ATP-binding protein
ORF02365 amino acid ABC transporter, permease and amino acid-binding protein
ORF02370 membrane protein, putative
ORF02371 transcriptional regulator, TetR family, putative
ORF02373 ribosomal protein S4 (rpsD)
ORF02374 conserved hypothetical protein
ORF02375 replicative DNA helicase (dnaC)
ORF02376 ribosomal protein L9 (rplI)
ORF02377 DHH family protein
ORF02378 glucose inhibited division protein A (gidA)
ORF02380 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (trmU)
ORF02381 L-serine dehydratase, iron-sulfur-dependent, beta subunit (sdhB)
ORF02382 L-serine dehydratase, iron-sulfur-dependent, alpha subunit (sdhA)
ORF02385 cobalt transport family protein
ORF02386 ABC transporter, ATP-binding protein
ORF02387 ABC transporter, ATP-binding protein, FRAMESHIFT
ORF02388 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (pgsA)
ORF02389 peptidase, M16 family
ORF02390 conserved hypothetical protein
ORF02391 conserved hypothetical protein
ORF02392 recF protein (recF)
ORF02396 inosine-5'-monophosphate dehydrogenase (guaB)
ORF02397 transcriptional regulator, ArgR family
ORF02400 arginine deiminase (arcA)
ORF02402 ornithine carbamoyltransferase (argF)
ORF02404 carbamate kinase (arcC)
ORF02405 tryptophanyl-tRNA synthetase (trpS)
ORF02407 conserved hypothetical protein

Table 8: GBS genes shared with GAS and pneumococcus**ORFxxxx Annotation**

ORF02408	ABC transporter, ATP-binding protein
ORF02409	ABC transporter, permease protein, putative
ORF02410	conserved hypothetical protein TIGR00246
ORF02411	serine protease
ORF02412	partitioning protein, ParB family
ORF02413	chromosomal replication initiator protein DnaA (dnaA)
ORF02415	DNA polymerase III, beta subunit (dnan)
ORF02417	conserved hypothetical protein
ORF02419	conserved hypothetical GTP-binding protein
ORF02420	peptidyl-tRNA hydrolase (pth)
ORF02421	transcription-repair coupling factor (mfd)
ORF02423	S4 domain protein
ORF02424	cell division protein DivIC, putative
ORF02426	expressed protein of unknown function
ORF02427	MesJ/Ycf62 family protein
ORF02429	cell division protein FtsH (ftsH)

Table 9: GBS genes shared with pneumococcus**ORFxxxx Annotation**

ORF00017 phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (purH)
ORF00025 conserved hypothetical protein
ORF00029 acetyl xylan esterase, putative
ORF00042 aldehyde-alcohol dehydrogenase (adhE)
ORF00044 threonine synthase (thrC)
ORF00081 ribosomal protein L17 (rplQ)
ORF00090 conserved hypothetical protein
ORF00129 argininosuccinate synthase (argG)
ORF00156 oligopeptide ABC transporter, substrate-binding protein, putative
ORF00189 protease, putative
ORF00194 thioredoxin family protein
ORF00195 tRNA binding domain protein
ORF00217 conserved domain protein
ORF00218 PTS system, IIB component, putative
ORF00220 transketolase, N-terminal subunit
ORF00221 transketolase, C-terminal subunit
ORF00223 oxidoreductase, putative
ORF00282 acetyltransferase, GNAT family
ORF00290 IS1381, transposase OrfB
ORF00291 IS1381, transposase OrfA
ORF00293 conserved hypothetical protein
ORF00301 membrane protein, putative
ORF00343 ABC transporter, permease protein, putative
ORF00344 conserved hypothetical protein
ORF00382 aspartate kinase family protein
ORF00399 conserved hypothetical protein
ORF00439 cell wall surface anchor family protein
ORF00447 cytidine/deoxycytidylate deaminase family protein
ORF00450 5-formyltetrahydrofolate cyclo-ligase family protein
ORF00480 transcriptional regulator, MerR family
ORF00499 acetyltransferase, GNAT family
ORF00504 magnesium transporter, CorA family
ORF00521 VanZF domain protein
ORF00612 IS1381, transposase OrfA
ORF00613 IS1381, transposase OrfB
ORF00690 transmembrane protein Vexp1 (vex1)
ORF00691 ABC transporter, ATP-binding protein Vexp2 (vex2)
ORF00692 transmembrane protein Vexp3 (vex3)
ORF00714 conserved hypothetical protein
ORF00732 expressed cell wall surface anchor family protein, putative
ORF00774 ABC transporter, ATP-binding protein
ORF00778 ABC transporter, ATP-binding protein
ORF00780 conserved hypothetical protein
ORF00790 beta-glucuronidase
ORF00800 alpha amylase family protein
ORF00807 amino acid ABC transporter, permease protein
ORF00809 amino acid ABC transporter, amino acid-binding protein
ORF00814 conserved hypothetical protein
ORF00823 bacterial luciferase family protein
ORF00840 riboflavin biosynthesis protein RibD (ribD)
ORF00841 riboflavin synthase, alpha subunit (ribE)
ORF00842 riboflavin biosynthesis protein RibA (ribA)
ORF00843 riboflavin synthase, beta subunit (ribH)
ORF00866 penicillin-binding protein 2b
ORF00905 membrane protein, putative

Table 9: GBS genes shared with pneumococcus**ORFxXXXX Annotation**

ORF00910 major facilitator family protein
ORF00913 hydrolase, haloacid dehalogenase-like family
ORF00918 conserved hypothetical protein
ORF00945 conserved hypothetical protein
ORF00948 ABC transporter, ATP-binding protein
ORF00952 phosphomethylpyrimidine kinase (thiD)
ORF00953 hydroxyethylthiazole kinase (thiM)
ORF00954 thiamine-phosphate pyrophosphorylase (thiE)
ORF00961 GtrA family protein
ORF00967 1,4-alpha-glucan branching enzyme (glgB)
ORF00968 glucose-1-phosphate adenylyltransferase (glgC)
ORF00971 glycogen synthase (glgA)
ORF00985 acetyltransferase, GNAT family
ORF00990 magnesium transporter, CorA family, putative
ORF01022 nucleoside diphosphate kinase (ndk)
ORF01031 nucleoside diphosphate kinase domain protein
ORF01085 conserved hypothetical protein
ORF01087 IS1381, transposase OrfA
ORF01088 IS1381, transposase OrfB
ORF01098 ABC transporter, permease protein, putative
ORF01100 sensor histidine kinase
ORF01102 ABC transporter, substrate-binding protein
ORF01127 protease, putative
ORF01135 iron compound ABC transporter, permease protein
ORF01136 iron compound ABC transporter, permease protein
ORF01185 aspartate-semialdehyde dehydrogenase (asd)
ORF01217 conserved hypothetical protein
ORF01218 conserved hypothetical protein
ORF01219 formate/nitrite transporter family protein
ORF01226 oxidoreductase, short chain dehydrogenase/reductase family, FRAMESHIFT
ORF01254 homoserine kinase (thrB)
ORF01255 homoserine dehydrogenase (hom)
ORF01264 transcriptional regulator, Cro/CI family
ORF01268 thiol peroxidase (psad)
ORF01305 glycosyltransferase CpsJ(V) (cpsJ)
ORF01306 glycosyltransferase CpsO(V) (cpsO)
ORF01313 CpsD protein (cpsD)
ORF01314 cpsC protein (cpsC)
ORF01315 capsular polysaccharide biosynthesis protein CpsB (cpsB)
ORF01316 capsular polysaccharide biosynthesis protein CpsA (cpsA)
ORF01326 conserved hypothetical protein
ORF01333 alpha-acetolactate decarboxylase (budA)
ORF01334 acetolactate synthase, catabolic (ilvK)
ORF01337 MutT/nudix family protein
ORF01369 MATE efflux family protein
ORF01398 Tn5252, Orf 9 protein
ORF01399 Tn5252, Orf 10 protein
ORF01446 protease, putative
ORF01447 conserved hypothetical protein
ORF01449 conserved hypothetical protein
ORF01492 NADP-specific glutamate dehydrogenase (gdhA)
ORF01569 expressed cell wall surface anchor family protein
ORF01570 cell wall surface anchor family protein
ORF01574 polysaccharide biosynthesis protein
ORF01579 nucleotidyl transferase, putative